

2) INFORMATION FOR SEQ ID NO: 1053

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

20	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	TTGAAAAAAC	50
	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	GAATAGAATA	100
	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	ACGTATCGGT	150
	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	AAATACGAGC	200
	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	GTGCGAAAAA	250
25	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	TACTCTCGCC	300
	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	GAATATGAAA	350
	TCAACCATGT	TGATGTAGCA	TTTTCAGCTT	TGCATGGCAA	GTCAGGTGAA	400
	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	CTTTTGTAGG	450
	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	TTGACATACA	500
30	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	GGTTATTAAT	550
	AAAGATGATA	GGCCGGTGGC	AGCTACGTTT	ACCTATCCTG	TTTTTGTTAA	600
	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	AATAGCGCGG	650
	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	CAGCAAAATC	700
	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	CGGTATTGGG	750
35	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	AGGCTGCAGT	800
	ACGGAATCTT	TCGTATTCAT	CAGGAAGTCG	AGCCGGAAAA	AGGCTCTGAA	850
	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	AGCGAGGACG	900
	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	TGTAGAGGTC	950
	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	TGTACTGAAC	1000
40	GAAGTCAATA	CTCTGCCCCG	TTTCACGTCA	TACAGTCGTT	ATCCCCGTAT	1050
	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	CGCTTGATCG	1100
	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	ACTTTTTTAG	1150
	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	CACTTGGGAT	1200
	AATTTACCCG	GAAAACCGGT	TGACGGGTAT	GAAAGTAAAT	CGCATTGTAG	1250
45	GGACATTCGA	ATT				1263

2) INFORMATION FOR SEQ ID NO: 1054

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

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(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

5	CGGCCTATTA	TNCCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCAT	50
	AAAAACTGTT	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAG	100
	TTGCAATACT	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	150
	TCTGCAATAG	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	200
	ATACATTGGA	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	250
10	GCGCGGAATG	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	300
	AAAAAAATGC	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	350
	CCATGTTGAT	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	400
	GATCCATACA	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	450
	GATATTCAAA	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	500
15	TGCGAAAAAT	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	550
	ATGATAGGCC	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	600
	GCGCGTTCAG	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	650
	ATTGGACTION	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	700
	TTGAGCAGGC	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	750
20	AGTGCCGCGT	TAGTTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	800
	AATCTTTCGT	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	850
	CAGTTATAAC	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	900
	CAGGAAACGG	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	950
	CCGTGTGGAT	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	1000
25	TCAATACTCT	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	1050
	GCCGCTGCAG	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	1100
	AGCGTTAAAG	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	1150
	AATAGTACAC	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	1200
	TCACCGGAAA	ACCGGTTGAC	GGTTATAAGT	AA		1232
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2) INFORMATION FOR SEQ ID NO: 1055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

50	TACCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCAT	AAAAACTGTT	50
	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAG	TTGCAATACT	100
	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	TCTGCAATAG	150
	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	ATACATTGGA	200
	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	GCGCGGAATG	250
	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	AAAAAAATGC	300
55	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	CCATGTTGAT	350
	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	GATCCATACA	400
	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	GATATTCAAA	450
	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	TGCGAAAAAT	500
	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	ATGATAGGCC	550
60	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	GCGCGTTCAG	600

	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	ATTGGACTAC	650
	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	TTGAGCAGGC	700
	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	AGTGCCGCGT	750
	TAGCTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	AATCTTTCGT	800
5	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	CAGTTATAAC	850
	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	CAGGAAACGG	900
	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	CCGTGTGGAT	950
	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	TCAATACTCT	1000
	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	GCCGCTGCAG	1050
10	GTATTGCACT	TCCCGAAGTG	ATTGACCGCT	TGATCGTATT	AGCGTTAAAG	1100
	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTGTAGATGA	AATAGTACAC	1150
	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	TCACCGGAAA	1200
	ACCGGTTGAC	GGTTAGAA				1218

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2) INFORMATION FOR SEQ ID NO: 1056

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1265 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R688

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

	AATCACACCG	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	50
	TTGAAAAAAC	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	100
35	GAATAGAATA	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	150
	ACGTATCGGT	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	200
	AAATACGAGC	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	250
	GTGCGAAAAA	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	300
	TACTCTCGCC	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	350
40	GAATATGAAA	TCAACCATGT	TGATGTAGCA	TTTTTCAGCTT	TGCATGGCAA	400
	GTCAGGTGAA	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	450
	CTTTTGTAGG	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	500
	TTGACATACA	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	550
	GGTTATTAAT	AAAGATGATA	GGCCGGTGGC	AGCTACGTTT	ACCTATCCTG	600
45	TTTTTTGTAA	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	650
	AATAGCGCGG	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	700
	CAGCAAAATC	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	750
	CGGTATTGGG	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	800
	AGGCTGCAGT	ACGGAATCTT	TCGTATTTCAT	CAGGAAGTCG	AGCCGGAAAA	850
50	AGGCTCTGAA	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	900
	AGCGAGGACG	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	950
	TGTAGAGGTC	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	1000
	TGTACTGAAC	GAAGTCAATA	CTCTGCCCGG	TTTCACGTCA	TACAGTCGTT	1050
	ATCCCCGTAT	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	1100
55	CGCTTGATCG	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	1150
	ACTTTTTTTAG	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	1200
	CACTTGGGAT	AATTTCAACG	GAAAACCGGT	TGACGGTTAT	GAAGTAAATC	1250
	GCATTGTAGG	GACAT				1265

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2) INFORMATION FOR SEQ ID NO: 1057

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: R689

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
20	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
25	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
30	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
35	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
40	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTCT	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	1250
	ATTGTAGGGA	CATACGAAT				1269

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2) INFORMATION FOR SEQ ID NO: 1058

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1169 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R420

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
5	ATTCTCCAGA	ATACTCAGTG	TCACTAACCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTAACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
10	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
15	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750
	TTGACGATTG	GTGCTTGTGA	TGCGATTTCT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
20	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTCGTCAC	950
	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
25	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTGCTA				1169

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

45	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
	ATTCTCCAGA	ATACTCAGTG	TCACTAGCCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTGACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
50	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
55	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
60	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750

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 5
 TTTTGAAGAG
 CATTGCCTCT
 TATCGAAACT
 CAATCAAGGA
 CTGGGCACTC
 GAAATATTAG
 AACACATTAC
 GCCCCCGCAC
 GTGCTTGTGA
 AAATACCAAT
 CGCGCTTGAA
 TGGGATTGAC
 GCGATTTATT
 TAGAGCAATT
 AATTGATCAA
 TTAGTG
 TCGGATTTCT
 TAATCAGCGC
 TCACAGATCA
 TAAACGAAAT
 GCTATGATGG
 GATTGCACTG
 TAAAAACCAT
 CTTGTCGACG
 CACGATCACT
 AGGAGCAGGC
 CGAATCGATT
 CAACACCATG
 CGGAAGTCGG
 GCAGAGGAGG
 CCATTGAAAA
 GTTTTTTTTGA
 GTCCCAGCAC
 ACAGCTGCTT
 TTTTCGTCAC
 CCGGGATTTA
 GTTATCCTAC
 ACAAACGATG
 AAAATCAAGA
 800
 850
 900
 950
 1000
 1050
 1100
 1150
 1166

2) INFORMATION FOR SEQ ID NO: 1060

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1028 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus casseliflavus*
 25 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

30 AACATGAAAA AAATCGCCTT ATTTTTTGGAG GCAATTCACC GGAATACACC 50
 GTTTCCTTTAG CTTCAAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC 100
 CTATGACTAC GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT 150
 GGTACTTGTA TACAGGAGAA CTGGAAAAACA TCCGACAAGA CACGTGGTTG 200
 TTGGATACGA AACATAAACA GAAAATACAG CCGCTATTCTG AAGGAAACGG 250
 CTTTTGGCTA AGTGAAGAGC AGCAAACGTT GGTACCTGAT GTTTTATTTT 300
 35 CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT 350
 GAATTGATGA AGCTGCCTTA TGTAGGCTGC GGGGTGGCAG GTTCTGCCTT 400
 ATGTATGAAC AAATGGCTGC TGCATCAAGC TGCAGCAGCC ATTGGCGTAC 450
 AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGAACAA 500
 ATCGAAGCTT TTATCCAGAC CCATGGCTTC CCAGTTTTCT TTAAGCCTAA 550
 40 TGAAGCGGGC TCCTCAAAAG GGATCACTAA AGTCACCTGC GTTGAAGAAA 600
 TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTCCGC AGTGCTCCTA 650
 CAAAAAATA TTGCCGGTGT TGAGATCGGT TGCGGTATTT TGGGCAACGA 700
 CTCTTTGACT GTCGGTGCTT GTGACGCCAT TTCATTAGTA GACGGCTTTT 750
 TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAAAT CACCGTCCCT 800
 45 GCGCCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT 850
 GCTCTATCGT AGTCTTGGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTT 900
 TCACGGAGCG AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC 950
 TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGG TCGGCTTATC 1000
 CTATCAAGAA CTACTACAAA AACTGCTT 1028
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2) INFORMATION FOR SEQ ID NO: 1061

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

	AATATGAAAA	AAATCGCCTT	ATTTTTGGAG	GCAATTCACC	GGAGTACGCC	50
10	GTTTCTTTAG	CCTCAGCAAC	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	100
	CGATGACTAT	GACCTCTCTT	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	150
	GGTATTTGTA	TACAGGAGAA	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	200
	TTGGATACGA	AACATAAACA	GAAAATCCAG	CCGCTTTTTG	AAGGAAACGG	250
	CTTTTGGCTA	AGTGAAGAGC	AACAAACGTT	GGTTCCTGAT	GTTTTATTTC	300
15	CCATTATGCA	TGGCAAATAC	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	350
	GAATTGATGA	AACTACCTTA	TGTAGGCTGC	GGGGTGGCAG	CCTCTGCCTT	400
	ATGTATGAAC	AAATGGCTGC	TGCATCAAGC	AGCAGAAGCG	ATTGGCGTAC	450
	AAAGTGCTCC	TACGATTCTC	TTGACAAATC	AAGCCAACCA	GCAAGATCAA	500
	ATCGAAGCTT	TTATCCAGAC	CCATGGCTTT	CCGGTTTTTT	TTAAGCCTAA	550
20	TGAAGCGGGC	TCCTCAAAAG	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	600
	TCGCTTCTGC	CTTAAAAGAA	GCCTTTACTT	ATTGTTTCAGC	AGTGCTCCTA	650
	CAAAAAAATA	TTGCCGGTGT	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	700
	CTCTTTGACT	GTCGGTGCTT	GTGACGCTAT	TTCATTAGTA	GACGGCTTTT	750
	TCGATTTTGA	AGAAAAGTAC	CAGCTGATCA	GCGCCAAGAT	CACCGTTCCT	800
25	GCACCATTCG	CTGAAACGAT	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	850
	GCTCTATCGT	AGTCTTTGTC	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	900
	TCACGGATCA	AGGAGAACTA	TACTTGAATG	AAATCAATAC	TATGCCGGGC	950
	TTTACGAGTC	ACTCCCGCTA	TCCTGCCATG	ATGGCAGCGA	TCGGCTTATC	1000
30	CTATCAAGAA	CTACTACAAA	AACTGCTTGT			1030

2) INFORMATION FOR SEQ ID NO: 1062

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1031 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

	AAACATGAAA	AAAATCGCCA	TTATTTTTTG	AGGCAATTCA	CCGGAATACA	50
50	CCGTTTCTTT	AGCTTCAGCA	ACTAGCGCAA	TCGAAGCACT	CCAATCATCT	100
	CCCTATGACT	ACGACCTCTC	TTTGATCGGG	ATCGCCCCAG	ATGCTATGGA	150
	TTGGTACTTG	TATACAGGAG	AACTGGAAAA	CATCCGACAA	GACACGTGGT	200
	TGTTGGATAC	GAAACATAAA	CAGAAAATAC	AGCCGCTATT	CGAAGGAAAC	250
	GGCTTTTGGC	TAAGTGAAGA	GCAGCAAACG	TTGGTACCTG	ATGTTTTATT	300
55	TCCCATTATG	CATGGCAAAT	ACGGGGAAGA	TGGCAGTATC	CAAGGATTGT	350
	TTGAATTGAT	GAAGCTGCCT	TATGTAGGCT	GCGGGGTGGC	AGGTTCTGCC	400
	TTATGTATGA	ACAAATGGCT	GCTGCATCAA	GCTGCAGCAG	CCATTGGCGT	450
	ACAAAGTGCT	CCTACGATTC	TCTTGACAAA	TCAAGCCAAC	CAGCAAGAAC	500
	AAATCGAAGC	TTTTATCCAG	ACCCATGGCT	TCCCAGTTTT	CTTTAAGCCT	550
60	AATGAAGCGG	GCTCCTCAAA	AGGGATCACT	AAAGTCACCT	GCGTTGAAGA	600

AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC 650
 TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC 700
 GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTTCATTAG TAGACGGCTT 750
 TTTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC 800
 5 CTGCGCCATT GCCTGAAACG ATTGAAACCA AGGTCAAAGA ACAAGCTCAG 850
 CTGCTCTATC GTAGTCTTGG TCTTAAAGGT CTTGCTCGCA TCGACTTTTT 900
 TGTCACGGAG CGAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG 950
 GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCCGGCTTA 1000
 TCCTATCAAG AACTACTACA AAAACTGCTT G 1031
 10

2) INFORMATION FOR SEQ ID NO: 1063

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus casseliflavus*
 25 (B) STRAIN: R775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

AACATGAAAA AAATCGCCAT TATTTTTTGA GGCAATTCAC CGGAATACAC 50
 30 CGTTTCTTTA GCTTCAGCAA CTAGCGCAAT CGAAGCACTC CAATCATCTC 100
 CCTATGACTA CGACCTCTCT TTGATCGGGA TCGCCCCAGA TGCTATGGAT 150
 TGGTACTTGT ATACAGGAGA ACTGGAAAAC ATCCGACAAG ACACGTGGTT 200
 GTTGATACG AAACATAAAC AGAAAATACA GCCGCTATTT GAAGGAAACG 250
 GCTTTTGGCT AAGTGAAGAG CAGCAAACGT TAGTACCTGA TATTTTATTT 300
 35 CCCATTATGC ATGGCAAATA CGGGGAAGAT GGCAGTATCC AAGGATTGTT 350
 TGAATTGATG AAACCTACCTT ATGTAGGTTG CGGGGTGGCA GGTTCCTGCCT 400
 TATGTATGAA CAAATGGCTG CTGCATCAAG CTGCAGCAGC CATTGGCGTA 450
 CAAAGTGCTC CTACGATTCT CTTGACAAAT CAAGCCAACC AGCAAGAACA 500
 AATCGAAGCT TTTATCCAGA CCCATGGCTT CCCAGTTTTC TTTAAGCCTA 550
 40 ATGAAGCGGG CTCTTCAAAA GGGATCACTA AAGTCACCTG CGTTGAAGAA 600
 ATCGCTTCTG CCTTAAAAAA AGCCTTTACT TATTGTTCCG CAGTGCTCCT 650
 ACAAAAAAAT ATTGCCGGTG TTGAGATCGG TTGCGGTATT TTGGGCAACG 700
 ACTCTTTGAC TGTCGGTGCT TGTGACGCCA TTTTCATTAGT AGACGGCTTT 750
 TTCGATTTTG AAGAAAAGTA CCAGCTGATC AGCGCCAAAA TCACCGTCCC 800
 45 TGCGCCATTG CCTGAAACGA TTGAAACCAA GGTCAAAGAA CAAGCTCAGC 850
 TGCTCTATCG TAGTCTTGGT CTTAAAGGTC TTGCTCGCAT CGACTTTTTT 900
 GTCACGGATC AAGGAGAACT ATAATTGAAT GAAATCAATA CTATGCCGGG 950
 CTTTACGAGT CACTCCCGTT ATCCTGCCAT GATGGCAGCG GTCGGCTTAT 1000
 CCTATCAAGA ACTACTACAA AAACCTGCTT 1030
 50

2) INFORMATION FOR SEQ ID NO: 1064

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1032 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

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10 AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
   CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
   CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
   TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
   TGTTGGATAC GAAACAGAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
   GGCTTTTGGT TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
15 TCCCATTTATG CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
   TTGAATTGAT GAAGCTACCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
   TTATGTATGA ACAAATGGTT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
   ACAAAGTGCT CCTACGATTC TCTTGACAAA TCACGCCAAC CAGCAAGAAC      500
   AAATCGAAGC TTTTATCCAG ACCCATGGCT TTCCAGTTTT CTTTAAGCCT      550
20 AATGAAGCGG GTTCCTCAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600
   AATCGCTTCT GCCTTAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC      650
   TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC      700
   GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTCAATTAG TAGACGGCTT      750
   TTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC      800
25 CTGCGCCATT GCCTGAAACG ATTGAACTA AGGTCAAAGA ACAAGCTCAG      850
   CTGCTCTATC GTAGTCTTGG ACTTAAAGGT CTTGCTCGCA TCGACTTTTT      900
   TGTCACGGAT CAAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG      950
   GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCCGGTTA     1000
   TCCTATCAAG AACTACTACA AAAACTACTT GT                          1032
30

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2) INFORMATION FOR SEQ ID NO: 1065

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1034 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

```

50 AAAACATGA AAAAAATCGC CATTATTTT GGAGGCAATT CACCGGAATA      50
   CACCGTTTCT TTAGCTTCAG CAACTAGCGC AATCGAAGCA CTCCAATCAT      100
   CTCCCTATGA CTACGACCTC TCTTTGATCG GGATCGCCCC AGATGCTATG      150
   GATTGGTACT TGTATACAGG AGAACTGGAA AACATCCGAC AAGACACGTG      200
   GTTGTTGGAT ACGAAACATA AACAGAAAAT ACAGCCGCTA TTCGAAGGAA      250
   ACGGCTTTTG GCTAAGTGAA GAGCAGCAA CGTTGGTACC TGATGTTTTA      300
55 TTTCCCATTA TGCATGGCAA ATACGGGGAA GATGGCAGTA TCCAAGGATT      350
   GTTTGAATTG ATGAAGCTGC CTTATGTAGG CTGCGGGGTG GCAAGTTCTG      400
   CCTTATGTAT GAACAAATGG CTGCTGCATC AAGCTGCAGC AGCCATTGGC      450
   GTACAAAGTG CTCCTACGAT TCTCTTGACA AATCAAGCCA ACCAGCAAGA      500
   ACAAATCGAA GCTTTTATCC AGACCCATGG CTTTCCAGTT TTCTTTAAGC      550
60 CTAATGAAGC GGGCTCCTCA AAAGGGATCA CTAAAGTCAC CTGCGTTGAA      600

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5 GAAATCGCTT CTGCCTTAAA AGAAGCCTTT ACTTATTGTT CCGCAGTGCT 650
 CCTACAAAAA AATATTGCCG GTGTTGAGAT CCGTTGCGGT ATTTTGGGCA 700
 ACGACTCTTT GACTGTCGGT GCTTGTGACG CCATTTTCATT AGTAGACGGC 750
 TTTTTCGATT TTGAAGAAAA GTACCAGCTG ATCAGCGCCA AAATCACCGT 800
 CCCTGCGCCA TTGCCTGAAA CGATTGAAAC CAAGGTCAAA GAACAAGCTC 850
 AGCTGCTCTA TCGTAGTCTT GGTCTTAAAG GTCTTGCTCG CATCGACTTT 900
 TTTGTACACG ATCAAGGAGA ACTATACTTG AATGAAATCA ATACTATGCC 950
 GGGCTTTACG AGTCACTCCC GCTATCCTGC CATGATGGCA GCGGTCGGCT 1000
 TATCCTATCA AGAACTACTA CAAAACTGC TTGT 1034
 10

2) INFORMATION FOR SEQ ID NO: 1066

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1012 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 25 (B) STRAIN: R760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

30 CATGAAAAAA ATCGCCATTA TTTTGGAGG CAATTCACCG GAATACACCG 50
 TTTCTTTAGC CTCAGCAACT AGCGCAATCG AAGCACTCCA ATCATCTCCC 100
 TATGATTACG ACCTCTCTTT GATCGGGATC GCCCCAGATG CTATGGATTG 150
 GTACTTGTAT ACAGGAGAAC TGGAAAACAT CCGACAAGAC ACGTGGTTGT 200
 TGGATACGAA ACATACACAG AAAATCCAGC CACTTTTTTGA AGGAAACGGC 250
 TTTTGGATAA GTGAAGCGCA GCAAACGTTG GTACCTGATG TTTTATTTCC 300
 35 CATTATGCAT GGTAATACG GGAAGATGG CAGTATCCAA GGATTGTTTG 350
 AATTGATGAA GCTGCCTTAT GTAGGCTGTG GGGTGGCAGC CTCTGCCTTA 400
 TGTATGAACA AATGGTTATT GCATCAAGCA GCAGCAGCGA TTGGCGTACA 450
 AAGCGCTCCT ACGATTCTCT TGACAAATCA AGCCAACCAG CAAAGACAAA 500
 TCGAAGCCTT TATCCAGACC CATGGCTTTC CAGTTTTCTT TAAGCCTAAT 550
 40 GAAGCGGGCT CCTCAAAGG GATCACAAAA GTAACCTGTG TTGAAGAAAT 600
 CGCTCCTGCC TTGAAGGAAG CCTTCGCTTA TTGTTCCGCA GTGCTCTTAC 650
 AAAAAAATAT CGCTGGCGTT GAGATTGGTT GCGGTATCTT AGGCAACGAC 700
 TCTTTGACTG TCGGTGCTTG TGACGCTATT TCATTAGTAG ACGGCTTTTT 750
 CGATTTTGAA GAAAAGTACC AGTTGATCAG CGCCAAAATC ACCGTTCTTG 800
 45 CGCCATTGCC TGAAACGATT GAAACCAAAG TCAAAGAACA AGCTCAGCTG 850
 CTCTATCACA GTCTTGGTCT TAAAGGACTT GCTCGCATCG ACTTTTTTGT 900
 CACGGATCAA GGAGAACTAT ACTTGAATGA AATCAATACT ATGCCGGGCT 950
 TTACGAGTCA CTCCCGCTAT CCTGCCATGA TGGCAGCGGT CGGCTTATCC 1000
 TATCAAGAAT TA 1012
 50

2) INFORMATION FOR SEQ ID NO: 1067

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 721 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 5 (B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

	CTTACGCTTT	ATCGATTAGA	CACGGGNAGC	TTGTCCAATG	GGRAGCCGAT	50
10	TTGATTTTAT	GGATGAACGC	TCTCATCATG	CGGCAAATGG	AATATCATGC	100
	AATGAAGCGC	AAAATCGCAG	ACGTTTGCGC	TCCATCATGG	AAAACAGTGG	150
	GTTTGAAGCA	TATAGCCTCG	AATGGTGCCA	CTATGTATTA	AGAGACGAAC	200
	CATACCCCAA	TAGCTATTTT	GATTTCCCCG	TTAAATAAAC	TTTAAACCGT	250
	TGCACGGACA	AACTATATAA	GCTAACTCTT	TCGGCAGGAA	ACCCGACGTA	300
15	TGTAAGTGGT	TCTTAGGGAA	TTTATATATA	GTAGATAGTA	TTGAAGATGT	350
	AAGGCAGAGC	GATATTGCGG	TCATTATCTG	CGTGCGCTGC	GGCAAGATAG	400
	CCTGATAATA	AGACTGATCG	CATAGAGGGG	TGGTATTTCA	CACCGCCCAT	450
	TGTCAACAGG	CAGTTCAGCC	TCGTAAAT	CAGCATGGGT	ATCACTTATG	500
	AAAATTCATC	TACATTGGTG	ATAATAGTAA	ATCCAGTAGG	GCGAAATAAT	550
20	TGACTGTAAT	TTACGGGGCA	AAACGGCACA	ATCTCAAACG	AGATTGTGCC	600
	GTTTAAGGGG	AAGATTCTAG	AAATATTTCA	TACTTCCAAC	TATATAGTTA	650
	AGGAGGAGAC	TGAAAATGAA	GAAGTTGTTT	TTTTTATTGT	TATTGTTATT	700
	CTTAATATAC	TTAGGTTATT	G			721

25

2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 40 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

	ATTTTTAAGG	ATGAACGCTC	TTCATCATGC	GGCAAATGGA	ATATCATGCA	50
	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	CCATCATGGA	AAACAGTGGG	100
45	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	TATGTATTAA	GAGACGAACC	150
	ATACCCCAAT	AGCTATTTTG	ATTTCCCCGT	TAAATAAACT	TTTAACCGTT	200
	GCACGGACAA	ACTATATAAG	CTAACTCTTT	CGGCAGGAAA	CCCGACGTAT	250
	GTAAGTGGT	CTTAGGGAAT	TTATATATAG	TAGATAGTAT	TGAAGATGTA	300
	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	GTGCGCTGCG	GCAAGATAGC	350
50	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	GGTATTTTCA	ACCGCCCAT	400
	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	AGCATGGGTA	TCACTTATGA	450
	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	TCCAGTAGGG	CGAAATAATT	500
	GACTGTAATT	TACGGGGCAA	AACGGCACAA	TCTCAAACGA	GATTGTGCCG	550
	TTTAAGGGGA	AGATTCTAGA	AATATTTTCAT	ACTTCCAAC	ATATAGTTAA	600
55	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	TTTTATTGTT	ATTGTTATTC	650
	TTAATATACT	TAGGTTAT				668

60 2) INFORMATION FOR SEQ ID NO: 1069

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069

```

15  CGGCAAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTRAGCTT      50
    GTACCAATGG GAAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC      100
    GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT      150
    CCATCATGGA AAACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC      200
20  TATGTATTAA GAGACGAACC ATACCCCAAT AGCTATTTTG ATTTCCCCGT      250
    TAAATAAACT TTAAACCGTT GCACGGACAA ACTATATAAG CTAACCTCTT      300
    CGGCAGGAAA CCCGACGTAT GTAACGGTGT CTTAGGGAAT TTATATATAG      350
    TAGATAGTAT TGAAGATGTA AGGCAGAGCG ATATTGCGGT CATTATCTGC      400
    GTGCGCTGCG GCAAGATAGC CTGATAATAA GACTGATCGC ATAGAGGGGT      450
25  GGTATTTCAC ACCGCCCAT TGTCAACAGGC AGTTCAGCCT CGTTAAATTC      500
    AGCATGGGTA TCACTTATGA AAATTCATCT ACATTGGTGA TAATAGTAAA      550
    TCCAGTAGGG CGAAATAATT GACTGTAATT TACGGGGCAA AACGGCACAA      600
    TCTCAAACGA GATTGTGCCG TTAAAGGGGA AGATTCTAGA AATATTTTCAT      650
    ACTTCCAAC TATAGTTAA GGAGGAGACT GAAAATGAAG AAGTTGTTTT      700
30  TTTTATTGTT ATTGTTATTC TTAATATACT TAGGTTATGA CTACGTTAAT      750
    GAAANCCTGA                                     760
  
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2) INFORMATION FOR SEQ ID NO: 1070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070

```

50  AAAAGGAATA CGGGGCTTTC AAAAATCCAA GCCATAACCC GCGGGCAAGT      50
    GCCATTTGAT TCTTACGCTT TAATCGATTA GACACGGGTA AGCTTGTACC      100
    AATGGGGAAC CGATTTGATT TTAATGNATG AACGCTCTTC ATCATGCGGC      150
    AAATGGAATA TCATGCAATG AAGCGCAAAA TCGCAGACGT TTGCGCTCCA      200
55  TCATGGAAAA CAGTGGGTTT GAAGCATATA GCCTCGAATG GTGGCACTAT      250
    GTATTAAGAG ACGAACCATA CCCCAATAGC TATTTTGATT TCCCCGTTAA      300
    ATAAACTTTT AACCGTTGCA CGGACAAACT ATATAAGCTA ACTCTTTCGG      350
    CAGGAAACCC GACGTATGTA ACTGGTTCTT AGGGAATTTA TATATAGTAG      400
    ATAGTATTGA AGATGTAAGG CAGAGCGATA TTGCGGTCAT TATCTGCGTG      450
60  CGCTGCGGCA AGATAGCCTG ATAATAAGAC TGATCGCATA GAGGGGTGGT      500
  
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ATTTCACACC GCCCATTGTC AACAGGCAGT TCAGCCTCGT TAAATTCAGC 550
ATGGGTATCA CTTATGAAAA TTCATCTACA TTGGTGATAA TAGTAAATCC 600
AGTAGGGCGA AATAATTGAC TGTAATTTAC GGGGCAAAAC GGCACAATCT 650
CAAACGAGAT TGTGCCGTTT AAGGGGAAGA TTCTAGAAAT ATTTCATACT 700
5 TCCAACATA TAGTTAAGGA GGAGACTGAA AATGAAGAAG TTGTTTTTTT 750
TTATTGTTAT TGTTATTCTT AATATACTTA GGTATGACT ACGTTAATGA 800
A 801

10

2) INFORMATION FOR SEQ ID NO: 1071

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R684

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

TTGTACCAAT GGGGAGCCGA TTTGATTTTA TGGATGAACG CTCTCATCAT 50
GCGGCAAATG GAATATCATG CAATGAAGCG CAAAATCGCA GACGTTTGCG 100
CTCCATCATG GAAAACAGTG GGTTTGAAGC ATATAGCCTC GAATGGTGGC 150
30 ACTATGTATT AAGAGACGAA CCATACCCCA ATAGCTATTT TGATTTCCCC 200
GTTAAATAAA CTTTTAACCG TTGCACGGAC AAACATATATA AGCTAACTCT 250
TTCGGCAGGA AACCCGACGT ATGTAAGTGG TTCTTAGGGA ATTTATATAT 300
AGTAGATAGT ATTGAAGATG TAAGGCAGAG CGATATTGCG GTCATTATCT 350
GCGTGCGCTG CGGCAAGATA GCCTGATAAT AAGACTGATC GCATAGAGGG 400
35 GTGGTATTTT ACACCGCCCA TTGTCAACAG GCAGTTCAGC CTCGTTAAT 450
TCAGCATGGG TATCACTTAT GAAAATTCAT CTACATTGGT GATAATAGTA 500
AATCCAGTAG GGCGAAATAA TTGACTGTAA TTTACGGGGC AAAACGGCAC 550
AATCTCAAAC GAGATTGTGC CGTTTAAGGG GAAGATTCTA GAAATATTTT 600
ATACTTCCAA CTATATAGTT AAGGAGGAGA CTGAAAATGA AGAAGTTGTT 650
40 TTTTTTATTG TTATTGTTAT TCTTAATATA CTTAGGTTAT GACTACGTTA 700
ATGAAGCACT G 711

45 2) INFORMATION FOR SEQ ID NO: 1072

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072

60

	GCCATTGATC	TTACGCTTTA	TCGATTAGAC	ACGGGTNAGC	TTGTACCAAT	50
	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	GCGGCAAATG	100
	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	CTCCATCATG	150
	GAAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	ACTATGTATT	200
5	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	GTTAAATAAA	250
	CTTTTAACCG	TTGCACGGAC	AACTATATA	AGCTAACTCT	TTCGGCAGGA	300
	AACCCGACGT	ATGTAAGTGG	TTCTTAGGGA	ATTTATATAT	AGTAGATAGT	350
	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	GCGTGCGCTG	400
	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	GTGGTATTTT	450
10	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	TCAGCATGGG	500
	TATCACTTAT	GAAAATTTCAT	CTACATTGGT	GATAATAGTA	AATCCAGTAG	550
	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	AATCTCAAAC	600
	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	ATACTTCCAA	650
	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	TTTTTTTATTG	700
15	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	ATGAAGCACT	750
	G					751

20 2) INFORMATION FOR SEQ ID NO: 1073

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 685 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

35	ATTTGATTTT	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	50
	GCAATGAAGC	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	100
	GGGTTTGAAG	CATATAGCCT	CGAATGGTGG	CACTATGTAT	TAAGAGACGA	150
	ACCATACCCC	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	200
40	GTTGCACGGA	CAAACTATAT	AAGCTAACTC	TTTCGGCAGG	AAACCCGACG	250
	TATGTAAGT	GTTCTTAGGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	300
	GTAAGGCAGA	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	350
	AGCCTGATAA	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	400
	ATTGTCAACA	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	450
45	TGAAAATTCA	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	500
	ATTGACTGTA	ATTTACGGGG	CAAAACGGCA	CAATCTCAAA	CGAGATTGTG	550
	CCGTTTAAGG	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	600
	TAAGGAGGAG	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	650
	TTCTTAATAT	ACTTAGGTTA	TGACTACGTT	AATGA		685

50

2) INFORMATION FOR SEQ ID NO: 1074

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

	ATCGATTAGA	CACGGGTGAG	CTTGTACCAA	TGGGGAGCCG	ATTTGATTTT	50
10	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	GCAATGAAGC	100
	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	GGGTTTGAAG	150
	CATATAGCCT	CGAATGGTGG	CACTATGTAT	TAAGAGACGA	ACCATACCCC	200
	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	GTTGCACGGA	250
	CAAACTATAT	AAGCTAACTC	TTTCGGCAGG	AAACCCGACG	TATGTAAGT	300
15	GTTCTTAGGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	GTAAGGCAGA	350
	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	AGCCTGATAA	400
	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	ATTGTCAACA	450
	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	TGAAAATTCA	500
	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	ATTGACTGTA	550
20	ATTTACGGGG	CAAAACGGCA	CAATCTCAAA	CGAGATTGTG	CCGTTTAAGG	600
	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	TAAGGAGGAG	650
	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	TTCTTAATAT	700
	ACTTAGGTTA	TGACTACGTT	AATGAAGCAC	TG		732

25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 670 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R691

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

	TCTCATCATG	CGGCAAATGG	AATATCATGC	AATGAAGCGC	AAAATCGCAG	50
	ACGTTTGCGC	TCCATCATGG	AAAACAGTGG	GTTTGAAGCA	TATAGCCTCG	100
45	AATGGTGGCA	CTATGTATTA	AGAGACGAAC	CATACCCCAA	TAGCTATTTT	150
	GATTTCCCCG	TTAAATAAAC	TTTTAACCGT	TGCACGGACA	AACTATATAA	200
	GCTAACTCTT	TCGGCAGGAA	ACCCGACGTA	TGTAAGTGGT	TCTTAGGGAA	250
	TTTATATATA	GTAGATAGTA	TTGAAGATGT	AAGGCAGAGC	GATATTGCGG	300
	TCATTATCTG	CGTGCGCTGC	GGCAAGATAG	CCTGATAATA	AGACTGATCG	350
50	CATAGAGGGG	TGGTATTTCA	CACCGCCCAT	TGTCAACAGG	CAGTTCAGCC	400
	TCGTAAATTT	CAGCATGGGT	ATCACTTATG	AAAATTCATC	TACATTGGTG	450
	ATAATAGTAA	ATCCAGTAGG	GCGAAATAAT	TGACTGTAAT	TTACGGGGCA	500
	AAACGGCACA	ATCTCAAACG	AGATTGTGCC	GTTTAAGGGG	AAGATTCTAG	550
	AAATATTTCA	TACTTCCAAC	TATATAGTTA	AGGAGGAGAC	TGAAAATGAA	600
55	GAAGTTGTTT	TTTTTATTGT	TATTGTTATT	CTTAATATAC	TTAGGTTATG	650
	ACTACGTTAA	TGAAGCACTG				670

60 2) INFORMATION FOR SEQ ID NO: 1076

610

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: DG131/3 serotype OX3:H8
 (C) ACCESSION NUMBER: Z36901

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

ATGAAAATAA	TAATTTT TAG	AGTGCTAACT	TTTTTCTTTG	TTATCTTTTC	50
TGTTAATGTG	GTTGCGAAGG	AATTTACCTT	AGATTTCTCG	ACAGCAAAGA	100
CGTATGTAGA	TTGCTGAAT	GTCATTGCT	CTGCAATAGG	TACTCCATTA	150
20 CAGACTATTT	CATCAGGAGG	TACGTCTTTA	CTGATGATTG	ATAGTGGCAC	200
AGGGGATAAT	TTGTTTGCAG	TTGATGTCAG	AGGGATAGAT	CCAGAGGAAG	250
GGCGGTTTAA	TAATCTACGG	CTTATTGTTG	AACGAAATAA	TTTATATGTG	300
ACAGGATTTG	TTAACAGGAC	AAATAATGTT	TTTTATCGCT	TTGCTGATTT	350
TTCACATGTT	ACCTTTCCTG	GTACAACTGC	GGTTACATTG	TCTGGTGACA	400
25 GTAGCTATAC	CACGTTACAG	CGTGTTGCGG	GGATCAGTCG	TACGGGGATG	450
CAGATAAATC	GCCATTCGTT	GACTACTTCT	TATCTGGATT	TAATGTCGCA	500
TAGCGGAACC	TCACTGACGC	AGTCTGTGGC	AAGAGCGATG	TTACGGTTTG	550
TTACTGTGAC	AGCTGAAGCT	TTACGTTTTC	GGCAAATTCA	GAGGGGATTT	600
CGTACAACAC	TTGATGATCT	CAGTGGGCGT	TCTTATGTAA	TGACTGCTGA	650
30 AGATGTTGAT	CTTACGTTGA	ACTGGGGAAG	GTTGAGTAGT	GTCCTGCCTG	700
ACTATCATGG	ACAAGACTCT	GTTGCTGTTG	GAAGAATTTC	TTTTGGAAGT	750
GTTAATGCAA	TTCTGGGTAG	CGTGGCATT	ATACTGAATT	GTCATCATCA	800
TGCATCGCGA	GTTGCCAGAA	TTGTACCTAA	TGAGTTTCCT	TCTATGTGCC	850
CGGTAGATGG	AAGAGTGGCT	GGGATTACGC	ACAATAAAAT	ATTGTGGGAC	900
35 TCATCCACTC	TGGGGGCAAT	TTTGATACGC	AGGGCTATTA	GCAGTTGA	948

2) INFORMATION FOR SEQ ID NO: 1077

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1259 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: 94C serotype O48:H21
 (C) ACCESSION NUMBER: extracted from Z37725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

55 CACCTGTATA	TGAAGTGTAT	ATTATTTAAA	TGGGTACTGT	GCCTGTTACT	50
GGGTTTTTCT	TCGGTATCCT	ATTCCCGGGA	GTTTACGATA	GACTTTTTCGA	100
CCCAACAAAG	TTATGTCTCT	TCGTAAATA	GTATACGGAC	AGAGATATCG	150
ACCCCTCTTG	AACATATATC	TCAGGGGACC	ACATCGGTGT	CTGTTATTAA	200
60 CCACACCCCA	CCGGGCAGTT	ATTTTGCTGT	GGATATACGA	GGGCTTGATG	250

	TCTATCAGGC	GCGTTTTGAC	CATCTTCGGC	TGATTATTGA	GCAAAATAAT	300
	TTATATGTGG	CCGGGTTCGT	TAATACGGCA	ACAAATACTT	TCTACCGTTT	350
	TTCAGATTTT	ACACATATAT	CAGTGCCCGA	TGTGACAACG	GTTTCCATGA	400
	CAACGGACAG	CAGTTATACC	ACTCTGCAAC	GTGTCGCAGC	GCTGGAACGT	450
5	TCCGGAATGC	AAATCAGTCG	TCACTCACTG	GTTTCATCAT	ATCTGGCGTT	500
	AATGGAGTTC	AGTGGTAATA	CAATGACCAG	AGATGCATCC	AGAGCAGTTC	550
	TGCGTTTTGT	CACTGTCACA	GCAGAAGCCT	TACGCTTCAG	GCAGATACAG	600
	AGAGAATTTC	GTCAGGCACT	GTCTGAAACT	GCTCCTGTGT	ATACCATGAC	650
	GCCGGGAGAC	GTGGACCTCA	CTCTGAACTG	GGGGCGAATC	AGCAATGTGC	700
10	TTCCGGAGTA	TCGGGGAGAG	GATGGTGTCA	GAGTGGGGAG	AATATCCTTT	750
	AATAATATAT	CAGCGATACT	GGGTACTGTG	GCCGTTATAC	TGAATTGCCA	800
	TCATCAGGGG	GCGCGTTCTG	TTCGCGCCGT	GAATGAAGAG	AGTCAACCAG	850
	AATGTCAGAT	AACTGGCGAC	AGGCCCGTTA	TAAAAATAAA	CAATACATTA	900
	TGGGAAAGTA	ATACAGCTGC	AGCGTTTCTG	AACAGAAAGT	CACAGTTTTT	950
15	ATATACAACG	GGTAAATAAA	GGAGTTAAGT	ATGAAGAAGA	TGTTTATGGC	1000
	GGTTTTATTT	GCATTAGTTT	CTGTTAATGC	AATGGCGGCG	GATTGTGCTA	1050
	AAGGTAAAAT	TGAGTTTTTC	AAGTATAATG	AGGATGACAC	ATTTACAGTG	1100
	AAGGTTGACG	GGAAAGAATA	CTGGACCAGT	CGCTGGAATC	TGCAACCGTT	1150
	ACTGCAAAGT	GCTCAGCTGA	CAGGAATGAC	TGTCACAATC	AAATCCAGTA	1200
20	CCTGTGAATC	AGGCTCCGGA	TTTGCTGAAG	TGCAGTTTAA	TAATGACTGA	1250
	GGCATAACC					1259

25 2) INFORMATION FOR SEQ ID NO: 1078

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - 30 (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1079

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 bases
 - 45 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

19

55

2) INFORMATION FOR SEQ ID NO: 1080

- (i) SEQUENCE CHARACTERISTICS:
- 60 (A) LENGTH: 25 bases

612

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080

10 TATAGCTACT GTCACCAGAC AATGT 25

2) INFORMATION FOR SEQ ID NO: 1081

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081

25 ATGTCAGAGG GATAGATCCA 20

2) INFORMATION FOR SEQ ID NO: 1082

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082

40 TTGARCRAAA TAATTTATAT GTG 23

45 2) INFORMATION FOR SEQ ID NO: 1083

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

TGATGATGRC AATTCAGTAT 20

60

2) INFORMATION FOR SEQ ID NO: 1084

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

15

2) INFORMATION FOR SEQ ID NO: 1085

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GCTCCTGTGC GTGG

34

30

2) INFORMATION FOR SEQ ID NO: 1086

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

45 CTACTCCCGC CTTTGGGTT

20

50

2) INFORMATION FOR SEQ ID NO: 1087

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

60

5 2) INFORMATION FOR SEQ ID NO: 1088

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

20

2) INFORMATION FOR SEQ ID NO: 1089

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1090

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

AATAGCGCGG ACGAATTGGA C

21

50

2) INFORMATION FOR SEQ ID NO: 1091

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

5 AACGCGGCAC TGTTTCCCAA

20

2) INFORMATION FOR SEQ ID NO: 1092

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

20

TCGGCAAGAC AATATGACAG C

21

25 2) INFORMATION FOR SEQ ID NO: 1093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSsa-165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

40

TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
CGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACCTGCTT	200
45 TTTTAAAGTA	TAGGTATAAA	ATACAATTGA	TTAAAATAGT	AAAGGAAATG	250
AATCATGAAA	CAATTAACTA	AGCCTTTATA	CTTTTACCTA	TTACTTTTTA	300
TTACAACAAC	ACTGATTGGC	GCGTTACTAT	TATATTTGCC	AATCACAGGT	350
AAACATCCTA	TTGATTTTGT	GGACGCCCGT	T		381

50

2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

GGTAAAACAG GTACTTCTAA CTA

23

5

2) INFORMATION FOR SEQ ID NO: 1095

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

20 CGATAGAAGC AGCAGGACAA

20

2) INFORMATION FOR SEQ ID NO: 1096

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

40

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAAG GGATCACWAA AGTMAC

26

55

2) INFORMATION FOR SEQ ID NO: 1098

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 23 bases

617

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098

10 TCTTCAAAAT CGAAAAAGCC GTC 23

2) INFORMATION FOR SEQ ID NO: 1099

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099

25 TCAAAAGGGA TCACWAAAGT MAC 23

2) INFORMATION FOR SEQ ID NO: 1100

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100

40 GTAAAKCCCG GCATRGTRTT GATTTC 26

2) INFORMATION FOR SEQ ID NO: 1101

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

55 GACGGYTTTT TYGATTTTGA AGA 23

60 2) INFORMATION FOR SEQ ID NO: 1102

618

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAG ACC

23

15

2) INFORMATION FOR SEQ ID NO: 1103

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

20

30

2) INFORMATION FOR SEQ ID NO: 1104

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

GGATCAACAC AGTAGAACCG

20

45

2) INFORMATION FOR SEQ ID NO: 1105

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

50 CTCCTACGAT TCTCTTGAYA AATCA

25

2) INFORMATION FOR SEQ ID NO: 1106

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

15

CAACCGATCT CAACACCGGC AAT

23

20 2) INFORMATION FOR SEQ ID NO: 1107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

CTCATTTGAC TTCCTCCTTT GCT

23

35

2) INFORMATION FOR SEQ ID NO: 1108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

GTAAGAATCG GAAAAGCGGA AGG

23

50

2) INFORMATION FOR SEQ ID NO: 1109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

ACATCGTGAT CGCTAAAAGG AGC

23

5

2) INFORMATION FOR SEQ ID NO: 1110

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

20 ACGAGAAAGA CAACAGGAAG ACC

23

2) INFORMATION FOR SEQ ID NO: 1111

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

35

CTTTTCCGG CTCGWYTTCC TGATG

25

40 2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

GGCTGYGATA TTCAAAGCTC

20

55

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

10

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

25

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

40

TTTCGGGCTG TGAGGTCGGB TGHGCG

26

2) INFORMATION FOR SEQ ID NO: 1116

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

55

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

60

2) INFORMATION FOR SEQ ID NO: 1117

622

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: 94
 (C) ACCESSION NUMBER: U94526
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

	AAATTTCGATC	CGCACTACAT	CGGAATTACA	AAAAACGGTG	TATGGAAGCT	50
	ATGCAAGAAG	CCATGTACGG	AATGGGAAGC	CGACAGTCTC	CCCGCCATAC	100
	TCTCCCCGGA	TAGGAAAACG	CATGGGCTGC	TTGTCATGAA	AGAAAGCGAA	150
20	TACGAAACAC	GGCGTATTGA	TGTGGCTTTC	CCGGTTTTGC	ATGGCAAATG	200
	CGGGGAGGAT	GGTGCGATAC	AGGGGCTGTT	TGTATTGTCT	GGTATCCCCT	250
	ATGTGGGCTG	TGATATTCAA	AGCTCCGCAG	CTTGCAATGA	CAAATCACTG	300
	GCCTACATTC	TTACAAAAAA	TGCGGGCATC	GCCGTTCCCG	AATTTCAAAT	350
	GATTGATAAA	GGTGACAAGC	CGGAGGCGGG	TGCGCTTACC	TACCCTGTCT	400
25	TTGTGAAGCC	GGCACGGTCA	GGTTCGTCCT	TTGGCGTAAC	CAAAGTAAAC	450
	GGTACGGAAG	AACTTAACGC	TGCGATAGAA	GCGGCAGGAC	AATATGATGG	500
	AAAAATCTTA	ATTGAGCAAG	CGATTTCCGG	CTGTGAGGTC	GGGTGTGCGG	550
	TCATGGGGAA	CGAGGATGAT	TTGATTGTCG	GCGAAGTGGA	TCAAATCCGG	600
	CTGAGCCACG	GTATCTTCCG	CATCCATCAG	GAAAACGAGC	CGGAAAAAGG	650
30	CTCAGAAAAT	GCGATGATTA	CAGTTCCCGC	AGACATTCCG	GTCGAGGAAC	700
	GAAATCGGGT	GCAGGAAACG	GCAAAGAAAG	TATATCGGGT	GCTTGGATGC	750
	AGAGGGCTTG	CCCGTGTTGA	TCTTTTTTTG	CAGGAGGATG	GCGGCATCGT	800
	T					801

35

2) INFORMATION FOR SEQ ID NO: 1118

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

50 TTTTCWGAGC CTTTTTCCGG CTCG 24

2) INFORMATION FOR SEQ ID NO: 1119

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119

5 TTTCGGGCTG TGAGGTCGGB TGHGC

25

2) INFORMATION FOR SEQ ID NO: 1120

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120

20

TTTCGGGCTG TGAGGTCGGB TGHG

24

25 2) INFORMATION FOR SEQ ID NO: 1121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121

TGTTTGWATT GTCYGGYATC CC

22

40

2) INFORMATION FOR SEQ ID NO: 1122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

TGGTGCATTG CTACGTGG

18

55

2) INFORMATION FOR SEQ ID NO: 1123

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

10 TTTCTGGGCTG TGAGGTCGGB TG 22

2) INFORMATION FOR SEQ ID NO: 1124

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

25 GATTGTGRTCC ACYTCGCCRA CA 22

2) INFORMATION FOR SEQ ID NO: 1125

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

40 ACTCACAAC TGGGATGGATG 20

45 2) INFORMATION FOR SEQ ID NO: 1126

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

60 TTATGGTTGT GCTGGTTGAG G 21

2) INFORMATION FOR SEQ ID NO: 1127

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA

20

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2) INFORMATION FOR SEQ ID NO: 1128

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA

20

30

2) INFORMATION FOR SEQ ID NO: 1129

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

45 ATGATGACHG AMATGATGAA AAC

23

50

2) INFORMATION FOR SEQ ID NO: 1130

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130

60

5 2) INFORMATION FOR SEQ ID NO: 1131

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131

CATCTGGAGC TACRTARCCA GT

22

20

2) INFORMATION FOR SEQ ID NO: 1132

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132

AGTGAAAARA TGGCTGCTGC

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2) INFORMATION FOR SEQ ID NO: 1133

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133

CATCAAGAAC ACTGGCTAYG TAG

23

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2) INFORMATION FOR SEQ ID NO: 1134

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

5 CTAGATAGAG CTAAAACCTT CCT

23

2) INFORMATION FOR SEQ ID NO: 1135

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

20

CATTATGCAA ACGCCATTTC AAG

23

25 2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

ACTTGTCCAC GTTSGATRTC T

21

40

2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

AATTAATGGC TGCWGTGAY GAA

23

55

2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 1032 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*
 (C) ACCESSION NUMBER: M75132

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

	ATGAAAAAAAA	TTGCCGTTTT	ATTTGGAGGG	AATTCTCCAG	AATACTCAGT	50
	GTCAC TAACC	TCAGCAGCAA	GTGTGATCCA	AGCTATTGAC	CCGCTGAAAT	100
15	ATGAAGTAAT	GACCATTGGC	ATCGCACCAA	CAATGGATTG	GTATTGGTAT	150
	CAAGGAAACC	TCGCGAATGT	TCGCAATGAT	ACTTGGCTAG	AAGATCACAA	200
	AAACTGTCAC	CAGCTGACTT	TTTCTAGCCA	AGGATTTATA	TTAGGAGAAA	250
	AACGAATCGT	CCCTGATGTC	CTCTTTCCAG	TCTTGCATGG	GAAGTATGGC	300
	GAGGATGGCT	GTATCCAAGG	ACTGCTTGAA	CTAATGAACC	TGCCTTATGT	350
20	TGGTTGCCAT	GTCGCTGCCT	CCGCATTATG	TATGAACAAA	TGGCTCTTGC	400
	ATCAACTTGC	TGATACCATG	GGAATCGCTA	GTGCTCCCAC	TTTGCTTTTA	450
	TCCCGCTATG	AAAACGATCC	TGCCACAATC	GATCGTTTTA	TTCAAGACCA	500
	TGGATTCCCG	ATCTTTATCA	AGCCGAATGA	AGCCGGTTCT	TCAAAAGGGA	550
	TCACAAAAGT	AACTGACAAA	ACAGCGCTCC	AATCTGCATT	AACGACTGCT	600
25	TTTGCTTACG	GTTCTACTGT	GTTGATCCAA	AAGGCGATAG	CGGGTATTGA	650
	AATTGGCTGC	GGCATCTTAG	GAAATGAGCA	ATTGACGATT	GGTGCTTGTG	700
	ATGCGATTTC	TCTTGTCGAC	GGTTTTTTTG	ATTTTGAAGA	GAAATACCAA	750
	TTAATCAGCG	CCACGATCAC	TGTCCCAGCA	CCATTGCCTC	TCGCGCTTGA	800
	ATCACAGATC	AAGGAGCAGG	CACAGCTGCT	TTATCGAAAC	TTGGGATTGA	850
30	CGGGTCTGGC	TCGAATCGAT	TTTTTTCGTCA	CCAATCAAGG	AGCGATTAT	900
	TTAAACGAAA	TCAACACCAT	GCCGGGATTT	ACTGGGCACT	CCCGCTACCC	950
	AGCTATGATG	GCGGAAGTCG	GGTTATCCTA	CGAAATATTA	GTAGAGCAAT	1000
	TGATTGCACT	GGCAGAGGAG	GACAAACGAT	GA		1032

35

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1768 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: X56895

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

	GATATCGTTA	CGCTTCATGT	GCCGCTCAAT	ACGGATACGC	ACTATATTAT	50
55	CAGCCACGAA	CAAATACAGA	GAATGAAGCA	AGGAGCATTT	CTTATCAATA	100
	CTGGGCGCGG	TCCACTTGTA	GATACCTATG	AGTTGGTTAA	AGCATTAGAA	150
	AACGGGAAAC	TGGGCGGTGC	CGCATTGGAT	GTATTGGAAG	GAGAGGAAGA	200
	GTTTTTCTAC	TCTGATTGCA	CCCAAAAACC	AATTGATAAT	CAATTTTAC	250
	TTAAACTTCA	AAGAATGCCT	AACGTGATAA	TCACACCGCA	TACGGCCTAT	300
60	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAACCA	TTAAAAACTG	350

	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	400
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	450
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	500
	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	550
5	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	600
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	650
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	700
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	750
	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	800
10	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	850
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	900
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	950
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	1000
	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	1050
15	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	1100
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	1150
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	1200
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	1250
	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1300
20	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1350
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1400
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTAGAT	GAAATAGTAC	1450
	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1500
	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAGTT	1550
25	GGCTGAATCG	CTTTTGAAGG	CAAAAGAACT	GGCTGCTACC	CAAGGGTACG	1600
	GATTGCTTCT	ATGGGACGGT	TACCGTCCTA	AGCGTGCTGT	AAACTGTTTT	1650
	ATGCAATGGG	CTGCACAGCC	GGAAAATAAC	CTGACAAAGG	AAAGTTATTA	1700
	TCCAATATT	GACCGAACTG	AGATGATTTT	AAAAGGATAC	GTGGCTTCAA	1750
	AATCAAGCCA	TAGCCGCG				1768
30						

2) INFORMATION FOR SEQ ID NO: 1140

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (C) ACCESSION NUMBER: L29638

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

	GTAAGAATCG	GAAAAGCGGA	AGGAAGAAAA	ACATGAAAAA	AATCGCCATT	50
50	ATTTTTGGAG	GCAATTCACC	GGAATACACC	GTTTCTTTAG	CTTCAGCAAC	100
	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	CTATGACTAC	GACCTCTCTT	150
	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	GGTACTTGTA	TACAGGAGAA	200
	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	TTGGATACGA	AACATAAACA	250
	GAAAATACAG	CCGCTATTCG	AAGGAAACGG	CTTTTGGCTA	AGTGAAGAGC	300
55	AGCAAACGTT	GGTACCTGAT	GTTTTATTTT	CCATTATGCA	TGGCAAATAC	350
	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	GAATTGATGA	AGCTGCCTTA	400
	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	ATGTATGAAC	AAATGGCTGC	450
	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	AAAGTGCTCC	TACGATTCTC	500
	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	ATCGAAGCTT	TTATCCAGAC	550
60	CCATGGCTTC	CCAGTTTCT	TTAAGCCTAA	TGAAGCGGGC	TCCTCAAAG	600

	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	TCGCTTCTGC	CTTAAAAGAA	650
	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	CAAAAAAATA	TTGCCGGTGT	700
	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	CTCTTTGACT	GTCGGTGCTT	750
	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	TCGATTTTGA	AGAAAAGTAC	800
5	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	GCGCCATTGC	CTGAAACGAT	850
	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	GCTCTATCGT	AGTCTTGGTC	900
	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	TCACGGAGCG	AGGAGAATA	950
	TACTTGAATG	AAATCAATAC	TATGCCGGGC	TTTACGAGTC	ACTCCCGCTA	1000
	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	CTATCAAGAA	CTACTACAAA	1050
10	AACTGCTTGT	CTTAGCAAAG	GAGGAAGTCA	AATGAG		1086

2) INFORMATION FOR SEQ ID NO: 1141

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3946 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 25 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: extracted from M97297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

30	ATGAATAACA	TCGGCATTAC	TGTTTATGGA	TGTGAGCAGG	ATGAGGCAGA	50
	TGCATTCCAT	GCTCTTTCGC	CTCGCTTTGG	CGTTATGGCA	ACGATAATTA	100
	ACGCCAACGT	GTCGGAATCC	AACGCCAAAT	CCGCGCCTTT	CAATCAATGT	150
	ATCAGTGTGG	GACATAAATC	AGAGATTTCC	GCCTCTATTC	TTCTTGCGCT	200
	GAAGAGAGCC	GGTGTGAAAT	ATATTTCTAC	CCGAAGCATC	GGCTGCAATC	250
35	ATATAGATAC	AACTGCTGCT	AAGAGAATGG	GCATCACTGT	CGACAATGTG	300
	GCGTACTCGC	CGGATAGCGT	TGCCGATTAT	ACTATGATGC	TAATTCTTAT	350
	GGCAGTACGC	AACGTAAAAT	CGATTGTGCG	CTCTGTGGAA	AAACATGATT	400
	TCAGGTTGGA	CAGCGACCGT	GGCAAGGTAC	TCAGCGACAT	GACAGTTGGT	450
	GTGGTGGGAA	CGGGCCAGAT	AGGCAAAGCG	GTTATTGAGC	GGCTGCGAGG	500
40	ATTTGGATGT	AAAGTGTTGG	CTTATAGTCG	CAGCCGAAGT	ATAGAGGTAA	550
	ACTATGTACC	GTTTGATGAG	TTGCTGCAAA	ATAGCGATAT	CGTTACGCTT	600
	CATGTGCCGC	TCAATACGGA	TACGCACTAT	ATTATCAGCC	ACGAACAAAT	650
	ACAGAGAATG	AAGCAAGGAG	CATTTCTTAT	CAATACTGGG	CGCGGTCCAC	700
	TTGTAGATAC	CTATGAGTTG	GTAAAGCAT	TAGAAAACGG	GAAACTGGGC	750
45	GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
	TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
	TGCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
	TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAAG	950
	GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
50	TCAGAGGAGC	ATGACGTATC	GGTAAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
	CATTAATAAA	GAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
	GTGTATGGAA	AATGTGCGAA	AAACCTTGCG	CGGAATGGGA	AAACGACAAT	1150
	TGCTATTTCAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
	TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
55	CTTTGCATGG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTTGAA	1300
	TTGTCCGGTA	TCCCTTTTGT	AGGCTGCGAT	ATTCAAAGCT	CAGCAATTTG	1350
	TATGGACAAA	TCGTTGACAT	ACATCGTTGC	GAAAAATGCT	GGGATAGCTA	1400
	CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
	TTTACCTATC	CTGTTTTTGT	TAAGCCGGCG	CGTTCAGGCT	CATCCTTCGG	1500
60	TGTGAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550

	CAAGACAATA	TGACAGCAAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
	GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCGCGTTAG	TTGTTGGCGA	1650
	GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCGTATT	CATCAGGAAG	1700
	TCGAGCCGGA	AAAAGGCTCT	GAAAACGCAG	TTATAACCGT	TCCCGCAGAC	1750
5	CTTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
	TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCG	TGTGGATATG	TTTTTACAAG	1850
	ATAACGGCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
	TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
	CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTTAAAGGGG	TGATAAGCAT	2000
10	GGAAATAGGA	TTTACTTTTT	TAGATGAAAT	AGTACACGGT	GTTTCGTTGGG	2050
	ACGCTAAATA	TGCCACTTGG	GATAATTTCA	CCGGAAAACC	GGTTGACGGT	2100
	TATGAAGTAA	ATCGCATTGT	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
	GAAGGCAAAA	GAAGTGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
	ACGGTTACCG	TCCTAAGCGT	GCTGTAAACT	GTTTTATGCA	ATGGGCTGCA	2250
15	CAGCCGGAAA	ATAACCTGAC	AAAGGAAAGT	TATTATCCCA	ATATTGACCG	2300
	AACTGAGATG	ATTTCAAAG	GATACGTGGC	TTCAAAATCA	AGCCATAGCC	2350
	GCGGCAGTGC	CATTGATCTT	ACGCTTTATC	GATTAGACAC	GGGTGAGCTT	2400
	GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
	GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	2500
20	CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
	TATGTATTAA	GAGACGAACC	ATACCCCAAT	AGCTATTTTG	ATTTCCCCGT	2600
	TAAATAAACT	TTTAACCGTT	GCACGGACAA	ACTATATAAG	CTAACTCTTT	2650
	CGGCAGGAAA	CCCGACGTAT	GTAAGTGGT	CTTAGGGAAT	TTATATATAG	2700
	TAGATAGTAT	TGAAGATGTA	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	2750
25	GTGCGCTGCG	GCAAGATAGC	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	2800
	GGTATTTTAC	ACCGCCCAT	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	2850
	AGCATGGGTA	TCACTTATGA	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	2900
	TCCAGTAGGG	CGAAATAATT	GACTGTAAAT	TACGGGGCAA	AACGGCACAA	2950
	TCTCAAACGA	GATTGTGCCG	TTTAAGGGGA	AGATTCTAGA	AATATTTTCAT	3000
30	ACTTCCAAC	ATATAGTTAA	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	3050
	TTTTATTGTT	ATTGTTATTC	TTAATATACT	TAGGTTATGA	CTACGTTAAT	3100
	GAAGCACTGT	TTTCTCAGGA	AAAAGTCGAA	TTTCAAAATT	ATGATCAAAA	3150
	TCCCAAAGAA	CATTTAGAAA	ATAGTGGGAC	TTCTGAAAAT	ACCCAAGAGA	3200
	AAACAATTAC	AGAAGAACAG	GTTTATCAAG	GAAATCTGCT	ATTAATCAAT	3250
35	AGTAAATATC	CTGTTCCGCA	AGAAAGTGTG	AAGTCAGATA	TCGTGAATTT	3300
	ATCTAAACAT	GACGAATTAA	TAAATGGATA	CGGGTTGCTT	GATAGTAATA	3350
	TTTATATGTC	AAAAGAAATA	GCACAAAAT	TTTCAGAGAT	GGTCAATGAT	3400
	GCTGTAAAGG	GTGGCGTTAG	TCATTTTATT	ATTAATAGTG	GCTATCGAGA	3450
	CTTTGATGAG	CAAAGTGTGC	TTTACCAAGA	AATGGGGGCT	GAGTATGCCT	3500
40	TACCAGCAGG	TTATAGTGAG	CATAATTCAG	GTTTATCACT	AGATGTAGGA	3550
	TCAAGCTTGA	CGAAAATGGA	ACGAGCCCCT	GAAGGAAAGT	GGATAGAAGA	3600
	AAATGCTTGG	AAATACGGGT	TCATTTTACG	TTATCCAGAG	GACAAAACAG	3650
	AGTTAACAGG	AATTCAATAT	GAACCATGGC	ATATTCGCTA	TGTTGGTTTA	3700
	CCACATAGTG	CGATTATGAA	AGAAAAGAAT	TTCGTTCTCG	AGGAATATAT	3750
45	GGATTACCTA	AAAGAAGAAA	AAACCATTTT	TGTTAGTGTA	AATGGGGAAA	3800
	AATATGAGAT	CTTTTATTAT	CCTGTTACTA	AAAATACCAC	CATTCATGTG	3850
	CCGACTAATC	TTCGTTATGA	GATATCAGGA	AACAATATAG	ACGGTGTAAT	3900
	TGTGACAGTG	TTTCCCGGAT	CAACACATAC	TAATTCAGG	AGGTAA	3946

50

2) INFORMATION FOR SEQ ID NO: 1142

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

5

2) INFORMATION FOR SEQ ID NO: 1143

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

20 CAATTAGCTT AGCAATAGGT GTTGG

25

2) INFORMATION FOR SEQ ID NO: 1144

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

35

TGTYTTCCAA GTTTCAGCTC

20

40 2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

AACATATTKG GTTGATAGGT

20

55

2) INFORMATION FOR SEQ ID NO: 1146

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

60

(B) TYPE: Nucleic acid

633

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

GGGATTACCT ATGCCAATAT GAT

23

10

2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

AGCTGTGTTA GCVCGAACAT CTTG

24

25

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

40

GACTTTGTTT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149

55

TCCYACWATT TCTTTTGWG

20

60 2) INFORMATION FOR SEQ ID NO: 1150

634

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150

TGATAATCAC ACCGCATACG

20

15

2) INFORMATION FOR SEQ ID NO: 1151

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151

TGCTGTCATA TTGTCTTGCC

20

30

2) INFORMATION FOR SEQ ID NO: 1152

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

20

45

2) INFORMATION FOR SEQ ID NO: 1153

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

60 CTCGTATGTC CCTACAATGC

20

2) INFORMATION FOR SEQ ID NO: 1154

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

15

GTTTGAAGCA TATAGCCTCG

20

20 2) INFORMATION FOR SEQ ID NO: 1155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

CAGTGCTTCA TTAACGTAGT C

21

35

2) INFORMATION FOR SEQ ID NO: 1156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

GTTGAAATGC ATCACGAACA ATT

23

50

2) INFORMATION FOR SEQ ID NO: 1157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

AAGAACGTTT CAGTTAAGGA AAT

23

5

2) INFORMATION FOR SEQ ID NO: 1158

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

20 AAGAGGTAAT GTCTGTGGT

19

2) INFORMATION FOR SEQ ID NO: 1159

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

35

TGAAGGTTTG CCAGGTGA

18

40 2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

CGTTTCTGTT AAAGAAATTA GAAG

24

55

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid

60

637

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

10

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

25

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

40

GTTGGTTTCA ACGTTAAGAA C

21

2) INFORMATION FOR SEQ ID NO: 1164

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

55

GGTTTCAACG TCAAGAAC

18

60

2) INFORMATION FOR SEQ ID NO: 1165

638

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

GGTTTCAACG TGAAGAAC

18

15

2) INFORMATION FOR SEQ ID NO: 1166

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

ACGTTAAGAA TGTTTCTGTC AA

22

30

2) INFORMATION FOR SEQ ID NO: 1167

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 14 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

14

45

2) INFORMATION FOR SEQ ID NO: 1168

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

60 GAACAATTGG TTGAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1169

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: SP-665
(C) ACCESSION NUMBER: AF139883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

20

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
25 TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
30 GCTTG GTTAG	CGATT CAGTT	AGAACA AAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
35 CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAAC TCCGA	950
40 TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
45 TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTCCG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAA AAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
50 CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
TGTCGGAACT	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGACT	TATGGA ACTG	GGCGTGGAGC	CTATCTTCCT	1650
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
55 AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCTG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTTGT	ATTCAAAAAT	1950
60 GGAGCTCGCC	CAATATGGAC	TGAACCCTCT	ACTCAACAAT	CCTCAACAGC	2000

TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

5

2) INFORMATION FOR SEQ ID NO: 1170

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

20 ACGAATTGGA CTACGCAATT

20

2) INFORMATION FOR SEQ ID NO: 1171

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

35

ACGAGGATGA TTTGATTGTC

20

40 2) INFORMATION FOR SEQ ID NO: 1172

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1560 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: 64147
(C) ACCESSION NUMBER: X13136

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

GATCCTCTAA	ATGATTCTCA	GGTGGCTGTT	ATTGCCTCTA	TTTCAAAGGA	50
GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	GGATAGAAAG	GTTTTGGAAA	100
CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	CCAGTGAAAA	AGCTGGTCTC	150
60 CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	AAAGGCTATT	CTCTAAATGA	200

	CCGTGTAGGA	ACCTCCTATT	TGGAAAAGCA	ATATGAAGAG	ACCTTACAAG	250
	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	ACAAATATGG	CAACATGGAA	300
	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	GGAAACAATA	TCAAGCTGAC	350
	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	TGCTTTGCTG	AAAAGTTATT	400
5	TCAATTCAGA	GTTGGGAAAT	GGTGGAGCCA	AGTATTCTGA	AGGTGTCTAT	450
	GCAGTCGCCC	TTAACCCAAA	AACAGGTGCT	GTTTTGTCTA	TGTCAGGAAT	500
	TAAACATGAC	TTGAAAACAG	GAGAGTTGAC	GCCGGATTCC	TTGGGAACGG	550
	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	TCAAAGCAGC	GACCATCAGC	600
	TCTGGTTGGG	AAAATGGAGT	CTTGTCAGGA	AATCAGACCT	TGACAGACCA	650
10	GTCCATTGTC	TTTCAAGGTT	CAGCTCCAAT	TAATTCTTGG	TATCCTGCCT	700
	TTTCTAGACC	AATGCCGATT	ACGGCGGTTT	AGGCTCTAGA	GTATTCATCC	750
	AATGCTTATA	TGGTCCAAAC	AGCCCTAGGT	CTTATGGGGC	AGACCTATCA	800
	ACCCAATATG	TTTGTCGGCA	CCAGCAATCT	AGAGTCTGCT	ATGGGGAAAT	850
	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	GTTCTGCGAC	CGGAATTGAC	900
15	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	AAAGAGTATA	GCTTTGCTAA	950
	TTTCATTACC	AATGCCTTTG	GGCAGTTTGA	TAACTATACG	CCGATGCAGT	1000
	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	ATGGTGTTTC	TGTGGCTCCT	1050
	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	GATAAGGGAG	GAATATATCCG	1100
	CTTGATTTCAG	CAACTGCAAC	CGACAGAGAT	GAATAAGGTC	AATATATCCG	1150
20	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	TTTATCAGGT	TGCCCATGGT	1200
	ACTAGTGAAT	TGACAACTGG	ACGTGCCTTT	TCAAATGGCG	CCTTGGTATC	1250
	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	CTATGTGGCA	GATGGTCAGC	1300
	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	CCCCATCTGA	TAATCCCCAA	1350
	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	ACCAACCTTA	CAAATGGTGT	1400
25	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	CCTCTATAAC	CAACATCATC	1450
	CAATGAATTA	GAAAGGAACA	TATGCTTTAT	CCAACACCTA	TTGCTAAGCT	1500
	AATTGACAGT	TATTCGAAGT	TACCGGGTAT	CGGGATTAAG	ACGGCTACCC	1550
	GTTTGGCCTT					1560

30

2) INFORMATION FOR SEQ ID NO: 1173

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 40 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- 45 (C) ACCESSION NUMBER: Z49096

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

	GAGTCCCGAT	TGCTGAGGAT	GCAACCTCCT	ATAATGTCTA	TGCGGTCATT	50
50	GATGAGAACT	ATAAGTCAGC	AACGGGTAAG	ATTCTTTACG	TAGAAAAAAC	100
	ACAATTTAAC	AAGGTTGCAG	AGGTCTTTCA	TAAGTATCTG	GACATGGAAG	150
	AATCCTATGT	AAGAGAGCAA	CTCTCGCAAC	CTAATCTCAA	GCAAGTTTCC	200
	TTTGGAGCAA	AGGGAAATGG	GATTACCTAT	GCCAATATGA	TGACTATCAA	250
	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	300
55	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGTCTA	350
	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTGC	TGGGAACTTC	400
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGCATTG	450
	TTACCTATGA	AAAGGATCGT	CTGGGCAATA	TTGTACCCGG	AACAGAACTG	500
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	550
60	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	600

	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	650
	ATTCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	700
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	750
	AACCAGGATC	AGCCTTTAAG	GTCATGATGT	TAGCTTCTTC	TATTGATAAT	800
5	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	850
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAGGGTTTG	ACTACTGGTG	900
	GGATGATGAC	TTTCTCACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAACG	950
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTG GTTG	ATTATCTAAA	1000
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	1050
10	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATT	1100
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	1150
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	1200
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1250
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1300
15	AGTTGGGACG	GACCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1350
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1400
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1450
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1500
	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1550
20	GGAGAATTTG	CCACCCCAAT	CTTGAGCGG	GCTTCAGCTA	TGAAAGAATC	1600
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1650
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1700
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1750
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1800
25	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1850
	AGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1900
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTGT	TCAGAAGCAA	GATGTTTCGA	1950
	CTAATACAGC	TATCAAAAAC	ATTAAAAAAA	TTAAATTAAC	TTTAGGAGAC	2000
	TAATATG					2007
30						

2) INFORMATION FOR SEQ ID NO: 1174

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- 40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

45 GAACGTGGTG AAGTTCGC

18

2) INFORMATION FOR SEQ ID NO: 1175

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- 55 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

60

5 2) INFORMATION FOR SEQ ID NO: 1176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

TACTGGTGTA GAAATGTTC

19

20

2) INFORMATION FOR SEQ ID NO: 1177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

GCTCAACAAG TTCCAGATTA

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2) INFORMATION FOR SEQ ID NO: 1178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2456 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC8325
50 (C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

55	ATGAACTGAT TATACTTAAC ATTA AAAAAG ATGATAACAC CTTCTACACC	50
	TCCATATCAC AAAAAATTAT AACATTATTT TGACATAAAT ACTACATTTG	100
	TAATATACTA CAAATGTAGT CTTATATAAG GAGGATATTG ATGAAAAAGA	150
	TAAAAATTGT TCCA CT TATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA	200
	TATTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT	250
	TGAAGATAAA AATTTC AAAC AAGTTTATAA AGATAGCAGT TATATTTCTA	300
60	AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT	350

	AATAGTTTAG	GCGTTAAAGA	TATAAACATT	CAGGATCGTA	AAATAAAAAA	400
	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	ATTAAAACAA	450
	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	TAAAGAAGAT	500
	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	CAGGAATGCA	550
5	GAAAGACCAA	AGCATAACATA	TTGAAAATTT	AAAATCAGAA	CGTGGTAAAA	600
	TTTTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	ACATATGAGA	650
	TTAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	AAGCAATCGC	700
	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAACAACAAA	TGGATCAAAA	750
	TTGGGTACAA	GATGATACCT	TCGTTCCACT	TTAAAACCGT	TAAAAAAATG	800
10	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	CAACTAATGA	850
	AACAGAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	CATCTATTAG	900
	GTTATGTTGG	TCCCATTAAC	TCTGAAGAAT	TAAAACAAAA	AGAATATAAA	950
	GGCTATAAAG	ATGATGCAGT	TATTGGTAAA	AAGGGACTCG	AAAAACTTTA	1000
	CGATAAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	ATCGTTGACG	1050
15	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	GAAAAAAGAT	1100
	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	AGAGTATTTA	1150
	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	CACCCTCAAA	1200
	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	CGTCTATCCA	1250
	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	CCGAAGATAA	1300
20	AAAAGAACCT	CTGCTCAACA	AGTTCCAGAT	TACAACCTCA	CCAGGTTCAA	1350
	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	AACATTAGAC	1400
	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	AAGATAAATC	1450
	TTGGGGTGTT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	GGTAATATCG	1500
	ACTTAAACAA	AGCAATAGAA	TCATCAGATA	ACATTTTCTT	TGCTAGAGTA	1550
25	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	AAAAACTAGG	1600
	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	GCTCAAATTT	1650
	CAACAAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTC	AGGTTACGGA	1700
	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTCAA	TCTATAGCGC	1750
	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACCTTATTA	AAAGACACGA	1800
30	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	TATCAATCTA	1850
	TTAAATGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	AAGAAGATAT	1900
	TTATAGATCT	TATGCAAACCT	TAATTGGCAA	ATCCGGTACT	GCAGAACTCA	1950
	AAATGAAACA	AGGAGAAAGT	GGCAGACAAA	TTGGGTGGTT	TATATCATAT	2000
	GATAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	AAGATGTACA	2050
35	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	AAAGTGTATG	2100
	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	TGAATAACAA	2150
	AACAGTGAAG	CAATCCGTAA	CGATGGTTGC	TTCACTGTTT	TATTATGAAT	2200
	TATTAATAAG	TGCTGTTACT	TCTCCCTTAA	ATACAATTTT	TTCATTTTCA	2250
	TTGTATGTTG	AAAGTGACAC	TGTAACGAGT	CCATTTTCTT	TTTTTATGGA	2300
40	TTTCTTATTT	GTAATTTTCAG	CGATAACGTA	CAATGTATTA	CCTGGTATAC	2350
	AGTTTAATAA	ATTTAACGTT	ATTCATTTGT	GTTCTTGCTA	CAACTTCTTC	2400
	TCCGTATTTA	CCTTCTTCTA	CCCATAATTT	AAATGATATT	GAAAGTGTAT	2450
	GCATGC					2456

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2) INFORMATION FOR SEQ ID NO: 1179

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

60 ATTTGGTGAC GGGTGACTTT

20

2) INFORMATION FOR SEQ ID NO: 1180

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180

15 TCCACCGTTG CCAATCGCA

19

2) INFORMATION FOR SEQ ID NO: 1181

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181

30 AGCAGCTTAC TAGATGCCGT

20

35 2) INFORMATION FOR SEQ ID NO: 1182

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182

AACTGCAAGA GATCCTTTGG

20

50 2) INFORMATION FOR SEQ ID NO: 1183

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2535 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 175

(C) ACCESSION NUMBER: M18729

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(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	CAACAGTATG	TGGATATTAA	50
10	AAAGCAATAT	CCAGATGCTT	TTTTGCTCTT	TCGGATGGGT	GATTTTTTATG	100
	AATTATTTTA	TGAGGATGCG	GTCAATGCTG	CGCAGATTCT	GGAAATTTCC	150
	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	CCGATCCCTA	TGGCGGGTGT	200
	TCCCTATCAT	TCTGCCCAAC	AGTATATCGA	TGTCTTGATT	GAGCAGGGTT	250
	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	ATCCTAAACA	AGCAGTTGGG	300
15	GTTGTAAAC	GAGAGGTTGT	TCAGGTCATT	ACGCCAGGGA	CAGTGGTCGA	350
	TAGCAGTAAG	CCGGACAGTC	AGAATAATTT	TTTGGTTTCC	ATAGACCGCG	400
	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	ATTTGGTGAC	GGGTGACTTT	450
	TATGTGACAG	GTCTTTTGGA	TTTCACGCTG	GTTTGTGGGG	AAATCCGTAA	500
	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	TGACTTGTCT	GAGGAAGAAG	550
20	AACAAATCCT	CAGCCGCCAG	ATGAATCTGG	TACTCTCTTA	TGAAAAAGAA	600
	AGCTTTGAAG	ACCTTCATTT	ATTGGATTGT	CGATTGGCAA	CGGTGGAGCA	650
	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	TCATCGGACT	CAGATGAGGG	700
	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	ACGAAATTAA	GGATTTCTTG	750
	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	AGAATGCTCG	800
25	CTCAGGTAAG	AAACAAGGCA	GTCTTTTCTG	GCTTTTGGAT	GAAACCAAAA	850
	CGGCTATGGG	GATGCGTCTC	TTGCGTTCTT	GGATTCATCG	CCCCTTGATT	900
	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	GTAGTGCAGG	TCTTTCTCGA	950
	CCATTTCTTT	GAGCGTAGTG	ACTTGACAGA	CAGTCTCAAG	GGTGTTTATG	1000
	ACATTGAGCG	CTTGGCTAGT	CGTGTTCCTT	TTGGCAAAAC	CAATCCAAAG	1050
30	GATCTCTTGC	AGTTGGCGAC	TACCTTGTCT	AGTGTGCCAC	GGATTCGTGC	1100
	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	AGCCTATCTC	ATCGCACAAAC	1150
	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	TTAGCGCAGC	GATTGCTCCT	1200
	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	ATTATCCGGA	CTGGATTTGA	1250
	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	CAGAGAAGGG	ACTAGCTGGA	1300
35	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	ACTCTGGTAT	CAGCACGCTC	1350
	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	TATTTTCATG	TGACCAATTC	1400
	GCAACTGGGA	AATGTGCCAG	CCCACTTTTT	CCGCAAGGCG	ACGCTGAAAA	1450
	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	CCCGTATCGA	GGGAGATATG	1500
	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	GAATACGAAA	TATTTATGCG	1550
40	CATTCGTGAA	GAGGTCGGCA	AGTACATCCA	GCGTTTACAA	GCTCTAGCCC	1600
	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	GTCTGGCGGT	TGTGGCTGAA	1650
	ACCCAGCATT	TGATTGACCC	TGAGTTTGGT	GACGATTCAC	AAATTGATAT	1700
	CCGGAAGGGG	CGCCATGCTG	TCGTTGAAAA	GGTTATGGGG	GCTCAGACCT	1750
	ATATTCCAAA	TACGATTCAG	ATGGCAGAAG	ATACCAGTAT	TCAATTGGTT	1800
45	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	TATATGCGTC	AGTTAGCCAT	1850
	GACGGCGGTT	ATGGCCCAGC	TGGGTTCCCTA	TGTTCCCTGCT	GAAAGCGCCC	1900
	ATTTACCGAT	TTTTGATGCG	ATTTTACCC	GTATCGGAGC	AGCAGATGAC	1950
	TTGGTTTTCG	GTCAGTCAAC	CTTTATGGTG	GAGATGATGG	AGGCCAATAA	2000
	TGCCATTTTC	CATGCGACCA	AGAACTCTCT	CATTCTCTTT	GATGAATTGG	2050
50	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	CTCTTGCTCA	GTCCATCATC	2100
	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	ACCCTCTTTG	CGACCCACTA	2150
	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	ACAACACTTG	GTCAATGTCC	2200
	ACGTGGCAAC	TTTGAGCAG	GATGGGCAGG	TCACCTTCCT	TCACAAGATT	2250
	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	ATCCATGTTG	CCAAGATTGC	2300
55	TGGCTTGCCA	GCAGACCTTT	TAGCAAGGGC	GGATAAGATT	TTGACTCAGC	2350
	TAGAGAATCA	AGGAACAGAG	AGTCCTCCTC	CCATGAGACA	AACTAGTGCT	2400
	GTCACTGAAC	AGATTTCACT	CTTTGATAGG	GCAGAAGAGC	ATCCTATCCT	2450
	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	TATGACACCT	ATGCAGGTTA	2500
60	TGAATGTCTT	AGTAGAGTTA	AAACAGAAAC	TATAA		2535

2) INFORMATION FOR SEQ ID NO: 1184

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 623 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-05

15 (xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
20	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
25	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGAATC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
30	AAACCAATCC	AAAGGATCTC	TTG			623

2) INFORMATION FOR SEQ ID NO: 1185

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 621 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
40 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 45 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-06

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

50	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTCATCG	250
55	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGAATC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
60	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550

CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
AAACCAATCC AAAGGATCTC T 621

5

2) INFORMATION FOR SEQ ID NO: 1186

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 622 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-11

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(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

25 TGACGGGTGA CTTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCAGT ATGTTTCATCG 250
GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTTG 350
GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400
30 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTTGCGT TCTTGATTTC 450
ATCGCCCCTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500
CAGGTCTTTC TCGACCATT TTTTGAGCGT AGTGACTTGA CAGACAGTCT 550
CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
AAACCAATCC AAAGGATCTC TT 622

35

2) INFORMATION FOR SEQ ID NO: 1187

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 622 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

55 TGACGGGTGA CTTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCGGT ATGTTTCATCG 250
GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
60 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTTG 350

	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
5	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
	AAACCAATCC	AAAGGATCTC	TT			622

10 2) INFORMATION FOR SEQ ID NO: 1188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

25	GGGTGACTTT	TATGTAACGG	GGCTATTGGA	TTTCACGTTG	GTTTGTGGGG	50
	AAATTCGCAA	TCTCAAGGCT	AGAGAAGTGG	TGCTGGGTTA	TGACTTGTCT	100
	GAGGAAGAAG	AACAAATCCT	CAGTCGTCAG	ATGAATCTGG	TGCTTTCTTA	150
	TGAGAAGGAA	GGCTTTGAGG	ACCTTCATTT	ACTGGATCCA	CGACTGGCAG	200
30	CTGTGGAGCA	AGCGGCAGCT	AGTAAGCTCC	TCCAGTATGT	TCACCGGACC	250
	CAGATGCGGG	AATTGAACCA	CCTCAAACCA	GTTATCCGCT	ATGAAATCAA	300
	AGATTTCTTA	CAGATGGACT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	350
	AGAATGCCCG	TTCAGGCAAG	AAGCAAGGCA	GTCTTTTCTG	GCTTTTAGAT	400
	GAAACCAAGA	CGGCTATGGG	AATGCGTCTC	TTGCGTTCTT	GGATTCATCG	450
35	TCCTTTGATT	GATAAGGAGC	GAATCGTCCA	GCGTCAAGAG	GTGGTGCAGG	500
	TCTTTCTTGA	CCACTTCTTT	GAGCGTAGTG	ATTTAACGGA	CAGTCTTAAG	550
	GGTGTTTATG	ATATCGAACG	CTTGGCTAGT	CGGGTTTCTT	TTGGCAAGA	599

40

2) INFORMATION FOR SEQ ID NO: 1189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

55 (x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

	GGTGACGGGT	GACTTTTATG	TGACAGGTCT	TTTGGATTTT	ACGCTGGTTT	50
	GTGGGGAAAT	CCGCAATCTC	AAGGCTCGAG	AAGTGGTGCT	GGGTTATGAC	100
	TTGTCTGAGG	AAGAAGAACA	GATCCTTAGT	CGTCAGATGA	ATCTGGTACT	150
60	TTCCTATGAA	AAAGAAGGCT	TTGAAGACCT	TCATTTACTG	GATTCACGAT	200

650

5 TGGCAGCTGT GGAGCAAGCG GCATCTAGTA AACTGCTTCA GTATGTTCAT 250
 CGGACTCAGA TGAGGGAATT GAACCACCTC AAGCCTGTTA TCCGCTATGA 300
 AATCAAAGAT TTTTTCGAGA TGGATTATGC GACCAAGGCT AGTCTGGATT 350
 TGGTTGAGAA TGCCCGTTCA GGCAAGAAGC AAGGTAGTCT TTTTGGCTT 400
 TTGGATGAAA CCAAACAGC TATGGGAATG CGTCTCTTGC GGTCTTGGAT 450
 TCATCGCCCC CTGATTGATA AGGAACGAAT TGTCCAACGC CAAGAAGTTG 500
 TGCAGGTCTT TCTCGACCAT TTCTTTGAGC GTAGTGATTT GACAGACAGT 550
 CTCAAGGGTG TTTATGACAT TGAGCGCTTG GCTAGTCGTG TTTCTTTTGG 600
 CAAAACCAAT CCAAAGGATC TCTT 624
 10

2) INFORMATION FOR SEQ ID NO: 1190

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 25 (B) STRAIN: LSPQ 2583
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

30 TGACGGGTGA CTTTCAGGTG ACTAGTTTAG AGGACTTTGT CTTGGTCTGC 50
 GGGGAAATCC GCAATTTGAA AGCTAGGGAA GTGGTGCTGG GCTATGCCTT 100
 GCCAGAAGCT GAGGAGCAGG TTTTGGCTGG ACAGATGAAC CTTTTACTGT 150
 CCTATGTGGA GAAGGTTTTG GAGGATGTTC AGCTGCTGGG CGAGGAGCTG 200
 TCTCCTATGG AGCGTCAGGC AGCAGGGGAAA CTGCTGGAGT ATGTGCACCG 250
 GACCCAGATG AGGGAGCTCA GCCATTTGAA GAAGGCTCAG CATTATGAAA 300
 35 TCAAGGACTT CCTGCAAATG GACTATGCCA CCAAGGCGAG TCTGGATTTG 350
 ACAGAAAATG CTCGCTCGGG CAAGAAGCAC GGCAGTCTTT ATTGGCTGAT 400
 GGACGAGACT AAGACGGCCA TGGGCGGCCG CATGCTGCGC TCTTGGATCC 450
 AGCGTCCGCT GATTGATGAA GCGCGAATTA GCCAGCGACA GAATGTCGTT 500
 GAGGTTTTTC TGGATCATTT CTTTGAGCGG AGTGATTTGA CGGAGAGCCT 550
 40 CAAGGGGGTC TATGATATCG AGCGGCTGGC TAGTCGGGTG TCTTTTGGC 599

2) INFORMATION FOR SEQ ID NO: 1191

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903
 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

60 TGACGGGTGA CTTTCAGGTG ACTAGTTTAG AGGACTTTGC CCTGGTCTGC 50

	GGGGAAATCC	GTAATTTGAA	GGCTAGGGAA	GTGGTGCTGG	GCTATGCTTT	100
	GCCAGAAGCT	GAGGAGCAGG	TCTTGGCTGG	ACAGATGAAT	CTTTTGCTGT	150
	CCTATGTACA	GACGGCCTTG	GACGATGTCC	AGCTGCTGGG	CGAGGAACTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCGGGGAAA	TTGCTAGAGT	ATGTGCACCG	250
5	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCCCCAG	CATTATGAAA	300
	TCAAGGACTT	TCTGCAAATG	GATTATGCTA	CCAAGGCGAG	TCTGGATTTG	350
	ACAGAAAATG	CTCGCTCGGG	TAAGAAACAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACC	AAGACGGCCA	TGGGCGGCCG	TATGCTGCGC	TCTTGGATCC	450
	AGCGTCCGTT	GATTGATGAA	GTGCGAATTA	GCCAGCGGCA	GAATGTCGTC	500
10	GAGGTTTTTC	TGGAACATTT	CTTTGAGCGG	AGTGATTTGA	CGGAGAGCCT	550
	CAAGGGAGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGCA	600
	AGACCAATCC	AAAGGATCTC	TT			622

15

2) INFORMATION FOR SEQ ID NO: 1192

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - 20 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

GGTAAAACAG GAACCTCTAA CT

22

30

2) INFORMATION FOR SEQ ID NO: 1193

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

GGTAAGACAG GTACTTCTAA CT

22

45

2) INFORMATION FOR SEQ ID NO: 1194

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

55

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

60

5 2) INFORMATION FOR SEQ ID NO: 1195

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

CATTTCAGT AACACAACAG AATC

24

20

2) INFORMATION FOR SEQ ID NO: 1196

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTTCAGT GTAATACAAC AGAA

24

35

2) INFORMATION FOR SEQ ID NO: 1197

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1198

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

	AACGGGCGTC	TCGATAGAAA	AACACGTGAA	AATCCCAATG	ATTATAAACA	50
10	ATCAATATAC	GATTTTGCTG	AAGCTGTAAC	AAAAGGTATT	AAGGAACAAA	100
	CAAATAAAAA	TTAATAGGCA	ACTTAACCAG	AATCGTTAAA	ACTATATGAC	150
	GATTCTGGTT	TTTTAAATTC	AAAAAGTTTT	CTAAAAAATT	TACTTGCTTC	200
	TTTAAAGTAT	AGGTATGAAA	TACAATTGAT	TAAAATAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAATACT	GCCTTTATAC	TTTACCTAT	TACTTTTAT	300
15	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTGCCA	ATCACAKGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT	A		381

20 2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC 25

35 2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200

TCAAAGAAGA AACTAAAAAA GCTGT 25

50 2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201

AACGTAGGTG TCCTTCTTC

19

5

2) INFORMATION FOR SEQ ID NO: 1202

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202

20 GTGTTGAAAT GTTCCGTAAA CA

22

2) INFORMATION FOR SEQ ID NO: 1203

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203

35

GGIGARMGIG GIAAYGARAT G

21

40 2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

55

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid

50

655

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

10

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGTIG ARTCIGCCA

19

25

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

40

CCITCITCWC CIGGCATYTC

20

2) INFORMATION FOR SEQ ID NO: 1208

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

55

TCAAAAAGTT TTCTAAAAAA TTTAC

25

60 2) INFORMATION FOR SEQ ID NO: 1209

656

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

ACGGGCGTCC ACAAATCAA TAGGA

25

15

2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG

22

30

2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTA CAGGCTTTGA TCCC

24

45

2) INFORMATION FOR SEQ ID NO: 1212

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

60 CCICCIRGIG GIGAIACIGC WCC

23

2) INFORMATION FOR SEQ ID NO: 1213

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

15

AARGGIGGIA CIGCIGCIAT HCCIGG

26

20 2) INFORMATION FOR SEQ ID NO: 1214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

30

GGTAAAACAG GTACCTCTAA CTA

23

35

2) INFORMATION FOR SEQ ID NO: 1215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: D471
 (C) ACCESSION NUMBER: X65717

50

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

	AACAAAATAA AAGAACTTAC CTATTTTCCA TCCAAAATGT TTAGCAATCA	50
	TCATCTGCAA GGCAACGTAT TGCATGGCAT TGATGTGATG AGCAACTAAT	100
55	ATGTCATTAG AACGTTGCGT CAACTAGCA TCTAAATAAA GATCGAAATG	150
	CAGTTATCAA AAATGCAAGC TCCTATCGGC CCTTGTTTTA ATTATTACTC	200
	ACATTGCCTT AATGTATTTA CTTGCTTATT ATTAACCTTT TTGCTAAGTT	250
	AGTAGCGTCA GTTATTCATT GAAAGGACAT TATTATGAAA ATTCTTGTA	300
	CAGGCTTTGA TCCCTTTGGC GGCGAAGCTA TTAATCCTGC CCTTGAAGCT	350
60	ATCAAGAAAT TGCCAGCAAC CATTCATGGA GCAGAAATCA AATGTATTGA	400

	AGTTCCAACG	GTTTTTCAAA	AATCTGCCGA	TGTGCTCCAG	CAGCATATCG	450
	AAAGCTTTCA	ACCTGATGCA	GTCCTTTGTA	TTGGGCAAGC	TGGTGGCCGG	500
	ACTGGACTAA	CGCCAGAACG	CGTTGCCATT	AATCAAGACG	ATGCTCGCAT	550
	TCCTGATAAC	GAAGGGAATC	AGCCTATTGA	TACACCTATT	CGTGCAGATG	600
5	GTAAAGCAGC	TTATTTTTC	ACCTTGCCAA	TCAAAGCGAT	GGTTGCTGCC	650
	ATTCATCAGG	CTGGGCTTCC	TGCTTCTGTT	TCTAATACAG	CTGGTACCTT	700
	TGTTTGCAAT	CATTTGATGT	ATCAAGCCCT	TTACTTAGTG	GATAAATATT	750
	GTCCAAATGC	CAAAGCTGGG	TTTATGCATA	TTCCCTTTAT	GATGGAACAG	800
	GTTGTTGATA	AACCTAATAC	AGCTGCCATG	AACCTCGATG	ATATTACAAG	850
10	AGGAATTGAG	GCTGCTATTT	TTGCCATTGT	CGATTTCAAA	GATCGTTCCG	900
	ATTTAAAACG	TGTAGGGGGC	GCTACTCACT	GACTGTGACG	CTACTAAACC	950
	TATTTTAAAA	AAACAGAGAT	ATGAACAAAC	TCTGTTTTTT	TTGTGCTAAA	1000
	AATGAAAGAC	CTAGGGAAAC	TTTTCATCGG	TCTTTCTCAA	TTGTCATCTT	1050
	AATCTAATAC	TACTTCTAAC	ATCAGCGGGT	ATAGTTTGCC	AGTAATTAAG	1100
15	AAACGTTGTT	GATCTAAATG	AGCAATCCCA	TTCAAAACAT	TAAGGTCAGG	1150
	GTAATGGGAC	TTATCAAGAT	TTAAGGCTTT	TAACAAAGGA	CTAATATCAT	1200
	AGGTGGCTAC	CACCTTTCCA	GAATCAGGTT	GGAGTTTGAC	AATAGTATTG	1250
	GTTTGCCAAA	TATTGGCATA	GAGATAACCA	TCTACATACT	CTAATTCGTT	1300
	AAGCATTGAG	ATAGGGACAC	TTTCTATAGC	AACTAGT		1337

20

2) INFORMATION FOR SEQ ID NO: 1216

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

35 GGTAAGACTG GTACATCAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1217

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217

50

CAAATGCCAT TTCAAGTAAC ACAAC

25

55 2) INFORMATION FOR SEQ ID NO: 1218

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

60

659

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218

CAAACGCCAT TTCAAGTAAC ACAAC

25

10

2) INFORMATION FOR SEQ ID NO: 1219

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219

CAAATGCTAT TTCAAGTAAT ACAAC

25

25

2) INFORMATION FOR SEQ ID NO: 1220

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGCCAT TTCAAGTAAT ACGAC

25

40

2) INFORMATION FOR SEQ ID NO: 1221

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

55 GAYACICCG GICAYGTIGA YTT

23

60

2) INFORMATION FOR SEQ ID NO: 1222

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222
10 ATYGAYACIC CIGGICAYGT IGAYTT 26

15 2) INFORMATION FOR SEQ ID NO: 1223

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223
AYITCIARRT GIARYTCRCC CATICC 26

30 2) INFORMATION FOR SEQ ID NO: 1224

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224
CCIGYIHTIY TIGARCCIAT IATG 24

45 2) INFORMATION FOR SEQ ID NO: 1225

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225
TAICCRAACA TYTCISMIAR IGGIAC 26

60

2) INFORMATION FOR SEQ ID NO: 1226

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226

15 GTIRMRTAIC CRAACATYTC

20

2) INFORMATION FOR SEQ ID NO: 1227

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227

30

GTICCIYTIK CIGARATGTT YGGITA

26

35 2) INFORMATION FOR SEQ ID NO: 1228

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228

GTICCIYTIK CIGARATGTT YGGITAYGC

29

50 2) INFORMATION FOR SEQ ID NO: 1229

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229

TCCATYTGIG CIGCICCI GT IATCAT

26

5 2) INFORMATION FOR SEQ ID NO: 1230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2145 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (D) ACCESSION NUMBER: X00415

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

20 TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT 50
 CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA 100
 CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAA CCATAAAATC 150
 GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA 200
 25 GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG 250
 GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG 300
 GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCCATGC GTGTTCTCGA 350
 TGGTGCGGTA ATGGTTTACT GCGCAGTTGG TGGTGTTTCA CCGCAGTCTG 400
 AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCCGCG CATTGCGTTC 450
 30 GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCCTGAAAG TTGTTAACCA 500
 GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG 550
 GTGCTGAAGA ACATTTTACC GGTGTTGTTG ACCTGGTGAA AATGAAAGCT 600
 ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT 650
 CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG 700
 35 AATCCGCAGC TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT 750
 GAAGAACTGA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT 800
 GAACAACGAA ATCATCCTGG TAACCTGTGG TTCTGCGTTC AAGAACAAAG 850
 GTGTTTCAAGC GATGCTGGAT GCGGTAATTG ATTACCTGCC ATCCCCGGTT 900
 GACGTACCTG CGATCAACGG TATCCTGGAC GACGGTAAAG ACACTCCGGC 950
 40 TGAACGTCAC GCAAGTGATG ACGAGCCGTT CTCTGCACTG GCGTTCAAAA 1000
 TCGCTACCGA CCCGTTTGTT GGTAACCTGA CCTTCTTCCG TGTTTACTCC 1050
 GGTGTGGTTA ACTCTGGTGA TACCGTACTG AACTCCGTGA AAGCTGCACG 1100
 TGAGCGTTTC GGTCGTATCG TTCAGATGCA CGCTAACAAA CGTGAAGAGA 1150
 TCAAAGAAGT TCGCGCGGGC GACATCGCTG CTGCTATCGG TCTGAAAGAC 1200
 45 GTAACCACTG GTGACACCCT GTGTGACCCG GATGCGCCGA TCATTCTGGA 1250
 ACGTATGGAA TTCCCTGAGC CGGTAATCTC CATCGCAGTT GAACCGAAAA 1300
 CCAAAGCTGA CCAGGAAAAA ATGGGTCTGG CTCTGGGCCG TCTGGCTAAA 1350
 GAAGACCCGT CTTTCCGTGT ATGGACTGAC GAAGAATCTA ACCAGACCAT 1400
 CATCGCGGGT ATGGGCGAAC TGCACCTCGA CATCATCGTT GACCGTATGA 1450
 50 AGCGTGAATT CAACGTTGAA GCGAACGTAG GTAAACCGCA GGTTGCTTAC 1500
 CGTGAAACTA TCCGCCAGAA AGTTACCGAT GTTGAAGGTA AACACGCGAA 1550
 ACAGTCTGGT GGTCGTGGTC AGTATGGTCA TGTTGTTATC GACATGTACC 1600
 CGCTGGAGCC GGGTTCAAAC CCGAAAGGCT ACGAGTTCAT CAACGACATT 1650
 AAAGGTGGTG TAATCCCTGG CGAATACATC CCGGCCGTTG ATAAAGGTAT 1700
 55 CCAGGAACAG CTGAAAGCAG GTCCGCTGGC AGGCTACCCG GTAGTAGACA 1750
 TGGGTATTCT TCTGCACTTC GGTTCTTACC ATGACGTTGA CTCCTCTGAA 1800
 CTGGCGTTTA AACTGGCTGC TTCTATCGCC TTAAAGAAG GCTTTAAGAA 1850
 AGCGAAACCA GTTCTGCTTG AGCCGATCAT GAAGGTTGAA GTAGAAACTC 1900
 CGGAAGAGAA CACCGGTGAC GTTATCGGTG ACTTGAGCCG TCGTCGTGGT 1950
 60 ATGCTCAAAG GTCAGGAATC TGAAGTTACT GCGGTTAAGA TCCACGCTGA 2000

AGTACCGCTG	TCTGAAATGT	TCGGATACGC	AACTCAGCTG	CGTTCTCTGA	2050
CCAAAGGTCG	TGCATCATAC	ACTATGGAAT	TCCTGAAGTA	TGATGAAGCG	2100
CCGAGTAACG	TTGCTCAGGC	CGTAATTGAA	GCCCGTGGTA	AATAA	2145

5

2) INFORMATION FOR SEQ ID NO: 1231

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

20 GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC 37

2) INFORMATION FOR SEQ ID NO: 1232

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

35 GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC 42

2) INFORMATION FOR SEQ ID NO: 1233

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233

50 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

55 2) INFORMATION FOR SEQ ID NO: 1234

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

664

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234

ACTAAATAAA CGCTCATTCG

20

10

2) INFORMATION FOR SEQ ID NO: 1235

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235

GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC

38

25

2) INFORMATION FOR SEQ ID NO: 1236

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTCG CGTTGGTGGC TCGC

34

40

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

55 GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

60

2) INFORMATION FOR SEQ ID NO: 1238

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238
10 GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC 38

15 2) INFORMATION FOR SEQ ID NO: 1239

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239
GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC 33

30 2) INFORMATION FOR SEQ ID NO: 1240

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240
GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC 38

45 2) INFORMATION FOR SEQ ID NO: 1241

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241
GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC 35

60

2) INFORMATION FOR SEQ ID NO: 1242

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (E) STRAIN: BM4147-1
 (F) ACCESSION NUMBER: U39790

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

20	TTCTTAGAGA	CATTGAATAT	GCCTTATGTC	GGCGCAGGCG	TATTGACCAG	50
	TGCATGTGCC	ATGGATAAAA	TCATGACCAA	GTATATTTTA	CAAGCTGCTG	100
	GTGTGCCGCA	AGTTCCTTAT	GTACCACTAC	TTAAGAATCA	ATGGAAAGAA	150
	AATCCTAAAA	AAGTATTTGA	TCAATGTGAA	GGTTCCTTGC	TTTATCCGAT	200
	GTTTGTCAAA	CCTGCGAATA	TGGGTTCTAG	TGTCGGCATT	ACAAAGGCAG	250
25	AAAACCGAGA	AGAGCTGCAA	AATGCTTTAG	CAACAGCCTA	TCAGTATGAT	300
	TCTCGAGCAA	TCGTTGAACA	AGGAATTGAA	GCGCGCGAAA	TCGAAGTTGC	350
	TGTATTAGGA	AATGAAGATG	TTCGGACGAC	TTTGCCTGGC	GAAGTCGTAA	400
	AAGACGTAGC	ATTCTATGAT	TATGAAGCCA	AATATATCAA	TAATAAAATC	450
	GAAATGCAGA	TTCCAGCCGA	AGTGCCGGAA	GAAGTTTATC	AAAAAGCGCA	500
30	AGAGTACGCG	AAGTTAGCTT	ACACGATGTT	AGGTGGAAGC	GGATTGAGCC	550
	GGTGCGATTT	CTTTTTGACA	AATAAAAATG	AATTATTCCT	GAATGAATTA	600

35 2) INFORMATION FOR SEQ ID NO: 1243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2275 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (C) ACCESSION NUMBER: M38386

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

50

	GGTACCAAAG	AAAAAAACGA	ACGCCACAAC	CAACAGCCTC	TAAAGCAACA	50
	CCTGCTTCTG	AAATTGAGGG	AGATTTAGCA	AATGTCAATG	AGATTCTTTT	100
	GGTTCACGAT	GATCGTGTCG	GGTCAGCAAC	GATGGGAATG	AAAGTCTTAG	150
	AAGAAATTTT	AGATAAAGAG	AAAATTTCAA	TGCCGATTCG	AAAAATTAAT	200
55	ATTAATGAAT	TAACCTAACA	AACACAGGCT	TTAATTGTCA	CAAAAGCTGA	250
	ACTAACGGAA	CAAGCACGTA	AAAAAGCACC	GAAAGCGACA	CACTTATCAG	300
	TAAAAAGTTA	TGGTTAATCC	CCAAAAATAT	GAAACAGTGG	GTTTCGCTCT	350
	TAAAAGAAAG	TGCCTAGAGA	GGAAGAAAAC	AATGGAAAAT	CTTACGAATA	400
	TTTCAATTGA	ATTAAATCAA	CAGTTTAATA	CAAAAGAAGA	AGCTATTCGC	450
60	TTTTCGCGCC	AGAAACTAGT	CGAGGCAGGC	TGTGTTGAGC	CCGCTTATAT	500

	CGAAGCAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCCCAT	ATGGGGAATT	550
	TTATTGCCAT	TCCTCATGGA	ACAGAAGAAG	CCAAAAAATT	AGTGAAAAAA	600
	TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCGA	650
	AGAAGATGAA	AAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
5	AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
	GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800
	AAATTTAGCC	ATTGCTTAAA	GGAGAGAATA	AGAATGAACG	CAGTACATTT	850
	TGGAGCAGGA	AATATTGGAC	GCGGCTTTAT	TGGCGAAATT	TTAGCTAAAA	900
	CGGGTTTCAT	ATTACCGTTT	GTGGATGTTA	ATGGAAACCA	TCATCAAGCG	950
10	TTAAAAGAAC	GTAAAAGTTA	TACAATTGAA	TTGGCCGATG	CCTCACATCA	1000
	ACAAATTAAC	GTTGAAAATG	TGACCGGGTT	AAATAACATG	ACAGAACCAG	1050
	AAAAAGTAGT	AGAAGCAATT	GCGGAAGCCG	ATTTAGTCAC	GACGGCAATT	1100
	GGTCCTAATA	TTTTACCAAG	AATTGCTGAA	TTAATTGCTC	AAGGAATTGA	1150
	TGCACGTGCC	GAAGCAAATT	GTCAAAACGG	CCCGCTGGAT	ATTATCGCTT	1200
15	GTGAAAATAT	GATTGGTGGT	TCAACCTTTT	TAGCAGAAGA	AGTGGCCATA	1250
	ATATTTGAAA	AACCCAGCTT	ATCTGAACAA	TGGATTGGTT	TTCCTGATGC	1300
	GGCAGTTGAT	CGGATTGTTC	CATTACAAAA	ACATAAAGAT	CCACTTTTTG	1350
	TTCAAGTTGA	GCCTTTTTGT	GAATGGGTCA	TTGATGATAC	CAACCGAAAA	1400
	GCCAAAGAGA	TTCAGTTAGA	AGGCGTCATT	ACTTGTGCGAT	TAGAGCCGTA	1450
20	TATTGAACGA	AAATTATTTA	GTGTAACCAG	TGGCCATGCT	ACAGTTGCCT	1500
	ATACAGGGGC	GTTGTTAGGC	TATCAAACCA	TTGACGAAGC	GATGCAGGAC	1550
	GCCTTAGTGG	TAGCGCAACT	CAAATCAGTT	TTGCAGGAAA	CCGGTAAACT	1600
	TTTAGTGGCC	AAATGGAATT	TTGATGAACA	AGAACATGCA	GCCTATATTG	1650
	AAAAAATTAT	CAACCGTTTC	CAAATAAAT	ATATTTCAGA	TGCTATTACA	1700
25	CGTGTAGCAC	GGACACCAAT	CAGAAAATTA	GGTGCGCAAG	AACGGTTTAT	1750
	TCGACCAATC	CGTGAATTAC	AGGAACGCAA	TCTAGTGTCG	GCCGCATTTA	1800
	TAGCAATGAT	TGGTATTGTC	TTTAATTATC	ATGATCCAGA	AGATGAACAA	1850
	AGCCGTCAAT	TACAGGAAAT	GCTTGACCAA	GAAAGTGTTG	ATACAGTGGA	1900
	TCGCTGAAGT	AACGGGCATT	GAAGATCCAG	AAACGGTTAA	AAATATTAAA	1950
30	CAAAACGTAG	AACTGCTATG	CGCGACCACA	AGTAGCATAA	TTAACAAAAT	2000
	CCTTCTACCA	AGATACTTCA	CATTTCTTAA	TTAAAGAAAA	AACAACCGCG	2050
	CCTCACCTGA	GCCGACCCCC	AAAAGTTAGA	CCTAGAAATC	TAACTTTTGG	2100
	AGGTTTTTTT	GTATGGCAAA	ATACAGTTTT	GAAATTTAAA	CTTAAACTTG	2150
	TTCATGACTA	CTTATATGGT	CAAGGAGGTC	TAAGGTTTCT	CGCAAAGAAG	2200
35	TATGGGTTTA	AAGATAGTCT	CAAATAAGCA	AATGGATAAA	TGCCTATAAA	2250
	GAAC TTGGTG	AAGAAGGGGG	GATCC			2275

40 2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

55	GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
	TTGCGGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
	AATCTCATT	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
	CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
60	CCAGCCAAAA	CGATATTTTT	ATAATCATTA	CGTGAAAAAG	GTTTCCCTTC	250

ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

2) INFORMATION FOR SEQ ID NO: 1245

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245

GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAGAG 50
 CAACGAAAAC GGAACAAGCA TTAACCTAAC ATTTGAAGTT GCACTTCATT 100
 TAGGTGATGA CACAGTTCGT ACAGTTGCAA TGTCTTCCAC AGATGGACTT 150
 20 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
 TGGTGATGCA ACACTTGGTC GTGTATTAA CGTATTAGGT GATGCAATTG 250
 ACTTAGATGG TGAGGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
 CAAGCACCTG CATTCTGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350
 TGGTATTAAA GTAGTAGACT TACTTGCTCC TTACATTAAG GGTGGTAAGA 400
 25 TCGGTCTATT CGGTGGTGCC GGTGTAGGTA AAACGGTATT AATTCAGGAA 450
 TTAATCAATA ACATCGCACA AGAACACGGT GGTATCTCTG TATTCGCTGG 500
 TGTAGGTGAG CGTACTCGTG AGGGTAATGA CTTATACCAC GAAATGAGCG 550
 ATTCTGGCGT AATTAAGAAA ACTGCGATGG TATTCGGACA AATGAACGAG 600
 CCACCTGGAG CACGTCAACG TGTGCGTTA ACAGGTTTAA CAATGGCTGA 650
 30 GCATTTCCGT GATGAGCAAG GACAAGATGT ACTTCTGTTC ATCGATAATA 700
 TCTTCCGTTT CACGCAAGCA GGTCTGAAG TATCTGCCCT TCTTGGCCGT 750
 ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA 800
 ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTC 845

35

2) INFORMATION FOR SEQ ID NO: 1246

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 11986

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246

TGCACTTCAT TTAGGTGATG ACACAGTTCG TACAGTTGCA ATGTCTTCCA 50

5 CAGATGGACT TGTTTCGTGGC ACAGAAGTAG AAGATACTGG TAAAGCAATC 100
TCTGTACCAG TTGGTGATGT AACACTTGGT CGTGTATTTA ACGTATTAGG 150
TGATGCAATT GACTTAGATG GTGATGTTCC TGCGGATGTA CGTCGTGATC 200
CAATTCACCG TCAAGCGCCT GCATTCGAAG AGTTATCTAC TAAAGTAGAA 250
ATTCTTGAAA CTGGTATTAA AGTAGTAGAC TTAAGTCTCT CTTACATTAA 300
GGGTGGTAAG ATTGGTCTAT TCGGTGGTGC CGGCGTAGGT AAAACAGTAT 350
TAATTCAGGA ATTAATTAAT AACATCGCAC AAGAGCACGG TGGTATCTCT 400
GTATTCGCTG GTGTAGGTGA GCGTACTCGT GAAGGTAACG ACTTATACCA 450
CGAAATGAGC GATTCTGGCG TAATTAAGAA AACTGCGATG GTATTCGGAC 500
10 AAATGAACGA GCCACCTGGA GCACGTCAAC GTGTTGCATT AACAGGTTTA 550
ACAATGGCTG AACATTTCCG TGATGAGCAA GGACAAGACG TACTATTGTT 600
CATCGATAAC ATCTTCCGTT TCACGCAAGC GGGTTCTGAA GTATCTGCCC 650
TTCTTG 656

15

2) INFORMATION FOR SEQ ID NO: 1247

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247

CGAAAACGGA AGTATTAACT TAACATTTGA AGTTGCACTT CATTTAGGTG 50
ATGATACAGT TCGTACAGTT GCGATGTCTT CCACAGATGG ACTTGTTTCGT 100
35 GGCACAGAAG TAGAAGATAC TGGTAAACCA ATCTCTGTAC CAGTTGGTGA 150
TGTAACACTT GGTCGCGTAT TTAACGTATT AGGTGATGCA ATTGACTTAG 200
ATGGTGAGGT TCCTGCAGAT GTACATCGTG ATCCAATTCA CCGTCAAGCA 250
CCTGCATTCG AAGAATTATC TACTAAAGTA GAAATTCTTG AAAGTGGTAT 300
TAAAGTAGTA GACTTACTTG CTCCTTACAT TAAGGGTGGT AAGATCGGCC 350
40 TATTCGGTGG TGCCGGCGTA GGTAACACAG TATTAATTCA GGAATTAATT 400
AACAACATCG CACAAGAGCA CCGTGGTATC TCTGTATTCG CTGGTGTAGG 450
TGAGCGTACT CGTGAGGGTA ATGACTTATA CCACGAAATG AGCGATTCTG 500
GCGTAATCAA GAAAACTGCG ATGGTATTCG GACAAATGAA CGAGCCACCT 550
GGAGCACGTC AACGTGTTGC ATTAACAGGT TTAACAATGG CTGAGCATTT 600
45 CCGTGATGAG CAAGGACAAG ACGTACTTCT GTTCATCGAT AACATCTTCC 650
GTTTCACGCA AGCGGGTTCT GAAGTATCTG CCCTTCTTGG TCGTATGCCA 700
TCTGCGGTAG GTTACCAACC AACACTTGCA ACAGAAATGG GTCAATTACA 750
AGAGCGTATT ACATCTACAA ATAAAGGGTC TATCACGTCT A 791

50

2) INFORMATION FOR SEQ ID NO: 1248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: BGSC 4AC1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248

15	ATCTACAATG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAAGCATGAA	50
	CTTAACATTT	GAAGTTGCAC	TTCATTTAGG	TGATGATACA	GTTTCGTACAG	100
	TTGCGATGTC	TTCCACAGAT	GGACTTGTTT	GTGGCACAGA	AGTAGAAGAT	150
	ACTGGTAAAG	CAATCTCTGT	ACCAGTTGGT	GATGCAACAC	TTGGACGTGT	200
	ATTCAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAA	CTTCCTGCGG	250
20	ATGTACACCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAC	AGTATTAATT	CAGGAGTTAA	TCAATAACAT	CGCACAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
25	TAATGACTTA	TACCACGAAA	TGAGCGATTC	TGGCGTAATC	AAGAAAAC TG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
	GCATTAACAG	GTTTAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTA CTT	CTGTT CATCG	ATAACATCTT	CCGTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
30	CCAACACTTG	CAACAGAAAT	GGGTCAATTA	CAAGAGCGTA	TTACATCTAC	800
	AAATAAAGGG	TCTATCACGT	CTATC			825

35 2) INFORMATION FOR SEQ ID NO: 1249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249

50	ATCTACAACG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAAGTATTAA	50
	CTTAACATTT	GAAGTTGCAC	TTCATTTAGG	TGATGATACA	GTTTCGTACAG	100
	TTGCGATGTC	TTCCACAGAT	GGACTTGTTT	GTGGCACAGA	AGTAGAAGAT	150

	ACTGGTAAAC	CAATCTCTGT	ACCAGTTGGT	GATGTAACAC	TTGGTCGCGT	200
	ATTTAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAG	GTTCCTGCAG	250
	ATGTACATCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
5	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAAC	AGTATTAATT	CAGGAATTAA	TTAACAACAT	CGCACAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
	TAATGACTTA	TACCACGAAA	TGAGCGATTC	TGGCGTAATC	AAGAAAACCTG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
10	GCATTAACAG	GTTTAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTACTT	CTGTTTCATCG	ATAACATCTT	CCGTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
	CCAACACTTG	CAACAGAAAT	GGGTC			775

15

2) INFORMATION FOR SEQ ID NO: 1250

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 832 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10204

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250

	CCAGCAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAGC	50
	GAGCATCAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	GATGACACAG	100
35	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTCTG	TGGCACAGAA	150
	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	ATGTAACACT	200
	TGGTCGCGTA	TTCAACGTAT	TAGGTGATGC	AATTGACTTA	GATGGTGATG	250
	TTCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	ACCTGCATTC	300
	GAAGAACTAT	CTACAAGAAT	AGAAATTCTT	GAAACTGGTA	TTAAAGTAGT	350
40	AGATTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACG	GTATTAATTC	AGGAATTAAT	TAACAACATC	450
	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	GTGAGCGTAC	500
	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	GGCGTAATTA	550
	AGAAAACCTGC	GATGGTATTT	GGACAAATGA	ACGAGCCACC	TGGAGCACGT	600
45	CAACGTGTTG	CATTAACAGG	TTTAACAATG	GCTGAACATT	TCCGTGATGA	650
	GCAAGGACAA	GACGTACTAT	TGTTTCATCGA	TAACATCTTC	CGTTTCACGC	700
	AAGCAGGTTC	TGAAGTATCT	GCCCTTCTTG	GTCGTATGCC	ATCTGCGGTA	750
	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	AAGAGCGTAT	800
	TACATCTACA	AATAAAGGGT	CTATCACGTC	TA		832

50

2) INFORMATION FOR SEQ ID NO: 1251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251

15 AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100
 AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA GAAGTAGAAG 150
 ATACTGGTAA ACCAATCTCT GTACCAGTTG GTGATGTAAC ACTTGGTCGC 200
 20 GTATTTAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG AGGTTCCCTGC 250
 AGATGTACAT CGTGATCCAA TTCACCGTCA AGCACCTGCA TTCGAAGAAT 300
 TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT AGTAGACTTA 350
 CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTCG GTGGTGCCGG 400
 CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATTAACAAC ATCGCACAAAG 450
 25 AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG TACTCGTGAG 500
 GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA TCAAGAAAAC 550
 TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA CGTCAACGTG 600
 TTGCATTAAC AGGTTTAAAC ATGGCTGAGC ATTTCCGTGA TGAGCAAGGA 650
 CAAGACGTAC TTCTGTTCAT CGATAACATC TTCCGTTTCA CGCAAGCGGG 700
 30 TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG GTAGGTACC 750
 AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG TATTACATCT 800
 AC 802

35

2) INFORMATION FOR SEQ ID NO: 1252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252

AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100

	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	GAAGTAGAAG	150
	ATACTGGTAA	ACCAATCTCT	GTACCAGTTG	GTGATGTAAC	ACTTGGTCGC	200
	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	AGGTTCCCTGC	250
	AGATGTACAT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	TTCGAAGAAT	300
5	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	AGTAGACTTA	350
	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCG	GTGGTGCCGG	400
	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATTAACAAC	ATCGCACAAAG	450
	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	TCAAGAAAAC	550
10	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	CGTCAACGTG	600
	TTGCATTAAC	AGGCTTAACA	ATGGCTGAGC	ATTTCCGTGA	TGAGCAAGGA	650
	CAAGACGTAC	TTCTGTTCAT	CGATAACATC	TTCCGTTTCA	CGCAAGCGGG	700
	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	GTAGGTACC	750
	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	TATTACATCT	800
15	ACAAATAAAG	GGTCTATCAC	GTC			823

2) INFORMATION FOR SEQ ID NO: 1253

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253

35	CCAGAAATCT	ACAATGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	CATGAACTTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCGTGG	CACAGAAGTA	150
	GAAGATACTG	GTAAAGCAAT	CTCTGTACCA	GTTGGTGATG	CAACACTTGG	200
	ACGTGTATTC	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAAC TTC	250
40	CTGCGGATGT	ACACCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
	CCGGCGTAGG	TAAACAGTA	TTAATTCAGG	AATTAATCAA	TAACATCGCA	450
	CAAGAGCATG	GTGGTATCTC	TGTATTTCGCT	GGTGTAGGTG	AGCGTACTCG	500
45	TGAGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
	AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
50	TACCAACCGA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATT	798

2) INFORMATION FOR SEQ ID NO: 1254

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 767 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 7064

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254

	CATTTGAAGT	TGCACTTCAT	TTAGGTGATG	ACACAGTTCG	TACAGTTGCA	50
	ATGTCTTCCA	CAGATGGACT	TGTTCGTGGC	ACAGAAGTAG	AAGATACTGG	100
	TAAAGCAATC	TCTGTACCAG	TTGGTGATGC	AACACTTGGT	CGTGTATTTA	150
20	ACGTATTAGG	TGATGCAATT	GACTTAGATG	GTGAGGTTCC	TGCGGATGTA	200
	CGTCGTGATC	CAATTCACCG	TCAAGCACCT	GCATTCGAAG	AATTATCTAC	250
	TAAAGTAGAA	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TACTTGCTC	300
	CTTACATTAA	GGGTGGTAAG	ATCGGTCTAT	TCGGTGGTGC	CGGTGTAGGT	350
	AAAACGGTAT	TAATTCAGGA	ATTAATCAAT	AACATCGCAC	AAGAACACGG	400
25	TGGTATCTCT	GTATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAGGGTAATG	450
	ACTTATACCA	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	500
	GTATTCGGAC	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCGTT	550
	AACAGGTTTA	ACAATGGCTG	AGCATTTCCG	TGATGAGCAA	GGACAAGACG	600
	TACTTCTGTT	CATCGATAAT	ATCTTCCGTT	TCACGCAAGC	AGGTTCTGAA	650
30	GTATCTGCCC	TTCTTGGCCG	TATGCCATCT	GCGGTAGGTT	ACCAACCAAC	700
	ACTTGCAACA	GAAATGGGTC	AATTACAAGA	GCGTATTACA	TCTACAAATA	750
	AAGGGTCTAT	CACGTCT				767

35

2) INFORMATION FOR SEQ ID NO: 1255

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1174 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: C-14

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255

	GAAATGCGTG	AATCATTTTT	AGATTATGCG	ATGAGTGTTA	TCGTTGCTCG	50
	TGCATTGCCA	GATGTTTCGTG	ACGGTTTAAA	ACCAGTACAT	CGTCGTATAC	100

	TATATGGATT	AAATGAACAA	GGTATGACAC	CGGATAAATC	ATATAAAAAA	150
	TCAGCACGTA	TCGTTGGTGA	CGTAATGGGT	AAATATCACC	CTCATGGTGA	200
	CTTATCTATT	TATGAAGCAA	TGGTACGTAT	GGCTCAAGAT	TTCAGTTATC	250
	GTTATCCGCT	TGTTGATGGC	CAAGGTAACT	TTGGTTCAAT	GGATGGAGAT	300
5	GGCGCAGCAG	CAATGCGTTA	TACTGAAGCG	CGTATGACTA	AAATCACACT	350
	TGAACTGTTA	CGTGATATTA	ATAAAGATAC	AATAGATTTT	ATCGATAACT	400
	ATGATGGTAA	TGAAAGAGAG	CCGTCAGTCT	TACCTGCTCG	ATTCCCTAAC	450
	TTATTAGCCA	ATGGTGCATC	AGGTATCGCG	GTAGGTATGG	CAACGAATAT	500
	TCCACCACAT	AACCTAACAG	AATTAATCAA	TGGTGTACTT	AGCTTAAGTA	550
10	AGAACCCTGA	TATTTCAATT	GCTGAGTTAA	TGGAGGATAT	TGAAGGTCCT	600
	GATTTCCCAA	CTGCTGGACT	TATTTTAGGT	AAGAGTGGTA	TTAGACGTGC	650
	ATATGAAACA	GGTCGTGGTT	CAATTCAAAT	GCGTTCTCGT	GCAGTTATTG	700
	AAGAACGTGG	AGNCGGACGT	CAACGTATTG	TTGTCACTGA	AATTCCTTTC	750
	CAAGTGAATA	AGGCTCGTAT	GATTGAAAAA	ATTGCAGAGC	TCGTTCTGTA	800
15	CAAGAAAATT	GACGGTATCA	CTGATTTACG	TGATGAAACA	AGTTTACGTA	850
	CTGGTGTGCG	TGTCGTTATT	GATGTGCGTA	AGGATGCAAA	TGCTAGTGTC	900
	ATTTTAAATA	ACTTATACAA	ACAAACACCT	CTTCAAACAT	CATTTGGTGT	950
	GAATATGATT	GCACTTGTA	ATGGTAGACC	GAAGCTTATT	AATTTAAAAG	1000
	AAGCGTTGGT	ACATTATTTA	GAGCATCAAA	AGACAGTTGT	TAGAAGACGT	1050
20	ACGCAATACA	ACTTACGTAA	AGCTAAAGAT	CGTGCCCA	TTTTAGAAGG	1100
	ATTACGTATC	GCACTTGACC	ATATCGATGA	AATTATTTCA	ACGATTCTGT	1150
	AGTCAGATAC	AGATAAAGTT	GCAA			1174

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2) INFORMATION FOR SEQ ID NO: 1256

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 780 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10209

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256

	ATCTACAACG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAGCAAGCAT	50
	TAACTTAACA	TTTGAAGTTG	CACTTCATTT	AGGTGATGAC	ACAGTTCGTA	100
	CAGTTGCAAT	GTCTTCCACA	GATGGACTTG	TTCGTGGCAC	AGAAGTAGAA	150
45	GATACTGGTA	AAGCAATCTC	TGTACCAGTT	GGTGATGTAA	CACTTGGTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGA	GATGTTCTTG	250
	CGGATGTACG	TCGTGATCCA	ATTCACCGTC	AAGCGCCTGC	ATTCGAAGAG	300
	TTATCTACTA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
	ACTTGCTCCT	TACATTAAGG	GTGGTAAGAT	CGGTCTATTC	GGTGGTGCCG	400
50	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTAATCGTGA	500
	AGGTAACGAC	TTATACCACG	AAATGAGCGA	TTCTGGCGTA	ATTAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGAGC	ACGTCAACGT	600

GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
GCAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
GTTCTGAAGT	ATCTGCCCTT	CTTGGTCGTA	TGCCATCTGC	GGTAGGTTAC	750
CAGCCAACAC	TTGCAACAGA	AATGGGTCAA			780

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2) INFORMATION FOR SEQ ID NO: 1257

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 20 (B) STRAIN: CIP 7700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257

CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	ACGAAAACGG	50
25 AACAAGCATT	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGACA	100
CAGTTCGTAC	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
ACTTGGTCGT	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
AGGTTCCTGC	GGATGTACGT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
30 TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGTCTATTCG	400
GTGGTGCCGG	TGTAGGTAAA	ACGGTATTAA	TTCAGGAATT	AATCAATAAC	450
ATCGCACAAAG	AACACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	500
TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
35 TTAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
CGTCAACGTG	TTGCGTTAAC	AGGTTTAAAC	ATGGCTGAGC	ATTTCCGTGA	650
TGAGCAAGGA	CAAGATGTAC	TTCTGTTCAT	CGATAATATC	TTCCGTTTCA	700
CGCAAGCAGG	TTCTGAAGTA	TCTGCCCTTC	TTGGCCGTAT	GCCATCTGCG	750
GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
40 TATTACATCT	ACAAATA				817

2) INFORMATION FOR SEQ ID NO: 1258

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1404

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258

	CCAGAAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	TATTAACCTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCTGTG	CACAGAAGTA	150
10	GAAGATACTG	GTAAACCAAT	CTCTGTACCA	GTTGGTGATG	TAACACTTGG	200
	TCGCGTATTT	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAGGTTC	250
	CTGCAGATGT	ACATCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
15	CCGGCGTAGG	TAAAACAGTA	TTAATTCAGG	AATTAATTAA	CAACATCGCA	450
	CAAGAGCACG	GTGGTATCTC	TGTATTCGCT	GGTGTAGGTG	AGCGTACTCG	500
	TGAGGGTAAT	GACTTATAAC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
20	AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
	TACCAACCAA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATTAC	800
	ATCTACAAAT	AAAGGGTCTA	TCACGTCTA			829

25

2) INFORMATION FOR SEQ ID NO: 1259

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 844 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

40 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259

	TGGCGGAAAG	CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	50
45	ACGAAAACGG	TGAACTTAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	100
	GATGATACAG	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTCTG	150
	TGGCACAGAA	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	200
	ATGCAACACT	TGGTCGCGTA	TTTAACGTAT	TAGGTGATGC	TATTGACTTA	250
	GATGGTGAGG	TTCCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	300
50	ACCTGCATTC	GAAGAATTAT	CTACTAAAGT	AGAAATTCTT	GAAACTGGTA	350
	TTAAAGTAGT	AGACTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGC	400
	CTATTCGGTG	GTGCCGGTGT	AGGTAAAACA	GTATTAATTC	AGGAGTTAAT	450
	CAACAACATC	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	500

	GTGAGCGTAC	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	550
	GGCGTAATTA	AGAAAAC TGC	GATGGTATTC	GGACAAATGA	ACGAGCCACC	600
	TGGAGCACGT	CAACGTGTTG	CATTAACAGG	CTTAACAATG	GCTGAATATT	650
	TCCGTGATGA	GCAAGGACAA	GACGTACTTC	TGTTTCATCGA	TAATATCTTC	700
5	CGTTTCACGC	AAGCAGGTTC	TGAAGTATCT	GCCCTTCTTG	GCCGTATGCC	750
	ATCTGCGGTA	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	800
	AAGAGCGTAT	TACATCTACA	AATAAAGGGT	CTATCACGTC	TATC	844

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2) INFORMATION FOR SEQ ID NO: 1260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260

	AAGCTACCAG	AAATCTACAA	CGCCCTTACG	GTAAAACAGA	GCAACGAAAA	50
	CGGAACAAGC	ATTAAC TTAA	CATTTGAAGT	TGCACTTCAT	TTAGGTGATG	100
	ACACAGTTCG	TACAGTTGCA	ATGTCTTCCA	CAGATGGACT	TGTTCGTGGC	150
30	ACAGAAGTAG	AAGATACTGG	TAAAGCAATC	TCTGTACCAG	TTGGTGATGC	200
	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	TGATGCAATT	GACTTAGATG	250
	GTGAGGTTCC	TGCGGATGTA	CGCCGTGATC	CAATTCACCG	TCAAGCACCT	300
	GCATTCGAAG	AATTATCTAC	TAAAGTAGAA	ATTCTTGAAA	CTGGTATTAA	350
	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	GGGTGGTAAG	ATCGGTCTAT	400
35	TCGGTGGTGC	CGGTGTAGGT	AAAACAGTAT	TAATTCAGGA	ATTAATCAAC	450
	AACATCGCAC	AAGAACACGG	TGGTATCTCT	GTATTCGCTG	GTGTAGGTGA	500
	GCGTACTCGT	GAGGGTAATG	ACTTATACCA	CGAAATGAGC	GATTCAGGCG	550
	TAATTAAGAA	AACTGCGATG	GTATTCGGAC	AAATGAACGA	GCCACCTGGA	600
	GCGCGTCAAC	GTGTTGCGTT	AACAGGTTTA	ACAATGGCTG	AGCATTTCCG	650
40	TGATGAGCAA	GGACAAGACG	TTCTTCTGTT	CATCGATAAT	ATCTTCCGTT	700
	TCACGCAAGC	AGGTTCTGAA	GTATCTGCCC	TTCTTGGTCG	TATGCCATCT	750
	GCGGTAGGTT	ACCAACCAAC	ACTTGCAACA	GAAATGGGTC	AATTACAAGA	800
	GCGTATTACA	TCTACAAATA	AAGGGTCTAT	CACGTCTATC		840

45

2) INFORMATION FOR SEQ ID NO: 1261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4AZ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261

10	GCGGAAAGCT	ACCAGAAATC	TACAATGCCC	TTACGGTAAA	ACAAAGCAAC	50
	GAAAACGGAA	GCATGAACTT	AACATTTGAA	GTTGCACTTC	ATTTAGGTGA	100
	TGATACAGTT	CGTACAGTTG	CGATGTCTTC	CACAGATGGA	CTTGTTCTGTG	150
	GCACAGAAGT	AGAAGATACT	GGTAAAGCAA	TCTCTGTACC	AGTTGGTGAT	200
	GCAACACTTG	GACGTGTATT	CAACGTATTA	GGTGATGCAA	TTGACTTAGA	250
15	TGGTGAACCT	CCTGCGGATG	TACACCGTGA	TCCAATTCAC	CGTCAAGCAC	300
	CTGCATTCGA	AGAATTATCT	ACTAAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTAGTAG	ACTTACTTGC	TCCTTACATT	AAGGGTGGTA	AGATCGGCCT	400
	ATTCGGTGGT	GCCGGCGTAG	GTAAAACAGT	ATTAATTCAG	GAGTTAATCA	450
	ATAACATCGC	ACAAGAGCAC	GGTGGTATCT	CTGTATTTCG	TGGTGTAGGT	500
20	GAGCGTACTC	GTGAGGGTAA	TGACTTATAC	CACGAAATGA	GCGATTCTGG	550
	CGTAATCAAG	AAAACCTGCG	TGGTATTTCG	ACAAATGAAC	GAGCCACCTG	600
	GAGCACGTCA	ACGTGTTGCA	TTAACAGGTT	TAACAATGGC	TGAGCATTTTC	650
	CGTGATGAGC	AAGGACAAGA	CGTACTTCTG	TTCATCGATA	ACATCTTCCG	700
	TTTCACGCAA	GCGGGTTCTG	AAGTATCTGC	CCTTCTTGGT	CGTATGCCAT	750
25	CTGCGGTAGG	TTACCAACCA	ACACTTGCAA	CAGAAATGGG	TCAATTACAA	800
	GAGCGTATTA	CATCTACAAA	TAAAGGGTCT	ATCACGTCT		839

30 2) INFORMATION FOR SEQ ID NO: 1262

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4H2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262

45	AAGCTACCAG	AAATCTACAA	TGCCCTTACG	GTAAAACAAA	GCAACGAAAA	50
	CGGAAGCATG	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGATA	100
	CAGTTCGTAC	AGTTGCGATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
	GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
50	ACTTGGACGT	GTATTCAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
	AACTTCCTGC	GGATGTACAC	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
	TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
	AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCG	400

5 GTGGTGCCGG CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATCAATAAC 450
 ATCGCACAAAG AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG 500
 TACTCGTGAG GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA 550
 TCAAGAAAAC TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA 600
 5 CGTCAACGTG TTGCATTAAC AGGTTTAAAC ATGGCTGAGC ATTTCCGTGA 650
 TGAGCAAGGA CAAGACGTAC TTCTGTTCAT CGATAACATC TTCCGTTTCA 700
 CGCAAGCGGG TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG 750
 GTAGGTTACC AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG 800
 TATTACATCT ACAAATAAAG GGTCTATCAC GTC 833
 10

2) INFORMATION FOR SEQ ID NO: 1263

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 25 (B) STRAIN: BGSC 4Q1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263

30 CGAAAACGGA AGCATGAACT TAACATTTGA AGTTGCACTT CATTTAGGTG 50
 ATGATACAGT TCGTACAGTT GCGATGTCTT CCACAGATGG ACTTGTTTCGT 100
 GGCACAGAAG TAGAAGATAC TGGTAAAGCA ATTTCTGTAC CAGTTGGTGA 150
 TGTAACACTT GGACGTGTAT TCAACGTATT AGGTGATGCA ATTGACTTAG 200
 ATGGTGA ACT TCCTGCGGAT GTACACCGTG ATCCAATTCA CCGTCAAGCA 250
 CCTGCATTTCG AAGAATTATC TACTAAAGTA GAAATTCTTG AACTGGGTAT 300
 35 TAAAGTAGTA GACTTACTTG CTCCTTACAT TAAGGGTGGT AAGATCGGCC 350
 TATTCGGTGG TGCCGGTGTA GGTAAAACAG TATTAATTCA GGAATTAATT 400
 AACAAATCG CACAAGAGCA CGGTGGTATC TCTGTATTCG CTGGTGTAGG 450
 TGAGCGTACT CGTGAGGGTA ATGACTTATA CCACGAAATG AGCGATTCTG 500
 GCGTAATCAA GAAACTGCG ATGGTATTCG GACAAATGAA CGAGCCACCT 550
 40 GGAGCACGTC AACGTGTTGC ATTAACAGGT TTAACAATGG CTGAGCATTT 600
 CCGTGATGAG CAAGGACAAG ACGTACTTCT GTTCATCGAT AACATCTTCC 650
 GTTTCACGCA AGCGGGTTCT GAAGTATCTG CCCTTCTTGG TCGTATGCCA 700
 TCTGCGGTAG GTTACCAACC AACACTTGCA ACAGAAATGG GTCAATTACA 750
 AGAGCGTATT ACATCTACAA ATAAAGGGTC TATCACGTCT 790
 45

2) INFORMATION FOR SEQ ID NO: 1264

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264

10 AGTTGCACTT CATTAGGTG ATGATACAGT TCGTACAGTT GCGATGTCTT 50
 CCACAGATGG ACTTGTTTCGT GGCACAGAAG TAGAAGATAC TGGTAAACCA 100
 ATCTCTGTAC CAGTTGGTGA TGTAACACTT GGTCGCGTAT TTAACGTATT 150
 AGGTGATGCA ATTGACTTAG ATGGTGAGGT TCCTGCAGAT GTACATCGTG 200
 15 ATCCAATTCA CCGTCAAGCA CCTGCATTCG AAGAATTATC TACTAAAGTA 250
 GAAATTCTTG AAAGTGGTAT TAAAGTAGTA GACTTACTTG CTCCTTACAT 300
 TAAGGGTGGT AAGATCGGCC TATTCGGTGG TGCCGGCGTA GGTAAAACAG 350
 TATTAATTCA GGAATTAATT AACAAACATCG CACAAGAGCA CCGTGGTATC 400
 TCTGTATTCG CTGGTGTAGG TGAGCGTACT CGTGAGGGTA ATGACTTATA 450
 20 CCACGAAATG AGCGATTCTG GCGTAATCAA GAAAGTGGC ATGGTATTCG 500
 GACAAATGAA CGAGCCACCT GGAGCACGTC AACGTGTTGC ATTAACAGGT 550
 TTAACAATGG CTGAGCATTT CCGTGATGAG CAAGGACAAG ACGTACTTCT 600
 GTTCATCGAT AACATCTTCC GTTTCACGCA AGCGGGTTCT GAAG 644

25

2) INFORMATION FOR SEQ ID NO: 1265

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265

GGCGGAAAGC TACCAGAAAT CTACAACGCC CTTACGGTAA AACAGAGCAA 50
 CGAAAACGGA ACAAGCATTA ACTTAACATT TGAAGTTGCA CTTCAATTTAG 100
 45 GTGATGACAC AGTTCGTACA GTTGCAATGT CTTCCACAGA TGGACTTGTT 150
 CGTGGCACAG AAGTAGAAGA TACTGGTAAA GCAATCTCTG TACCAGTTGG 200
 TGATGCAACA CTTGGTTCGTG TATTTAACGT ATTAGGTGAT GCAATTGACT 250
 TAGATGGTGA GGTTCCTGCG GATGTACGTC GTGATCCAAT TCACCGTCAA 300
 GCACCTGCAT TCGAAGAATT ATCTACTAAA GTAGAAATTC TTGAAACTGG 350
 50 TATTAAAGTA GTAGACTTAC TTGCTCCTTA CATTAGGGT GGTAAGATCG 400
 GTCTATTCGG TGGTGCCGGT GTAGGTAAAA CGGTATTAAT TCAGGAATTA 450
 ATCAATAACA TCGCACAAGA ACACGGTGGT ATCTCTGTAT TCGCTGGTGT 500
 AGGTGAGCGT ACTCGTGAGG GTAATGACTT ATACCACGAA ATGAGCGATT 550

	CTGGCGTAAT	TAAGAAAAC	GCGATGGTAT	TCGGACAAAT	GAACGAGCCA	600
	CCTGGAGCAC	GTCAACGTGT	TGCGTTAACA	GGTTTAACAA	TGGCTGAGCA	650
	TTTCCGTGAT	GAGCAAGGAC	AAGATGTACT	TCTGTTCATC	GATAATATCT	700
	TCCGTTTCAC	GCAAGCAGGT	TCTGAAGTAT	CTGCCCTTCT	TGGCCGTATG	750
5	CCATCTGCGG	TAGGTTACCA	ACCAACACTT	GCAACAGAAA	TGGGTCAATT	800
	ACAAGAGCGT	ATTACATCTA	CAA			823

10 2) INFORMATION FOR SEQ ID NO: 1266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266

25	TGGTCCGAGR	CCCGATTCMA	TGAAATTATC	AAGGAAACCT	CCAAYTTCAT	50
	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	CCCATTTCTG	100
	GTTTCCAGGG	TGACAACATG	ATCGATSCCT	CTGCCAACTG	CCCATGGTAC	150
	AAGGGCTGGT	ACMAKGAGAC	TGCCGACAGG	CAAGYACTCT	GGCAAGACCC	200
30	TTCTTGAGGC	CATTGACGSC	ATTGAGCCCC	CCAMSCGTCC	TWCCGATAAA	250
	CCTCTCCGTC	TTCCTCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGMAC	300
	TGTTCTTGTC	GGACGTRTTG	AGACTGGAGT	CATCAAGCCC	GGTATGGTCG	350
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAAATG	400
	CACCACCAGC	AGCTTTCCGA	CGGTAWCCCC	GGTGACAACG	TCGGCTTCAA	450
35	CGTCAAGAAT	GTTTCCGTCA	AAGAAGTCCG	CCGTGGTAAC	GTTGCCTGGT	500
	GACTCTAAGA	ATGATCCCGC	MAWGGGCTGC	GATTCTTCA	ATGCYCAGGT	550
	CATCGTCCTC	AACCACCCTG	GTCAGGTTGG	CGCTGGTTAT	GCCCCAGTCC	600
	TCGAYTGCCA	TACTGCCCAC	ATTGCYTGCA	ARTTCGCTGA	GMTCMAGAG	650
	AAGATTGAYC	GCCGAACCGG	MAAGTCTGTT	GAGAACGCCC	CCAAGTTCAT	700
40	CAAGTCCGGT	GATGC				715

2) INFORMATION FOR SEQ ID NO: 1267

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 875 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 56220

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267

	GAGTCCTCTT	ATTTACTTTT	GTCATGACTA	CCTTACTAAT	CTGTCATAGA	50
	TCGTTACAAC	GAAATCGTCA	AGGAGACTTC	CAACTTCATC	AAGAAGGTCG	100
	GATACAACCC	CAAGAACGTT	CCTTTCGTTC	CTATCTCCGG	TTTCAACGGC	150
10	GACAACATGC	TTGAGCCCTC	CCCCAACTGC	CCCTGGTACA	AGGGTTGGGA	200
	GAAGGAGACC	AAGGCCGGTA	AGGTCACTGG	TAAGACCCTC	CTCGAGGCCA	250
	TCGACGCCAT	TGAGCCCCCT	ACCCGTCCCG	CCAACAAGGT	CAGTACTACC	300
	TCAATTACTT	GAAGTCTCTT	CATACGTTCC	GATTACTGAC	TGCTTCACAG	350
	CCCCTCCGTC	TTCCCCTCCA	GGACGTTTAC	AAGATCGGTG	GTATTGGAAC	400
15	GGTGCCCGTC	GGTCGTGTTG	AGACCGGTAC	CATCTCCCCT	GGTATGGTCG	450
	TTACCTTGTA	TGTATCCTGA	CCATCCCCCT	TGGCAATCAT	TACGTACTAA	500
	CTCACTCTTC	AGCGCTCCCG	CCAACGTCAC	CACTGAAGTC	AAGAGTGTTG	550
	AAATGCACCA	CCAGCAGCTC	GCTGCCGGTC	AGCCCGGTGA	CAACGTTGGT	600
	TTCAACGTGA	AGAACGTCTC	CGTCAAGGAA	ATCCGTCGTG	GTAACGTTGC	650
20	TGGTGATAGC	AAGAACGACC	CCCCTGCCGG	TGCTGCTTCC	TTCAACGCCC	700
	AGGTCATCGT	CCTCAACCAC	CCCGGTCAGG	TCGGTGCTGG	TTACGCCCCA	750
	GTCCTTGACT	GCCACACTGC	CCACATTGCT	TGCAAGTTCT	CTGAACCTCT	800
	TGAGAAGATT	GACCGTCGTA	CCGGAAAGTC	TGTTGAGGAC	CACCCCAAGT	850
	TCATCAAGTC	CGGTGACGCT	GCCAT			875

25

2) INFORMATION FOR SEQ ID NO: 1268

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*

40 (B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268

	GTGAGCGTGG	TATCACCATC	GATATTGCCC	TCTGGAAATT	CGAGACCCCG	50
45	AAGTACAGTG	TCAGTGTCAT	TGGTGAGTGC	TTTTTACCCC	TCTTAAGCAG	100
	ATTTCAACTT	CCAGAGTATC	TACTCTAACA	TATCCGCTTA	GATGCTCCCG	150
	GCCATCGTGA	CTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	200
	TGCGCTATCC	TCATCATTGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	TCTGCTTGCT	TTCACCCTTG	300
50	GTGTGAGGCA	ACTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCCGAGTCCC	GTTTCAACGA	AATCATCAAG	GAGGTTTCCA	ACTTCATCAA	400
	GAAGGTCGGA	TATAACCCCA	AGGCTGTTCC	CTTCGTGCCA	ATCTCTGGTT	450
	TCGAGGGTGA	CAACATGATT	GAACCCTCCC	CCAAGTGCAC	CTGGTACAAG	500

	GGCTGGAACA	AGGAGACTGC	CTCTGGCAAG	TCTTCTGGTA	AAACCCTTCT	550
	CGATGCCATT	GACGCCATTG	AACCCCCAAC	CCGTCCTACC	GATAAGCCTC	600
	TCCGTCTTCC	CCTCCAGGAT	GTTTACAAAA	TCTCTGGTAT	TGGCACTGTT	650
	CCCGTCGGAC	GTGTTGAGAC	TGGTGTGATC	AAGCCCGGTA	TGGTCGTGAC	700
5	TTTCGCTCCC	TCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACCAACAAC	CCAGGCTGGT	TACCCTGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTTT	CAGTCAAGGA	AGTCCGCCGT	GGCAACGTTG	CTGGCGACTC	850
	CAAAAATGAT	CCCCCAAGG	GCTGCGAATC	CTTCAATGCC	CAGGTCATCG	900
	TCCTTAACCA	CCCCGGCCAG	GTTGGCGCTG	GTTATGCCCC	AGTCCTCGAC	950
10	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCTGAACTCA	TTGAGAAGAT	1000
	CGACCGCCGT	ACTGGAAGT	CTGTTGAGAA	CAACCCCAAG	TTCATCAAGT	1050
	CTGGTGATGC	TGCTATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTG	1100
	GAGCCCTTCA	CTGACTATCC	CCCT			1124

15

2) INFORMATION FOR SEQ ID NO: 1269

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1043 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton rubrum*
 (B) STRAIN: WSA-224

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269

	GTGAGCGTGG	TATCACCATC	GATATCGCCC	TCTGGAAGTT	CGAGACCCCC	50
	AAGTACAATG	TCACCGTCAT	TGGTATGTTT	CTTTGCCTTG	TTCCCTCATG	100
35	TGGTTGTACC	ATATCTAACG	AGAGTAGACG	CCCCCGGTCA	CCGTGACTTC	150
	ATCAAGAACA	TGATCACTGG	TACCTCCCAG	GCTGACTGCG	CTATTCTCAT	200
	CATTGCTGCC	GGTACTGGTG	AGTTCGAGGC	TGGTATCTCC	AAGGATGGCC	250
	AGACCCGTGA	GCACGCTCTG	CTCGCCTTCA	CCCTCGGTGT	CAAGCAGCTC	300
	ATCGTTGCCA	TCAACAAGAT	GGACACCACC	GGCTGGTCCG	AGGATCGTTT	350
40	CAAGGAAATT	ATCAAGGAAG	TCACCAACTT	CATCAAGAAG	GTTGGCTACG	400
	ACCCCAAGGG	TGTTCCATTC	GTTCCAATCT	CTGGTTTCAA	CGGTGACAAAC	450
	ATGATTGAGG	CCTCCACCAA	CTGCCCATGG	TACAAGGGAT	GGAACAAGGA	500
	GACCAAGGCC	GGTGGTGCCA	AGTCCGGCAA	GACCCTCCTC	GAGGCCATCG	550
	ATGCCATCGA	CATGCCAACC	CGTCCTACCG	ACAAGCCCCT	CCGTCTCCCA	600
45	CTCCAGGATG	TCTACAAGAT	CTCTGGTATC	GGAAGTGTGC	CAGTCGGTCG	650
	TGTTGAGACC	GGTATCATCA	AGCCCGGTAT	GGTCGTCACC	TTNGCCCCCG	700
	CCAACGTCAC	CACTGAAGTC	AAGTCCGTYK	AAATGCACCA	CCAGCAGCTT	750
	CAGCAGGGTG	TCCCCGGTGA	CAACGTCGGC	TTCAATGTCA	AGAACGTTTC	800
	CGTCAAGGAA	GTCCGCCGTG	GTAACGTTGC	CGGTGACTCC	AAGAACGACC	850
50	CACCATCCGG	CTGTGCCTCC	TTCAACGCCC	AGGTCATYGT	CCTCAACCAC	900
	CCCGGCCAGA	TCGGTGCTGG	TTACGSTCCA	GTCCTCGACT	GCCACACTGS	950
	TCACATTGCT	TGCAAGTTCG	CTGAGCTCCT	CGAGAAGATT	GACCGCCGTA	1000
	CCGGTAAATC	CGTCGAAGCC	AACCCCAAGT	TCGTCAAGTC	TGG	1043

2) INFORMATION FOR SEQ ID NO: 1270

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Microsporium canis*
 (B) STRAIN: WSA-217
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270

	GCTGAGCGTG	AGCGTGGTAT	CACCATTGAT	ATCGCCCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACATGGTCA	CCGTCATCGG	TATGCTTTAT	CTGTTTCCCA	100
	TTTATAGTTG	CGACCAGTAA	CTAACAAAAA	GTAGATGCCC	CCGGGCACCG	150
20	TGACTTCATC	AAGAACATGA	TTACTGGTAC	CTCCCAGGCC	GACTGCGCTA	200
	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CTCGTGAGCA	CGCCCTGCTC	GCTTTCACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	TGGTCTGAGT	350
	CCCGTTTCGG	TGAAATCATC	AAGGAAGTCA	CCAACTTCAT	CAAGAAGGTC	400
25	GGCTACGACC	CCAAGGGTGT	CCCATTTCGT	CCAATCTCTG	GCTTCAACGG	450
	TGACAACATG	ATTGAGCCCT	CCACCAACTG	CCCATGGTAC	AAGGGATGGA	500
	ACAAGGAGAC	CAAGGCCGGT	GGCAAATCCT	CTGGTAAGAC	CCTCCTTGAG	550
	GCCATCGATG	CCATTGACAT	GCCCACTCGT	CCCACCGACA	AGCCTCTCCG	600
	TCTCCCCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	ACAGTACCAG	650
30	TCGGTCGTGT	TGAGACTGGT	ATCATCAAGC	CTGGTATGGT	TGTCACTTTY	700
	GCCCCCGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	TGCACCACCA	750
	GCAGCTYGTC	CAGGGTGTTT	CCGGTGACAA	CGTTGGCTTC	AACGTCAAGA	800
	ACGTYTCTGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	TGATTCCAAG	850
	AACGACCCAC	CAGCTGGCTG	CGCCTCTTTC	AAGGCCCAGG	TCATCGTCCT	900
35	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	CTTGACTGCC	950
	ACACTGCCCA	CATTGCTTGC	AAGTTCTCTG	AGCTTCTTGA	GAAGATTGAC	1000
	CGCCGTACTG	GTAAATCCGT	CGAAACCAGC	CCTAAGTTCG	TCAAGTCTGG	1050
	TGATGCCGCT	ATTGCCACCA	TGGTTCCATC	CAAGCCCATG	TGCGTTGAGG	1100
	CTTTC					1105

40

2) INFORMATION FOR SEQ ID NO: 1271

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1244 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:

50

(A) ORGANISM: *Aspergillus versicolor*

(B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271

5
 GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA AGTTCCAGAC 50
 CCCTAAGTAT GAGGTCACCG TCATTGGTAT GTTGTCTTTC TTGTGTTACC 100
 ATCGAAACAT ATCTAACCTA CAACTGCAGA CGCCCCCGGT CACCGTGACT 150
 TCATCAAGAA CATGATCACT GGTACCTCCC AGGCCGACTG CGCTATTCTC 200
 10 ATCATTGCTT CCGGTACTGG TGAATTTCGAG GCTGGTATCT CCAAGGATGG 250
 CCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTCGGT GTCCGTCAGC 300
 TCATCGTTGC CCTCAACAAG ATGGACACTG CTGGCTGGGC TGAGGCTCGT 350
 TACAACGAAA TCGTCAAGGA AACTTCCGGT TTCATCAAGA AGGTCGGCTA 400
 CAACCCCAAG TCGGTTCCCT TCGTCCCAT CTCCGGTTTC AACGGTGACA 450
 15 ACATGCTTGA GCCCTCCTCC AACTGCCCCT GGTACAAGGG TTGGGAGAAG 500
 GAGACCAAGG CTGGTAAGGC CACTGGTAAG ACCCTCCTCG AGGCCATCGA 550
 CGCCATTGAG CCTCCCGTCC GTCCCTCCAA CAAGCCTCTC CGTCTTCCCC 600
 TCCAGGATGT CTACAAGATC TCTGGTATTG GAACTGTCCC CGTCGGCCGT 650
 GTCGAGACCG GTACCATCGT CCCCGGTATG GTCGTCACCT TCGCTCCCGC 700
 20 CAACGTCACC ACTGAAGTCA AGTCCGTTGA GATGCACCAC CAGCAGCTCA 750
 AGGAGGGTGT TCCCGGTKAC AACGTTGGTT TCAACGTGAA GAACGTTTCC 800
 GTCAAGGAAG TCCGCCGTGG TAACGTCGCT GGTGACTCCA AGAACGACCC 850
 CCCTGCCGGT GCTGCCTCTT TCACCGCCCA GGTCATCGTC CTCAACCACC 900
 CCGGTCAGGT CGGCGCTGGT TACGCTCCCG TCCTCGACTG CCACACCGCT 950
 25 CACATTGCCT GCAAGTTCGC TGAGCTCCAG GAGAAGATCG ACCGCCGTAC 1000
 CGGAAAGTCT GTCGAATYTG CCCCCAAGTT CATCAAGTCT GGTGACGCCG 1050
 CTATCGTCAA GATGATTCCC TCCAAGCCCA TGTGTGTCGA GTCTTTCACT 1100
 GACTACCCTC CTYTCGGCCG TTTGCGCCGTC CGTGACGTAA GTTCTTTCCC 1150
 CAGCTTTTCG ATGCTACCCT TCTMTGAATC ACGTGTCATG TCTTGGCACC 1200
 30 CGCCCATCAC ATGACCACGC AACCTATAC CCCGCCACAC CCTT 1244

2) INFORMATION FOR SEQ ID NO: 1272

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1032 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Exophiala moniliae*

(B) STRAIN: WSA-219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272

50 GCTGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT GGAAGTTCGA 50
 GACCCCAAG TACTATGTCA CCGTCATCGA CGCCCCCGGT CATCGTGACT 100
 TCATCAAGAA CATGATCACT GGTACTTCCC AAGCTGACTG CGCCATTCTC 150
 ATCATTGCTG CCGGTACTGG TGAATTTCGAA GCCGGTATCT CCAAGGATGG 200

	TCAGACCCGT	GAGCACGCTC	TGCTTGCCTA	CACCCTGGGT	GTCAAGCAGC	250
	TCATTGTCGC	CATCAACAAG	ATGGACACTA	CCAAGTGGTC	TGAGGACCGT	300
	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	AGGTCGGCTA	350
	CAACCCCAAG	TCCGTTCCCTT	TCGTCCCCAT	CTCCGGCTTC	AACGGTGACA	400
5	ACATGATCGA	CGTCTCCACC	AACTGCCCCT	GGTACAAGGG	CTGGGAGAAG	450
	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTTG	AGGCCATCGA	500
	CGCCATTGAC	CCCCCTCTC	GTCCCACCGA	CAAGCCTYTC	CGTCTCCCTC	550
	TCCAGGATGT	GTACAAGATC	TCTGGTATCG	GAACGGTGCC	CGTCGGTCGT	600
	GTCGAGACTG	GTATCATCAA	GGCCGGTATG	GTCGTTACCT	TCGCTCCTGC	650
10	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	GAACAGCTCG	700
	CCGAGGGTGT	TCCAGGTGAC	AACGTCGGTT	TCAACGTCAA	GAACGTYTCC	750
	GTCAAGGAGG	TTCGTCGTGG	AAACGTTTGC	GGTGACTCCA	AGAACGACCC	800
	ACCCAAGGGC	GCTGATTCCT	TCAACGCCCA	GGTCATCGTC	TTGAACCACC	850
	CTGGTCAAGT	TGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	CCACACTGCC	900
15	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATCG	ATCGTCGKAC	950
	CGGAAAGTCG	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	GGTGACGCTG	1000
	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TG		1032

20

2) INFORMATION FOR SEQ ID NO: 1273

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hortaea werneckii*
 (B) STRAIN: ATCC 34944

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273

	TAACAGCCCG	TGCGACCGTC	TCGTCCAATA	ACTAATGATT	CGCAGGTACT	50
	ATGTCGTGAG	TATCCGGTCC	TTTTTTGTTA	ATTTACCAGA	AATGACGAAA	100
	TTTTTGACTA	ATTAACACAC	TCAGACCGTC	ATTGACGCCC	CGGGTCACCG	150
40	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCC	GACTGCGCTG	200
	TCCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTCGCCATCA	ATAAGATGGA	CACCACCAAG	TGGTCCGAGG	350
	AGCGTTACGG	CGAGATCATC	AAGGAGACCT	CTGCCTTCAT	CAAGAAGGTC	400
45	GGTTTCAACC	CGAAGCACGT	CCCGTTCGTC	CCGATCTCCG	GTTTCAACGG	450
	TGACAACATG	ATCGAGGCCT	YCACCAACTG	CCCGTGGTAC	AAGGGCTGGG	500
	AGAAGGAGAC	CAAGGCCAAG	GTCACCGGCA	AGACCCTYCT	TGAGGCCATT	550
	GACAACATCG	ACCCGCCGAG	CCGTCTTCC	GACAAGCCGC	TCCGTCTTCC	600
	CCTCCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGGACAGTC	CCAGTCGGCC	650
50	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTTAC	CTTCGCTCCG	700
	GCTGGTGTC	CCACTGAAGT	GAAGTCCGTT	GARATGCACC	ACGAGCAGCT	750
	CGCTGAGGGT	YTGCCGGGTG	ACAACGTCGG	CTTCAACGTC	AAGAACGTTT	800
	CCGTCAAGGA	GATCCGTCGT	GGCAACGTTG	CTGGTGACAG	CAAGGCTGAC	850

	CCGCCGAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	TCCTGAACCA	900
	CCCTGGCCAG	GTCGGTGCTG	GTTACGCTCC	AGTCCTGGAC	TGCCACACTG	950
	CCCACATTGC	CTGCAAGTTC	GGCGAGCTCC	TCGAGAAGAT	CGACCGTCGC	1000
	TYTGGCAAGT	CCATTGAAGC	CTYGCCTAAG	TACATCAAGT	CTGGTGACGC	1050
5	TGCCATYGTC	AAGATGATTC	CGTCCAAGCC	GATGTGCGTT	GAGCCATTCA	1100
	CTGAGT					1106

10 2) INFORMATION FOR SEQ ID NO: 1274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
 (B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274

25	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
	GTTCGAGACT	CCCCGCTACT	ATGTCACCGT	CATTGGTATG	TTGCTGTCAC	100
	CTCTCTCACA	CATGTCTCAC	CACTAACAAT	CAACAGACGC	CCCCGGCCAC	150
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGACTGCGC	200
30	CATTCTCATC	ATTGCCGCCG	GTA CTGGTGA	GTT CGAGGCT	GGTATCTCCA	250
	AGGATGGCCA	GACCCGTGAG	CACGCCCTGC	TCGCCTACAC	CCTCGGTGTC	300
	AAGAACCTCA	TTGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	350
	GTCCCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCA ACTTC	ATCAAGAAGG	400
	TCGGCTACAA	CCCCAAGGCT	GTCGCTTTTCG	TCCCCATCTC	CGGTTTCAAC	450
35	GGCGACAACA	TGCTTACTCC	CTCCACCAAC	TGCCCCCTGGT	ACAAGGGCTG	500
	GGAGCGTGAG	ATCAAGTCCG	GCAAGCTCAC	TGGCAAGACC	CTCCTCGAGG	550
	CCATTGACTC	CATCGAGCCC	CCCAAGCGTC	CCGTCGACAA	GCCCCCTYCGA	600
	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATTGGCA	CGGTTCCCGT	650
	CGGCCGTATC	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTMG	700
40	CCCCCTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	750
	CAGCTCTYTG	AGGGTCTTCC	CGGTGACAAC	GTCGGCTTCA	ACGTGAAGAA	800
	CGTYTCCGTC	AAGGAGATCC	GACGTGGCAA	CGTCGCTGGT	GACTCCAAGA	850
	ACGACCCCCC	TYTGGGTGCC	GCCTCTTTCA	CCGCCCAGGT	CATTGTCCTC	900
	AACCACCCTG	GCCAGGTCGG	TGCCGGTTAC	GCCCCCGTTY	TGGACTGCCA	950
45	CACTGCCCAC	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	1000
	GCCGA ACTGG	TAAGGCTGTT	GAGTCCGCCC	CCAAGTTCAT	CAAGTCTGGT	1050
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1100
	TTTCACTGAC	TACCCCCCT				1119

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2) INFORMATION FOR SEQ ID NO: 1275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Aureobasidium pullulans*
 (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275

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15 CTGAAGTCTG AGCGTGAGCG TGGTATCACT ATCGATATCG CCCTCTGGAA      50
   GTTCGAGACC CCCAAGTACA TGGTCACCGT CATCGATGCC CCCGGTCACC      100
   GTGATTTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC TGACTGCGCC      150
   ATTCTCATCA TTGCTGCCGG TACTGGTGAG TTCGAGGCTG GTATCTCCAA      200
   GGATGGCCAG ACTCGTGAGC ACGCTCTCCT CGCCTACACC CTTGGTGTCA      250
20 AGCAGCTCAT CGTTGCCATC AACAAAGATGG ACACCACCAA GTGGTCTGAG      300
   GCCCGTTACC AGGAGATCAT CAAGGAGACC TCCGGTTTCA TCAAGAAGGT      350
   CGGCTACAAC CCCAAGCACG TTCCCTTCGT CCCCATCTCC GGCTTCAACG      400
   GAGACAACAT GATCGAGGTC AGCTCCAAC TCCCTTGGTA CAAGGGTTGG      450
   GAGAAGGAGA CCAAGGCCAA GGCCACTGGC AAGACCCTCC TCGAGGCCAT      500
25 TGACGCCATC GACCCTCCTT CCCGTCCTAC CGACAAGCCC CTCCGTCTTC      550
   CCCTCCAGGA TGTCTACAAG ATCGGTGGTA TTGGCACGGT GCCCGTCGGT      600
   CGTGTTGAGA CCGGTAAGAT CATGGGTGGT ATGGTTGTCA CCTTCGCCCC      650
   CGCTGGTGTC ACCACCGAGG TCAAGTCCGT CGAGATGCAC CACGAGCAGC      700
   TCACCGAGGG TCTTCCCGGT GACAACGTCG GCTTCAACGT CAAGAACGTY      750
30 TCCGTCAAGG AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA      800
   CCCCCCAAG GGTGTGACT CCTTCAACGC CCAGGTCATC GTCCTGAACC      850
   ACCCTGGTCA GGTCGGTGCT GGTACGCAC CCGTCCTCGA CTGCCACACT      900
   GCCCACATTG CTTGCAAGTT YTCCGAGCTT GTTGAGAAGA TTGACCGCAG      950
   AACCGGCAAG TCCGTTGAGG CTGCCCCCAA GTTCATCAAG TCTGGTGACG     1000
35 CCGCCATCGT CAAGATGGTT CCCTCCAAGC CCATGTGTGT TGAGGCTTTC     1050
   ACCGACTACC CTCCTYTCGG TCGTTTCGCC GTCCGGTATG TTTTCTTCT      1100
   TCAATCATTC TTC                                     1113

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2) INFORMATION FOR SEQ ID NO: 1276

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 731 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 (B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276

	GGTCTGAGAC	CCGTTTCAAC	GAAATTATCA	AGGAAGTCAG	CAACTTCATC	50
5	AAGAAGGTCG	GATACAACCC	CAAGTCTGTT	CCCTTCGTGC	CAATCTCCGG	100
	TTTCGAGGGT	GACAACATGA	TTGAGCCTTC	CCCCAACTGC	CCTTGGTACA	150
	AGGGCTGGAA	CAAGGAGACT	GCTGCTGGCA	AGGCCGCCGG	TAAGACTCTT	200
	CTCGATGCCA	TTGACGCCAT	CGACCCCCCC	GTCCGTCCTA	CCGAGAAGCC	250
	TCTCCGTCTT	CCCCTCCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	300
10	TTCCCGTTGG	ACGTGTCGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTG	350
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TTGAAATGCA	400
	CCACCAGCAG	CTCCAGGCTG	GTTACCCTGG	TGACAACGTC	GGCTTCAACG	450
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCGGTGAC	500
	TCCAAGAACG	ACCCCCCCAA	GGGCTGCGAG	TCCTTCAACG	CCCAGGTCAT	550
15	CGTCCTCAAC	CACCCCGGCC	AGGTTGGCGC	TGGTTATGCC	CCAGTCCTCG	600
	ACTGCCACAC	TGCCACATT	GCTTGCAAGT	TCTCTGAGCT	CATCGAGAAG	650
	ATTGACCGCC	GTACCGGAAA	GTCTGTTGAG	GACAACCCCA	AGTTCATCAA	700
	GTCCGGTGAT	GCTGCTATCG	TCAAGATGAT	T		731

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2) INFORMATION FOR SEQ ID NO: 1277

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 1046 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Exophiala dermatitidis</i>
	(B) STRAIN: ATCC 76088

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277

	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCCCTCTG	GAAGTTCGAG	50
	ACCCCCAAGT	ACTATGTCAC	CGTCATCGAC	GCCCCGGGTC	ATCGTGACTT	100
40	TATCAAGAAC	ATGATCACTG	GTACCTCGCA	GGCCGACTGC	GCCATCTTGA	150
	TCATTGCCGC	CGGTACCGGT	GAATTCGAAG	CCGGTATCTC	CAAGGATGGT	200
	CAGACCCGTG	AGCACGCTCT	GCTCGCCTAC	ACCTTGGGTG	TCAAGCAGCT	250
	CATCGTCGCC	ATCAACAAGA	TGGACACCAC	CAAGTGGTCC	GAGGAGCGTT	300
	TCAACGAAAT	CATCAAGGAG	ACTTCCAAC	TCATCAAGAA	GGTCGGCTAC	350
45	AACCCCAAGG	CCGTTCTTT	CGTCCCCATC	TCCGGCTTCA	ACGGTGACAA	400
	CATGATTGAG	GTCTCCACCA	ACTGCCCGTG	GTACAAGGGA	TGGGAGAAGG	450
	AGTCCAAGGC	TGGCAAGGCC	ACCGGCAAGA	CCCTCCTCGA	GGCCATTGAC	500
	GCCATCGACC	CACCCACCCG	TCCCACCGAC	AAGCCTCTCC	GTCTCCCTCT	550
	CCAGGATGTC	TACAAGATCT	CTGGTATCGG	AACGGTTCCT	GTCGGTCGTG	600
50	TCGAGACCGG	TACCATCAAG	GCCGGTATGG	TCGTCACCTT	CGCTCCGGCC	650
	AACGTCACCA	CTGAAGTCAA	GTCCGTCGAA	ATGCACCACG	AGCAGCTCGC	700
	CGAGGGTYTG	CCAGGTGACA	ACGTTGGCTT	CAACGTCAAG	AACGTYTCCG	750
	TCAAGGAGGT	TCGTGCTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCG	800

	CCCAAGGGTG	CCGAGTCCTT	CAACGCCCAG	GTCATTGTCC	TCAACCACCC	850
	TGGTCAGATC	GGTGCCGGCT	ACGCTCCAGT	CTTGGATTGC	CACACTGCCC	900
	ACATTGCTTG	CAAGTTCGCC	GAGTTGCTCG	AGAAGATCGA	CCGTCGTACC	950
	GGAAAGTCCA	TCGAGAACAA	CCCCAAGTTC	ATCAAGTCTG	GTGATGCTGC	1000
5	CATCGTCAAG	ATGATTCCCA	GCAAGCCCAT	GTGTGTCGAG	GCTTTC	1046

2) INFORMATION FOR SEQ ID NO: 1278

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Fusarium moniliforme*
 (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278

25	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	TCGAGACTCC	50
	TCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GTCGCTCATA	CCTCATCCTA	100
	CTTCCTCATA	CTAACACATC	ATTCAGACGC	TCCCGGTAC	CGTGATTTC	150
	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGATTGCGC	CATTCTCATC	200
	ATTGCCGCCG	GTA CTGGTGA	GTTTCGAGGCT	GGTATCTCCA	AGGATGGCCA	250
30	GACCCGTGAG	CACGCTCTTC	TTGCCTACAC	CCTTGGTGTC	AAGAACCTCA	300
	TCGTGCGCAT	CAACAAGATG	GACACCACCA	AGTGGTCTGA	GGCCCGTTAC	350
	CAGGAGATCA	TCAAGGAGAC	CTCCTCTTTC	ATCAAGAAGG	TCGGCTACAA	400
	CCCCAAGGCT	GTCGCTTTCG	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	450
	TGCTTACCCC	CTCCACCAAC	TGCCCCCTGGT	ACAAGGGTTG	GGAGCGTGAG	500
35	ATCAAGTCCG	GCAAGCTCTC	CGGCAAGACC	CTCCTCGAGG	CCATTGACTC	550
	CATCGAGCCT	CCCAAGCGTC	CCGTTGACAA	GCCCCTCCGT	CTTCCCCTCC	600
	AGGATGTCTA	CAAGATCGGT	GGTATTGGAA	CGGTTCCCGT	CGGCCGTATT	650
	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTCG	CTCCCTCCAA	700
	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	CAGYTCAGTK	750
40	AGGGCCAGCC	CGGTGACAAC	GTTGGTTTCA	ACGTGAAGAA	CGTTTCCGTC	800
	AAGGACATCC	GACGTGGTAA	CGTCGCTGGT	GACTCCAAGA	ACGACCCCCC	850
	CCAGGGTGCC	GCTTCTTTCA	CCGCCAGGT	CATCGTCCTC	AACCACCCCG	900
	GCCAGGTCGG	TGCTGGTTAC	GCTCCTGTCC	TCGATTGCCA	CACTGCCCAC	950
	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	GCCGAACCGG	1000
45	TAAGGCTACT	GAGGCCGCTC	CCAAGTTCAT	CAAGTCTGGT	GACTCCGCCA	1050
	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GTGTCGAGGC	TTTCACTGAC	1100
	TACCCTCCT					1109

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2) INFORMATION FOR SEQ ID NO: 1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus terreus*
- (B) STRAIN: WSA-174

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279

	CCTGCAAGTG	GTCTGAGGAC	CGTTACAACG	AAATCGTGAA	GGAGACCTCC	50
15	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTC	CCTTCGTCCC	100
	CATCTCCGGT	TTCAACGGTG	ACAACATGCT	TGAGCCTTCC	CCCAACTGCC	150
	CCTGGTACAA	GGGTTGGGAG	AAGGAGGGCA	AGTCCGGCAA	GGTCACCGGT	200
	AAGACTCTCC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCGG	TCCGTCCTGC	250
	CAACAAGCCT	CTCCGTCTTC	CCCTCCAGGA	TGTGTACAAG	ATCTCTGGTA	300
20	TCGGAAGTGT	CCCCGTCGGC	CGTGTCGAGA	CTGGTGTTCAT	CACCCCCGGC	350
	ATGGTTGTTA	CCTTCGCTCC	TTCCAACGTC	ACCACTGAAG	TGAAGTCCGT	400
	TGAGATGCAC	CACCAGCAGC	TCAAGGAGGG	TCTCCCCGGT	GACAACGTTG	450
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AGGTCCGTCG	TGGTAACGTC	500
	GCTGGTGACT	CCAAGAACGA	CCCCCCTGCT	GGCGCTGCCT	CCTTCACCGC	550
25	CCAGGTCATC	GTTCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGCTACGCCC	600
	CCGTCCTCGA	CTGCCACACT	GCCCACATTG	CCTGCAAGTT	CGCTGAGCTC	650
	CAGGAGAAGA	TTGACCGCCG	TACCGGAAAG	TCTGTTGAGT	CTTCTCCCAA	700
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATC	CCTYCAAAGC	750
	CCATGTGCGT	CGAAG				765

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2) INFORMATION FOR SEQ ID NO: 1280

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 64746

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280

	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	GAAGTTCCAG	ACTCCCAAGT	50
50	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	CGCCCCGATA	TGTTTTGGTG	100
	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	150
	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	CTGCGCTATC	CTCATCATTTG	200
	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	TCTCCAAGGA	TGGCCAGACC	250

	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	GGTGTCAAGC	AGCTCATCGT	300
	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	GTCCGAGGAT	CGTTACAACG	350
	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	400
	AAGGCCGTTC	CCTTCGTMCC	CATCKCTGGC	TTCAACGGTG	ACAACATGCT	450
5	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	GGGATGGGAG	AAGGAGACCA	500
	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	TCGAGGCCAT	YGACGCCATT	550
	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	CTYCGTCTTC	CCCTCCAGGA	600
	TGTYTACAAG	ATCTCTGGTA	TCGGAACGGT	CCCTGTCGGC	CGTGTCGAGA	650
	CCGGTATCAT	CAAGCCCCGGC	ATGGTCGTCA	CCTTTGCCCC	CGCCAACGTC	700
10	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	CACCAGCAGC	TCCAGGAGGG	750
	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	CAAGAACGTT	TCCGTCAAGG	800
	AAGTCCSCCG	TGGTAACGTT	TGCGGTGACT	CCAAGAACGA	TCCCCCTCAG	850
	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	GTCCTCAACC	ACCCCGGTCA	900
	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	CTGCCACACT	GCCCACATTG	950
15	CTTGCAAGTT	CTYTGAGCTG	CTTGAGAAGA	TTGACCGCCG	TACCGGCAAG	1000
	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	TCCGGTGAWG	CCGCCATCGT	1050
	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	CGAGTCCTTC	ACTGACTACC	1100
	CCCCT					1105

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2) INFORMATION FOR SEQ ID NO: 1281

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 1343 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus laurentii*
- (B) STRAIN: ATCC 44096
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281

	GCCGAGCGAG	AGCGAGGTAT	CACCATCGAC	ATTGCTCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACAACGTCA	CCGTCATTGA	CGCCCCCGGA	CACCGAGACT	100
40	TCATCAAGAA	CATGATCACC	GGTACCTCCC	AGGCCGACTG	CGCCATCCTT	150
	ATCATTGCCA	CCGGTATCGG	AGAGTTCGAG	GCCGGTATCT	CTAAGGACGG	200
	TCAGACCCGA	GAGCACGCTT	TGCTCGCCTT	CACCCTCGGT	GTCAGGCAGC	250
	TCATCGTTGC	TTGCAACAAG	ATGGACACCT	GCAAGTGGTC	CGAGGACCGA	300
	TTCAACGAGA	TCGTCAAGGA	GACCAACGGT	TTCATCAAGA	AGGTCGGATA	350
45	CAACCCCAAG	GCTGTTCCCT	TCGTCCCCAT	CTCTGGATGG	CACGGAGACA	400
	AGTGAGTGCC	GTTCTTTGCG	TTGAGCCCTC	TTTGTCGCTC	CCCCTCCCTC	450
	TCAAGTGGCG	GCGGCGGTCT	CCACCCACAA	ATCGGGTGGC	GAATCCGCCA	500
	CACCCACCAC	TTCTCGCCAC	CGAGTGTGGC	ACTTCTTCCA	ACTCCTCTTT	550
	CCACTCCTCC	TCGTCTCGTC	TCTTTTTTTC	TCCGTTGTCT	TTGACAAGGG	600
50	GAGTGTGCTG	ATAGTAAAGC	ATGCTTGAGG	AGACCACCAA	CATGCCGTGG	650
	TACAAGGGAT	GGACCAAGGA	GACCAAGTCC	GGTGTCGTTA	AGGGTAAGAC	700
	CCTCCTCGAC	GCCATCGACG	CCATCGAGCC	TCCTCAACGA	CCCACCGACA	750
	AGCCCCTCCG	ACTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATCGGT	800

	ACGGTGCCCG	TCGGCCGAGT	CGAGACCGGT	GTCATCAAGG	CCGGGTAAGT	850
	CACGGGAGCC	TGACGGCTGT	TGTTGCCACA	CCCAACTTAT	ATCCAGTATG	900
	GTCGTCACCT	TCGCTCCTAC	CAACGTCACC	ACTGAGGTTA	AGTCCGTTGA	950
	GATGCACCAC	GAGCAGATCC	CTGAGGGTCT	TCCCGGAGAC	AACGTTGGTT	1000
5	TCAACGTGAA	GAACGTTTCC	ATCAAGGACA	TCCGACGAGG	AAACGTYTGC	1050
	TCCGACTCCA	AGAACGACCC	CGCTAAGGAG	GCCGCTTCTT	TCAACGCCCA	1100
	GGTCATTGTC	CTCAACCACC	CTGGACAGAT	TGGTGCCGGT	TACACCCCCG	1150
	TCCTCGACTG	CCACACCGCC	CACATTGCCT	GCAAGTTCGC	CGAGCTCATC	1200
	GAGAAGATCG	ACCGACGAAC	TGGTAAGACC	ATGGAGGCCG	CCCCCAAGTT	1250
10	CGTCAAGTCC	GGAGACGCCG	CCATTGTCAA	GCTCGTTGCC	CAGAAGCCCA	1300
	TCTGTGTCGA	GTCTTACTCT	GACTACCCTC	CCCTTGGACG	ATT	1343

15 2) INFORMATION FOR SEQ ID NO: 1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282

30	TGGTCCGAGG	CTCGTTTCAA	CGAAATCATC	AAGGAAGTCA	CCAACTTCAT	50
	CAAGAAGGTC	GGATACAACC	CCAAGTCTGT	TCCCTTCGTG	CCAATCTCTG	100
	GTTTCGAGGG	TGATAACATG	ATTGAGCCCT	CCACCAACTG	CCCCTGGTAC	150
	AAGGGCTGGA	CCAAGGAGAC	CGCTGCCGGC	AAGTCAACCG	GTAAGACTCT	200
35	TCTTGACGCC	ATTGATGCCA	TCGATCAACC	CTCCCGTCCT	ACCGACAAGC	250
	CCCTCCGTCT	TCCCCTCCAG	GATGTGTACA	AGATCTCCGG	TATTGGCACT	300
	GTTCCCGTTG	GACGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTCGT	350
	GACCTTCGCT	CCCTCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	400
	ACCACCAACA	GCTCTTGGCT	GGTAACCCCG	GTGACAACGT	CGGTTTCAAC	450
40	GTCAAGAACG	TTTCCGTCAA	GGAAGTCCGC	CGTGGCAACG	TTGCTGGTGA	500
	CTCAAAGAAC	GACCCCCCCA	AGGGCTGCGA	CTCCTTCAAC	GCCCAGGTCA	550
	TCGTCCTCAA	TCACCCCGGT	CAAGTTGGCG	CTGGTTATGC	CCCAGTCCTC	600
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TCCTCGAGAA	650
	GATTGACCGC	CGTACCGGAA	AGTCCACTGA	GAACAACCCC	AAGTTCATCA	700
45	AGTCTGGTGA	CGCCGCTATC	GTCAAGATGG	TTCC		734

2) INFORMATION FOR SEQ ID NO: 1283

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*
(B) STRAIN: ATCC 62877

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283

	CGTGAGCGTG	GTATCACCAT	CGACATTGCC	CTCTGGAAGT	TCGAGACTCC	50
	CCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GCTGTCACCT	CTCTCACACA	100
	TGTCTCACCA	CTAACAATCA	ACAGACGCCC	CCGGCCACCG	TGACTTCATC	150
15	AAGAACATGA	TCACTGGTAC	TTCCCAGGCC	GACTGCGCCA	TTCTCATCAT	200
	TGCCGCTGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	250
	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GAACCTCATT	300
	GTCGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTACCA	350
	GGAGATCATC	AAGGAGACCT	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	400
20	CCAAGGCTGT	CGCTTTCGTC	CCCATCTCCG	GTTTCAACGG	CGACAACATG	450
	CTTACTCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGCTGGG	AGCGTGAGAT	500
	CAAGTCCGGC	AAGCTCACTG	GCAAGACCCT	CCTCGAGGCC	ATTGACTCCA	550
	TCGAGCCCCC	CAAGCGTCCC	GTCGACAAGC	CCCTCCGACT	TCCCCTCCAG	600
	GATGTCTACA	AGATCGGTGG	TATTGGCACG	GTTCCCGTCG	GCCGTATCGA	650
25	GACTGGTGTC	ATCAAGCCCG	GTATGGTCGT	TACCTTCGCC	CCCTCCAACG	700
	TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACCACGAGCA	GCTCTYTGAG	750
	GGTCTTCCCG	GTGACAACGT	CGGCTTCAAC	GTKAAGAACG	TYTCCGTCAA	800
	GGAGATCCGA	CGTGGCAACG	TCGCTGGTGA	CTCCAAGAAC	GACCCCCCTY	850
	TGGGTGCCGC	CTCTTTCACC	GCCCAGGTCA	TTGTCCTCAA	CCACCCTGGC	900
30	CAGGTCGGTG	CCGGTTACGC	CCCCGTTYTG	GACTGCCACA	CTGCCCACAT	950
	TGCCTGCAAG	TTCGCCGAGA	TCCAGGAGAA	GATCGACCGC	CGAACTGGTA	1000
	AGGCTGTTGA	GTCCGCCCCC	AAGTTCATCA	AGTCTGGTGA	CTCCGCCATC	1050
	GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACTGACTA	1100
	CCCCCCT					1107

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2) INFORMATION FOR SEQ ID NO: 1284

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: ATCC 14285

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284

	GCTCAAGGCC	GAGCGTGAGC	GCGGTATCAC	CATCGATATT	GCTCTGTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TACGTCACCG	TCATTGACGC	CCCCGGTCAT	100
	CGCGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTTCGAGGCT	GGTATCTCCA	200
5	AGGATGGCCA	GACTCGTGAG	CACGCTCTGC	TCGCCTACAC	CCTGGGTGTG	250
	CGGCAGCTGA	TCGTCGCCAT	CAACAAGATG	GACACGGCCA	AGTGGGCTGA	300
	GGCTCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAAC TTC	ATCAAGAAGG	350
	TCGGCTACAA	CCCCAAGACT	GTTGCCTTCG	TCCCCATCTC	GGGCTTCCAC	400
	GGCGACAACA	TGCTTACTCC	CTCGACCAAC	TGCCCCCTGGT	ACAAGGGCTG	450
10	GGAGAAGGAG	GGCAAGAGCG	GCAAGGTTAC	CGGTAAGACT	CTGCTGGACG	500
	CCATTGACGC	CGTCGAGCCC	CCCAAGCGCC	CCACGGACAA	GCCCCTGCGT	550
	CTGCCCCCTCC	AGGATGTCTA	CAAGATCGGC	GGTATCGGCA	CTGTCCCTGT	600
	CGGCCGTATC	GAGACTGGTG	TCCTGAAGCC	CGGCATGGTC	GTCACCTTTG	650
	CCCCGTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
15	CAGCTTGTTG	AGGGTGTTCC	CGGCGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
	CGTYTCCGTC	AAGGAGATCC	GTGTTGGCAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCCCC	CTCGGGCGCC	GCCACCTTCA	ACGCCCAGGT	CATTGTCCTG	850
	AACCACCCCG	GCCAGGTCGG	CAACGGCTAC	GCCCCGGTTY	TGGACTGCCA	900
	CACCGCCAC	ATTGCCTGCA	AGTTCACCGA	GATCCTTGAG	AAGATCGACC	950
20	GCCGTACCGG	CAAGTCGGTT	GAGAACAACC	CCAAGTTCAT	CAAGTCGGGT	1000
	GACGCCGCCA	TTGTCAAGCT	GACGCCCTYG	AAGCCCATGT	GCGTT	1045

25 2) INFORMATION FOR SEQ ID NO: 1285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285

40	TTGCCAGTGG	TCCGAGGCC	GTTACAACGA	AATCGTCAAG	GAGACTTCCG	50
	GTTTCATCAA	GAAGGTCGGA	TACAACCCCA	AGTCCGTTGC	CTTCGTCCCC	100
	ATCTCCGGTT	TCAACGGTGA	CAACATGCTC	GAGGCCTCTA	CCAAGTCCCC	150
	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	GGCCGGTAAG	GCCACTGGTA	200
45	AGACCCTCCT	TGAGGCCATC	GACGCCATTG	AGCCCCCCAC	CCGTCCCTCC	250
	AACAAGCCCC	TCCGTCTTCC	CCTCCAGGAT	GTCTACAAGA	TCTCCGGTAT	300
	TGGAAC TGTC	CCCGTCGGCC	GTGTCGAGAC	TGGTGTTATC	ACCCCCGGCA	350
	TGGTCGTCAC	CTTCGCTCCT	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTT	400
	GAGATGCACC	ACCAGCAGCT	CAAGGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
50	TTTCAACGTC	AAGAACGTTT	CCGTCAAGGA	AATCCGTCGT	GGTAACGTTG	500
	CCTCCGACTC	CAAGAACGAC	CCCGCCTCCG	GCGCTGCCTC	TTTCAACGCC	550
	CAGGTCATCG	TTCTCAACCA	CCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	600
	CGTCCTCGAC	TGCCACACCG	CCCACATTGC	TTGCAAGTTC	TCTGAGCTTC	650

TTGAGAAGAT	TGACCGCCGT	ACCGGAAAGG	CTGTTGAAAC	CAGCCCCAAG	700
TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	CTTCCAAGCC	750
CATGTGCGKT	CCGA				764

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2) INFORMATION FOR SEQ ID NO: 1286

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 971 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 16264

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286

ACCATCGATA	TCGCGCTCTG	GAAGTTCGAG	ACTCCCAAGT	ACTTCGTCAC	50
CGTCATCGAT	GCCCCTGGTC	ATCGTGACTT	CATCAAGAAC	ATGATCACTG	100
25 GTACCTCCCA	GGCTGATTGT	GCTATTCTCA	TCATTGCCGC	TGGTACTGGT	150
GAGTTCGAGG	CCGGTATCTC	CAAGGATGGC	CAGACCCGTG	AGCATGCTCT	200
GCTCGCCTAC	ACCCTGGGCG	TGAAGCAGCT	TATCGTCGCC	ATCAACAAGA	250
TGGACACCAC	CAAATGGTCT	GAGGATCGTT	TCAACGAAAT	CATCAAGGAG	300
ACTTCCAACT	TCATCAAGAA	GGTCGGATAC	AACCCCAAGT	CCGTTCCATT	350
30 CGTGCCCATC	TCCGGCTTCA	ACGGTGACAA	CATGATCGAC	GTCTCCACCA	400
ATGCCCCCTG	GTACAAGGGC	TGGGAAAAGG	AGTCCAAGGC	TGGCAAGGCC	450
ACCGGCAAGA	CCCTCCTTGA	GGCTATCGAC	TCCATCGACC	CTCCTGCTCG	500
TCCCACCGAC	AAGCCTCTCC	GTCTCCCCT	CCAGGATGTC	TACAAGATTT	550
CTGGTATCGG	CACGGTGCCC	GTCGGTCGTG	TTGAGACTGG	TACCATCAAG	600
35 GCCGGTATGG	TCGTCACCTT	TGCCCCCGCC	AACGTCACCA	CTGAAGTCAA	650
GTCCGTCGAA	ATGCACCACG	AACAGCTYGC	CGAGGGCGTT	CCGGGTGACA	700
ACGTCGGCTT	CAACGTCAAG	AACGTYTCCG	TGAAGGAGGT	TCGTCGTGGA	750
AACGTTGCTG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTG	CCGACTCCTT	800
CAACGCCCAG	GTCATCGTCC	TCAACCACCC	TGGTCAGGTC	GGTGCTGGCT	850
40 ACGCCCCGGT	CTTGGATTGC	CACACTGCCC	ACATTGCCTG	CAAGTTCTYT	900
GAGCTCCTCG	AGAAGATCGA	TCGTCGKACC	GGCAAGTCCA	TGGAAAACAA	950
CCCCAAGTTC	ATCAAGTCTG	G			971

45

2) INFORMATION FOR SEQ ID NO: 1287

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Exserohilum rostratum*
(B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287

	GGTCTGAGGA	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	50
10	AAGAAGGTCG	GCTACAACCC	CAAGCACGTT	CCCTTCGTCC	CCATCTCCGG	100
	TTTCAACGGA	GACAACATGA	TCGAGGCCTC	CAGCAACTGC	CCCTGGTACA	150
	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACTGGTAA	GACCCTCCTT	200
	GAGGCCATTG	ACGCCATCGA	CCCTCCCAGC	CGTCCTACCG	ACAAGCCCCT	250
	CCGTCTTCCC	CTCCAGGATG	TCTACAAGAT	TGGTGGTATT	GGCACGGTTC	300
15	CCGTCGGTCG	TGTCGAGACC	GGTATCATCA	AGGCCGGTAT	GGTCGTCACC	350
	TTCGCCCCCG	CTGGTGTCAC	CACTGAAGTC	AAGTCCGTCG	AGATGCACCA	400
	CGAGCAGCTT	ACCGAGGGTG	TCCCCGGTGA	CAACGTCGGC	TTCAACGTCA	450
	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GTAACGTTGC	CGGTGACTCC	500
	AAGAACGACC	CCCCCAAGGG	CTGCGAGTCT	TTCAACGCTC	AGGTCATTGT	550
20	CCTCAACCAC	CCTGGTCAGG	TCGGTGCCGG	TTACGCGCCA	GTCCTCGACT	600
	GCCACACCGC	CCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	CGAGAAGATT	650
	GACCGCCGTA	CCGGAAAGTC	TGTCGAAGCC	TCTCCCAAGT	TCATCAAGTC	700
	TGGTGACGCG	GCCATCGTCA	AGATGGTTCC	CT		732

25

2) INFORMATION FOR SEQ ID NO: 1288

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 337 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: HER 1236

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288

	AATGGATCCT	GTATACGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTRC	50
	TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTGGAAAT	CGCGGAAGCA	100
45	CTTGTACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
	TCTTGTACCG	AAAGCAGAGA	TTGAAGGCCA	TATGGGTGAC	TCACACGTAG	200
	GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTMGTAAGCT	TTCAGGAGCA	250
	ATCAACAAAT	CARRARCAAT	WGCAATCTTT	ATTAACCAAA	TTCGWGAAAA	300
	AGTTGGGGTT	ATGTTTCGGAA	ACCCAGAAAC	AACTCCA		337

50

2) INFORMATION FOR SEQ ID NO: 1289

700

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289

15 AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTTC 50
 TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA 100
 CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC 150
 TCTTGTACCG AAAGCAGAGA TTGAAGGCGA TATGGGTGAC TCACACGTAG 200
 20 GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA 250
 ATCAACAAAT CARAARCAAT TGCAATCTTT ATTAACCAAA TTCGTGAAAA 300
 AGTTGGGGTT ATGTTGCGAA ACCCAGAAAC AACTCC 336

25 2) INFORMATION FOR SEQ ID NO: 1290

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290

GAYTAYGCIA TGISIGTIAT HGT 23

40 2) INFORMATION FOR SEQ ID NO: 1291

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291

GCIYTICIG AYGTINGIGA YGG

23

5 2) INFORMATION FOR SEQ ID NO: 1292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292

ARISCYTCIA RIATRTGIGC

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20

2) INFORMATION FOR SEQ ID NO: 1293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293

ATGGCTGAAT TACCTCAATC

20

35

2) INFORMATION FOR SEQ ID NO: 1294

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294

ATGATTGTTG TATATCTTCT TCAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1295

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295

CAGAAAGTTT GAAGCGTTGT 20

15 2) INFORMATION FOR SEQ ID NO: 1296

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296

AACGATTCGT GAGTCAGATA 20

30 2) INFORMATION FOR SEQ ID NO: 1297

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297

CGGTCAACAT TGAGGAAGAG CT 22

45 2) INFORMATION FOR SEQ ID NO: 1298

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298

ACGAAATCGA CCGTCTCTTT TTC

23

10

2) INFORMATION FOR SEQ ID NO: 1299

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 2711 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

(A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: 601055
(C) ACCESSION NUMBER: X71437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299

	ATGGCTGAAT	TACCTCAATC	AAGAATAAAT	GAACGAAATA	TTACCAGTGA	50
	AATGCGTGAA	TCATTTTITAG	ATTATGCGAT	GAGTGTTATC	GTTGCTCGTG	100
30	CATTGCCAGA	TGTTCGTGAC	GGTTTAAAC	CAGTACATCG	TCGTATACTA	150
	TATGGATTAA	ATGAACAAGG	TATGACACCG	GATAAATCAT	ATAAAAAATC	200
	AGCACGTATC	GTTGGTGACG	TAATGGGTAA	ATATCACCTT	CATGGTGACT	250
	CATCTATTTA	TGAAGCAATG	GTACGTATGG	CTCAAGATTT	CAGTTATCGT	300
	TATCCGCTTG	TTGATGGCCA	AGGTAACCTT	GGTTCAATGG	ATGGAGATGG	350
35	CGCAGCAGCA	ATGCGTTATA	CTGAAGCGCG	TATGACTAAA	ATCACACTTG	400
	AACTGTTACG	TGATATTAAT	AAAGATACAA	TAGATTTTAT	CGATAACTAT	450
	GATGGTAATG	AAAGAGAGCC	GTCAGTCTTA	CCTGCTCGAT	TCCCTAATTT	500
	ATTAGCCAAT	GGTGCATCAG	GTATCGCGGT	AGGTATGGCA	ACGAATATTC	550
	CACCACATAA	CTTAACAGAA	TTAATCAATG	GTGTACTTAG	CTTAAGTAAG	600
40	AACCCTGATA	TTTCAATTGC	TGAGTTAATG	GAAGATATTG	AAGGTCCTGA	650
	TTTCCCAACT	GCTGGACTTA	TTTTAGGTAA	GAGTGGTATT	AGACGTGCAT	700
	ATGAAACAGG	TCGTGGTTCA	ATTCAAATGC	GTTCTCGTGC	AGTTATTGAA	750
	GAACGTGGAG	GCGGACGTCA	ACGTATTGTT	GTCACTGAAA	TTCTTTTCCA	800
	AGTGAATAAG	GCTCGTATGA	TTGAAAAAAT	TGCAGAGCTC	GTTCGTGACA	850
45	AGAAAATTGA	CGGTATCACT	GATTTACGTG	ATGAAACAAG	TTTACGTACT	900
	GGTGTGCGTG	TCGTTATTGA	TGTGCGTAAG	GATGCAAATG	CTAGTGTCAT	950
	TTTAAATAAC	TTATACAAAC	AAACACCTCT	TCAAACATCA	TTTGGTGTGA	1000
	ATATGATTGC	ACTTGTAAT	GGTAGACCGA	AGCTTATTAA	TTTAAAAGAA	1050
	GCGTTGGTAC	ATTATTTAGA	GCATCAAAAG	ACAGTTGTTA	GAAGACGTAC	1100
50	GCAATATAAC	TTACGTAAAG	CTAAAGATCG	TGCCCATATT	TTAGAAGGGT	1150
	TACGTATCGC	ACTTGACCAT	ATCGATGAAA	TTATTTCAAC	GATTCGTGAG	1200
	TCAGATACAG	ATAAAGTTGC	AATGGAAAGC	TTGCAACAAC	GCTTCAAAC	1250
	TTCTGAAAAA	CAAGCTCAAG	CTATTTTAGA	CATGCGTTTA	AGACGTCTAA	1300

	CAGGTTTAGA	GAGAAACAAA	ATTGAAGCTG	AATATAATGA	GTTATTAAAT	1350
	TATATTAGTG	AATTAGAAGC	CATCTTAGCT	GATGAAGAAG	TGTTATTACA	1400
	GTTAGTTAGA	GATGAATTGA	CTGAAATTAG	AGATCGTTTC	GGTGATGAGC	1450
	GTCGTACAGA	AATTCAATTA	GGTGGATTTG	AAGACTTAGA	GGACGAAGAC	1500
5	TTAATTCCAG	AAGAACAAAT	AGTAATTACT	TTGAGCCATA	ATAACTACAT	1550
	TAAACGTTTG	CCGGTATCTA	CATATCGTGC	TCAAAACCGT	GGTGGTCGTG	1600
	GTGTTCAAGG	TATGAATACA	TTGGAAGAAG	ATTTTGTGAG	TCAATTGGTA	1650
	ACTTTAAGTA	CACATGACCA	TGTATTGTTC	TTTACTAACA	AAGGTCGTGT	1700
	ATACAAACTA	AAAGGTTATG	AAGTGCCTGA	GTTATCAAGA	CAGTCTAAAG	1750
10	GTATTCCTGT	AGTGAATGCT	ATTGAACTTG	GAAATGATGA	AGTCATTAGT	1800
	ACAATGATTG	CTGTAAAGA	CCTTGAAAGT	GAAGACAAC	TCTTAGTGTT	1850
	TGCAACTAAA	CGTGGTGTTG	TTAAACGTTT	AGCATTAAGT	AACTTCTCAA	1900
	GAATAAATAG	AAATGGTAAG	ATTGCGATTT	CGTTCAGAGA	AGATGATGAG	1950
	TTAATTGCAG	TTCGTTTAAC	AAGTGGTCAA	GAAGATATCT	TGATTGGTAC	2000
15	ATCACATGCA	TCATTAATTC	GATTCCCTGA	ATCAACATTA	CGTCCTTTAG	2050
	GCCGTACAGC	AACGGGTGTG	AAAGGTATTA	CACTTCGTGA	AGGTGACGAA	2100
	GTTGTAGGGC	TTGATGTAGC	TCATGCAAAC	AGTGTTGATG	AAGTATTAGT	2150
	AGTTACTGAA	AATGGTTATG	GTAAACGTAC	GCCAGTTAAT	GACTATCGTT	2200
	TATCAAATCG	TGGTGGTAAA	GGTATTAAAA	CAGCTACGAT	TACTGAGCGT	2250
20	AATGGTAATG	TTGTATGTAT	CACTACAGTA	ACTGGTGAAG	AAGATTTAAT	2300
	GATTGTTACT	AATGCCGGTG	TCATTATTCG	ACTAGATGTT	GCAGATATTT	2350
	CTCAAATGG	TCGTGCAGCA	CAAGGTGTTC	GCTTAATTCG	CTTAGGCGAT	2400
	GATCAATTTG	TTTCAACGGT	TGCTAAAGTA	AAAGAGGATG	CAGATGAAGT	2450
	AAATGAAGAT	GAACAATCTA	CTGTATCTGA	AGATGGTACT	GAACAACAAC	2500
25	GTGAAGCGGT	TGTAAATGAT	GAAACACCAG	GAAATGCAAT	TCATACTGAA	2550
	GTGATTGATT	CAGAAGAAAA	TGATGAAGAT	GGACGTATTG	AAGTAAGACA	2600
	AGATTTTCATG	GATCGTGTTG	AAGAAGATAT	ACAACAATCA	TCAGATGAAG	2650
	ATGAAGAATA	A				2711

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2) INFORMATION FOR SEQ ID NO: 1300

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 2628 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: K12

45 (C) ACCESSION NUMBER: X57174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300

	ATGAGCGACC	TTGCGAGAGA	AATTACACCG	GTCAACATTG	AGGAAGAGCT	50
50	GAAGAGCTCC	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	100
	TGCCAGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	150
	GCCATGAACG	TACTAGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCTGC	200
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCATCCCCAT	GGTGACTCGG	250

	CGGTCTATGA	CACGATCGTC	CGCATGGCGC	AGCCATTCTC	GCTGCGTTAT	300
	ATGCTGGTAG	ACGGTCAGGG	TAACTTCGGT	TCTATCGACG	GCGACTCTGC	350
	GGCGGCAATG	CGTTATACGG	AAATCCGTCT	GGCGAAAATT	GCCCATGAAC	400
	TGATGGCCGA	TCTCGAAAAA	GAGACGGTCG	ATTTCGTTGA	TAACTATGAC	450
5	GGCACGGAAA	AAATTCCGGA	CGTCATGCCA	ACCAAAATTC	CTAACCTGCT	500
	GGTGAACGGT	TCTTCCGGTA	TCGCCGTAGG	TATGGCAACC	AACATCCCGC	550
	CGCACAACCT	GACGGAAGTC	ATCAACGGTT	GTCTGGCGTA	TATTGATGAT	600
	GAAGACATCA	GCATTGAAGG	GCTGATGGAA	CACATCCCGG	AGCCGGACTT	650
	CCCGACGGCG	GCAATCATTA	ACGGTCGTCG	CGGTATTGAA	GAAGCTTACC	700
10	GTACCGGTCG	CGGCAAGGTG	TATATCCGCG	CTCGCGCAGA	AGTGGAAGTT	750
	GACGCCAAAA	CCGGTCGTGA	AACCATTATC	GTCCACGAAA	TTCCGTATCA	800
	GGTAAACAAA	GCGCGCCTGA	TCGAGAAGAT	TGCGGAACTG	GTAAAAGAAA	850
	AACGCGTGGA	AGGCATCAGC	GCGCTGCGTG	ACGAGTCTGA	CAAAGACGGT	900
	ATGCGCATCG	TGATTGAAGT	GAAACGCGAT	GCGGTCGGTG	AAGTTGTGCT	950
15	CAACAACCTC	TACTCCCAGA	CCCAGTTGCA	GGTTTCTTTC	GGTATCAACA	1000
	TGGTGGCATT	GCACCATGGT	CAGCCGAAGA	TCATGAACCT	GAAAGACATC	1050
	ATCGCGGCGT	TTGTTCGTCA	CCGCCGTGAA	GTGGTGACCC	GTCGTACTAT	1100
	TTTCGAACTG	CGTAAAGCTC	GCGATCGTGC	TCATATCCTT	GAAGCATTAG	1150
	CCGTGGCGCT	GGCGAACATC	GACCCGATCA	TCGAACTGAT	CCGTCATGCG	1200
20	CCGACGCCTG	CAGAAGCGAA	AACTGCGCTG	GTTGCTAATC	CGTGGCAGCT	1250
	GGGCAACGTT	GCCGCGATGC	TCGAACGTGC	TGGCGACGAT	GCTGCGCGTC	1300
	CGGAATGGCT	GGAGCCAGAG	TTCGGCGTGC	GTGATGGTCT	GTACTACCTG	1350
	ACCGAACAGC	AAGCTCAGGC	GATTCTGGAT	CTGCGTTTGC	AGAAACTGAC	1400
	CGGTCTTGAG	CACGAAAAAC	TGCTCGACGA	ATACAAAGAG	CTGCTGGATC	1450
25	AGATCGCGGA	ACTGTTGCGT	ATTCTTGGA	GCGCCGATCG	TCTGATGGAA	1500
	GTGATCCGTG	AAGAGCTGGA	GCTGGTTCGT	GAACAGTTCG	GTGACAAACG	1550
	TCGTACTGAA	ATCACCGCCA	ACAGCGCAGA	CATCAACCTG	GAAGATCTGA	1600
	TCACCCAGGA	AGATGTGGTC	GTGACGCTCT	CTCACCAGGG	CTACGTTAAG	1650
	TATCAGCCGC	TTTCTGAATA	CGAAGCGCAG	CGTCGTGGCG	GGAAAGGTAA	1700
30	ATCTGCCGCA	CGTATTAAAG	AAGAAGACTT	TATCGACCGA	CTGCTGGTGG	1750
	CGAACACTCA	CGACCATATT	CTGTGCTTCT	CCAGCCGTGG	TCGCGTCTAT	1800
	TCGATGAAAG	TTTATCAGTT	GCCGGAAGCC	ACTCGTGGCG	CGCGCGGTCG	1850
	TCCGATCGTC	AACCTGCTGC	CGCTGGAGCA	GGACGAACGT	ATCACTGCGA	1900
	TCCTGCCAGT	GACCGAGTTT	GAAGAAGGCG	TGAAAGTCTT	CATGGCGACC	1950
35	GCTAACGGTA	CCGTGAAGAA	AACTGTCCTC	ACCGAGTTCA	ACCGTCTGCG	2000
	TACCGCCGGT	AAAGTGGCGA	TCAAACCTGGT	TGACGGCGAT	GAGCTGATCG	2050
	GCGTTGACCT	GACCAGCGGC	GAAGACGAAG	TAATGCTGTT	CTCCGCTGAA	2100
	GGTAAAGTGG	TGCGCTTTAA	AGAGTCTTCT	GTCCGTGCGA	TGGGCTGCAA	2150
	CACCACCGGT	GTTCGCGGTA	TTCGCTTAGG	TGAAGGCGAT	AAAGTCGTCT	2200
40	CTCTGATCGT	GCCTCGTGGC	GATGGCGCAA	TCCTCACCGC	AACGCAAAAC	2250
	GGTTACGGTA	AACGTACCGC	AGTGGCGGAA	TACCCAACCA	AGTCGCGTGC	2300
	GACGAAAGGG	GTTATCTCCA	TCAAGGTTAC	CGAACGTAAC	GGTTTAGTTG	2350
	TTGGCGCGGT	ACAGGTAGAT	GA CTGCGACC	AGATCATGAT	GATCACCGAT	2400
	GCCGGTACGC	TGGTACGTAC	TCGCGTTTCG	GAAATCAGCA	TCGTGGGCCG	2450
45	TAACACCCAG	GGCGTGATCC	TCATCCGTAC	TGCGGAAGAT	GAAAACGTAG	2500
	TGGGTCTGCA	ACGTGTTGCT	GAACCGGTTG	ACGAGGAAGA	TCTGGATACC	2550
	ATCGACGGCA	GTGCCGCGGA	AGGGGACGAT	GAAATCGCTC	CGGAAGTGGA	2600
	CGTTGACGAC	GAGCCAGAAG	AAGAATAA			2628

50

2) INFORMATION FOR SEQ ID NO: 1301

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301
10 GTIMGIAWIM GICCIGSIAT GTA 23

15 2) INFORMATION FOR SEQ ID NO: 1302

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302

TAIADIGGIG GIKKIGCIAT RTA 23

30 2) INFORMATION FOR SEQ ID NO: 1303

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303

GGIGAIGAIID YIMGIGARGG 20

45 2) INFORMATION FOR SEQ ID NO: 1304

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1304

5

CIARYTTIKY ITTIGTYTG

19

10 2) INFORMATION FOR SEQ ID NO: 1305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305

ATGGTGACTG CATTGTCAGA TG

22

25

2) INFORMATION FOR SEQ ID NO: 1306

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306

GTCTACGGTT TTCTACAACG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1307

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1923 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: M86227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307

5	ATGGTGACTG	CATTGTCAGA	TGTAAACAAC	ACGGATAATT	ATGGTGCTGG	50
	GCAAATACAA	GTATTAGAAG	GTTTAGAAGC	AGTACGTAAA	AGACCAGGTA	100
	TGTATATAGG	ATCGACTCAG	AGAGAGTTGC	ACATTAGTGT	GGAAATTGTC	150
	GATAATAGTA	TCGATGAAGC	ATTAGCTGGT	TATGCAAATA	AAATTGAAGT	200
	TGTTATTGAA	AAAGATAACT	GGATTAAAGT	AACGGATAAC	GGACGTGGTA	250
10	TCCCAGTTGA	TATTCAAGAA	AAAATGGGAC	GTCCAGCTGT	CGAAGTTATT	300
	TTAACTGTTT	TACATGCTGG	TGGTAAATTC	GGCGGTGGCG	GATACAAAGT	350
	ATCTGGTGGT	TTACATGGTG	TTGGTTCATC	AGTTGTAAAC	GCATTGTCAC	400
	AAGACTTAGA	AGTATATGTA	CACAGAAATG	AGACTATATA	TCATCAAGCA	450
	TATAAAAAAG	GTGTACCTCA	ATTTGACTTA	AAAGAAGTTG	GCACAACTGA	500
15	TAAGACAGGT	ACTGTCATTC	GTTTTAAAGC	AGATGGAGAA	ATCTTCACAG	550
	AGACAACGTG	ATACAACAT	GAAACATTAC	AGCAGCGTAT	TAGAGAGCTT	600
	GCTTCTTAA	ACAAAGGAAT	TCAAATCACA	TTAAGAGATG	AACGTGATGA	650
	AGAAAACGTT	AGAGAAGACT	CCTATCACTA	TGAGGGCGGT	ATTAAATCGT	700
	ACGTTGAGTT	ATTGAACGAA	AATAAAGAAC	CTATTCATGA	TGAGCCAATT	750
20	TATATTCATC	AATCTAAAGA	TGATATTGAA	GTAGAAATTG	CGATTCAATA	800
	TAATCAGGA	TATGCCACAA	ATCTTTTAAC	TTACGCAAAT	AACATTCATA	850
	CGTACGAAGG	TGGTACGCAT	GAAGACGGAT	TCAAACGTGC	ATTAACGCGT	900
	GTCTTAAATA	GTTATGGTTT	AAGTAGCAGA	TATGAAGAAG	AAAAGATAGC	950
	TTCTGGTGAA	GATACACGAG	AAGGTATGAC	AGCAATTATA	TCTATCAAAC	1000
25	ATGGTGATCC	TCAATTTCGAA	GGTCAAACGA	AGACAAAATT	AGGTAATTCT	1050
	GAAGTGCGTC	AAGTTGTAGA	TAAATTATTC	TCAGAGCACT	TTGAACGATT	1100
	TTTATATGAA	AATCCACAAG	TCGCACGTAC	AGTGGTTGAA	AAAGGTATTA	1150
	TGGCGGCACG	TGCACGTGTT	GCTGCGAAAA	AAGCGCGTGA	AGTAACACGT	1200
	CGTAAATCAG	CGTTAGATGT	AGCAAGTCTT	CCAGGTAAAT	TAGCCGATTG	1250
30	CTCTAGTCAA	AGTCCTGAAG	AATGTGAGAT	TTTCTTAGTC	GAAGGGGACT	1300
	CTGCCGGAGG	GTCTACAAAA	TCTGGTCGTG	ACTCTAGAAC	GCAGGCGATT	1350
	TTACCATTAC	GAGGTAAGAT	ATTAAATGTT	GAAAAAGCAC	GATTAGATAG	1400
	AATTTTGAAT	AACAATGAAA	TTCGTCAAAT	GATCACAGCA	TTTGGTACAG	1450
	GAATCGGTGG	CGACTTTGAT	CTAGCGAAAG	CAAGATATCA	CAAAATCGTC	1500
35	ATTATGACTG	ATGCCGATGT	GGATGGAGCG	CATATTAGAA	CATTGTTATT	1550
	AATATTCTTC	TATCGATTTA	TGAGACCGTT	AATTGAAGCA	GGCTATGTGT	1600
	ATATTGCACA	GCCACCGTTG	TATAAACTGA	CACAAGGTAA	ACAAAAGTAT	1650
	TATGTATACA	ATGATAGGGA	ACTTGATAAA	CTTAAATCTG	AATTGAATCC	1700
	AACACCAAAA	TGGTCTATTG	CGCTATACAA	AGGTCTTGGA	GAAATGAATG	1750
40	CAGATCAATT	ATGGGAAACA	ACAATGAACC	CTGAGCACCG	CGCTCTTTTA	1800
	CAAGTAAAC	TTGAAGATGC	GATTGAAGCG	GACCAAACAT	TTGAAATGTT	1850
	AATGGGTGAC	GTTGTAGAAA	ACCGTAGACA	ATTTATAGAA	GATAATGCAG	1900
	TTTATGCAAA	CTTAGACTTC	TAA			1923

45

2) INFORMATION FOR SEQ ID NO: 1308

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308

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ATGTAYGTIA TIATGGAYMG IGC

23

10 2) INFORMATION FOR SEQ ID NO: 1309

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309

ATIATYTTT TICCYTTICC YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1310

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310

ATIATITSIA TIACYTCRTC

20

40

2) INFORMATION FOR SEQ ID NO: 1311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311

GARATGAARA TIMGIGGIGA RCA

23

5 2) INFORMATION FOR SEQ ID NO: 1312

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312

AARTAYATIA TICARGARMG IGC

23

20

2) INFORMATION FOR SEQ ID NO: 1313

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313

AMIAYICKRT GIGGITTITT YTT

23

35

2) INFORMATION FOR SEQ ID NO: 1314

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314

TAIGAITTYA CIGAISMICA RGC

23

50

2) INFORMATION FOR SEQ ID NO: 1315

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315

ACIATIGCIT CIGCYTGIKS YTC 23

15

2) INFORMATION FOR SEQ ID NO: 1316

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316

GTGAGTGAAA TAATTCAAGA TT 22

30

2) INFORMATION FOR SEQ ID NO: 1317

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317

CACCAAATC ATCTGTATCT AC 22

45

2) INFORMATION FOR SEQ ID NO: 1318

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318

ACCTAYTCSA TGTACGTRAT CATGGA

26

10

2) INFORMATION FOR SEQ ID NO: 1319

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319

AGRTCGTCIA CCATCGGYAG YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1320

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2259 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(B) STRAIN: K-12 MG1655
40 (C) ACCESSION NUMBER: AE000384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320

	ATGAGCGATA	TGGCAGAGCG	CCTTGCGCTA	CATGAATTTA	CGGAAAACGC	50
45	CTACTTAAAC	TACTCCATGT	ACGTGATCAT	GGACCGTGCG	TTGCCGTTTA	100
	TTGGTGATGG	TCTGAAACCT	GTTCAGCGCC	GCATTGTGTA	TGCGATGTCT	150
	GAAGTGGGCC	TGAATGCCAG	CGCCAAATTT	AAAAAATCGG	CCCGTACCGT	200
	CGGTGACGTA	CTGGGTAAAT	ACCATCCGCA	CGGCGATAGC	GCCTGTTATG	250
	AAGCGATGGT	CCTGATGGCG	CAACCGTTCT	CTTACCGTTA	TCCGCTGGTT	300
50	GATGGTCAGG	GGAAGTGGGG	CGCGCCGGAC	GATCCGAAAT	CGTTCGCGGC	350
	AATGCGTTAC	ACCGAATCCC	GGTTGTCGAA	ATATTCCGAG	CTGCTATTGA	400
	GCGAGCTGGG	GCAGGGGACG	GCTGACTGGG	TGCCAAACTT	CGACGGCACT	450
	TTGCAGGAGC	CGAAAATGCT	ACCTGCCCCGT	CTGCCAAACA	TTTGTCTTAA	500

	CGGCACCACC	GGTATTGCCG	TCGGCATGGC	GACCGATATT	CCACCGCATA	550
	ACCTGCGTGA	AGTGGCTCAG	GCGGCAATCG	CATTAATCGA	CCAGCCGAAA	600
	ACCACGCTCG	ATCAGCTGCT	GGATATCGTG	CAGGGGCCGG	ATTATCCGAC	650
	TGAAGCGGAA	ATTATCACTT	CGCGCGCCGA	GATCCGTAAA	ATCTACGAGA	700
5	ACGGACGTGG	TTCAGTGCGT	ATGCGCGCGG	TGTGGAAGAA	AGAAGATGGC	750
	GCGGTGGTTA	TCAGCGCATT	GCCGCATCAG	GTTTCAGGTG	CGCGCGTACT	800
	GGAGCAAATT	GCTGCGCAAA	TGCGCAACAA	AAAGCTGCCG	ATGGTTGACG	850
	ATCTGCGCGA	TGAATCTGAC	CACGAGAACC	CGACCCGCCT	GGTGATTGTG	900
	CCGCGTTCCA	ACCGCGTGGA	TATGGATCAG	GTGATGAACC	ACCTCTTCGC	950
10	TACCACCGAT	CTGGAAAAGA	GCTATCGTAT	TAACCTTAAT	ATGATCGGTC	1000
	TGGATGGTCG	TCCGGCGGTG	AAAAACCTGC	TGGAAATCCT	CTCCGAATGG	1050
	CTGGTGTTCC	GCCGCGATAC	CGTGCGCCGC	CGACTGAACT	ATCGTCTGGA	1100
	GAAAGTCCTC	AAGCGCCTGC	ATATCCTCGA	AGGTTTGCTG	GTGGCGTTTC	1150
	TCAATATCGA	CGAAGTGATT	GAGATCATTC	GTAATGAAGA	TGAACCGAAA	1200
15	CCGGCGCTGA	TGTCGCGGTT	TGGCCTTACG	GAAACCCAGG	CGGAAGCGAT	1250
	CCTCGAACTG	AAACTGCGTC	ATCTTGCCAA	ACTGGAAGAG	ATGAAGATTC	1300
	GCGGTGAGCA	GAGTGAAGTG	GAAAAAGAGC	GCGACCAAGT	GCAGGGCATT	1350
	TTGGCTTCCG	AGCGTAAAAT	GAATAACCTG	CTGAAGAAAG	AACTGCAGGC	1400
	AGACGCGCAA	GCCTACGGTG	ACGATCGTCG	TTCGCCGTTG	CAGGAACGCG	1450
20	AAGAAGCGAA	AGCGATGAGC	GAGCACGACA	TGCTGCCGTC	TGAACCTGTC	1500
	ACCATTGTGC	TGTCGCAGAT	GGGCTGGGTA	CGCAGCGCTA	AAGGCCATGA	1550
	TATCGACGCG	CCGGGCCTGA	ATTATAAAGC	GGGTGATAGC	TTCAAAGCGG	1600
	CGGTGAAAGG	TAAGAGCAAC	CAACCGGTAG	TGTTTGTTGA	TTCCACCGGT	1650
	CGTAGCTATG	CCATTGACCC	GATTACGCTG	CCGTCGGCGC	GTGGTCAGGG	1700
25	CGAGCCGCTC	ACCGGCAAAT	TAACGTTGCC	GCCTGGGGCG	ACCGTTGACC	1750
	ATATGCTGAT	GGAAAGCGAC	GATCAGAAAC	TGCTGATGGC	TTCCGATGCG	1800
	GGTTACGGTT	TCGTCTGCAC	CTTTAACGAT	CTGGTGGCGC	GTAACCGTGC	1850
	AGGTAAGGCT	TTGATCACCT	TACCGGAAAA	TGCCCATGTT	ATGCCGCCGG	1900
	TGGTGATTGA	AGATGCTTCC	GATATGCTGC	TGGCAATCAC	TCAGGCAGGC	1950
30	CGTATGTTGA	TGTTCCCGGT	AAGTGATCTG	CCGCAGCTGT	CGAAGGGCAA	2000
	AGGCAACAAG	ATTATCAACA	TTCCATCGGC	AGAAGCCGCG	CGTGGAGAAG	2050
	ATGGTCTGGC	GCAATTGTAC	GTTCTGCCGC	CGCAAAGCAC	GCTGACCATT	2100
	CATGTTGGGA	AACGCAAAAT	TAAACTGCGC	CCGGAAGAGT	TACAGAAAGT	2150
	CACTGGCGAA	CGTGGACGCC	GCGGTACGTT	GATGCGCGGT	TTGCAGCGTA	2200
35	TCGATCGTGT	TGAGATCGAC	TCTCCTCGCC	GTGCCAGCAG	CGGTGATAGC	2250
	GAAGAGTAA					2259

40 2) INFORMATION FOR SEQ ID NO: 1321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2403 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: KMP9
(C) ACCESSION NUMBER: D67074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321

	GTGAGTGAAA	TAATTCAAGA	TTTATCACTT	GAAGATGTTT	TAGGTGATCG	50
5	CTTTGGAAGA	TATAGTAAAT	ATATTATTCA	AGAGCGTGCA	TTGCCAGATG	100
	TTCGTGATGG	TTTAAAACCA	GTACAACGTC	GTATTTTATA	TGCAATGTAT	150
	TCAAGTGGTA	ATACACACGA	TAAAAATTTT	CGTAAAAGTG	CGAAAACAGT	200
	CGGTGATGTT	ATTGGTCAAT	ATCATCCACA	TGGAGACTTC	TCAGTGTACA	250
	AAGCAATGGT	CCGTTTAAAGT	CAAGACTGGA	AGTTACGACA	TGTCTTAATA	300
10	GAAATGCATG	GTAATAATGG	TAGTATCGAT	AATGATCCGC	CAGCGGCAAT	350
	GCGTTACACT	GAAGCTAAGT	TAAGCTTACT	AGCTGAAGAG	TTATTACGTG	400
	ATATTAATAA	AGAGACAGTT	TCTTTCATTC	CAAACATATGA	TGATACGACA	450
	CTCGAACCAA	TGGTATTGCC	ATCAAGATTT	CCTAACTTAC	TAGTGAATGG	500
	TTCTACAGGT	ATATCTGCAG	GTTACGCGAC	AGATATACCA	CCACATAATT	550
15	TAGCTGAAGT	GATTCAAGCA	ACACTTAAAT	ATATTGATAA	TCCGGATATT	600
	ACAGTCAATC	AATTAATGAA	ATATATTAAA	GGTCCTGATT	TTCCAACCTGG	650
	TGGTATTATT	CAAGGTATTG	ATGGTATTAA	AAAAGCTTAT	GAATCAGGTA	700
	AAGGTAGAAT	TATAGTTCGT	TCTAAAGTTG	AAGAAGAAAC	TTTACGCAAT	750
	GGACGTAAAC	AGTTAATTAT	TACTGAAATT	CCATATGAAG	TGAACAAAAG	800
20	TAGCTTAGTA	AAACGTATCG	ATGAATTACG	TGCTGACAAA	AAAGTCGATG	850
	GTATCGTTGA	AGTACGTGAT	GAAACTGATA	GAAGTGGTTT	ACGAATAGCA	900
	ATTGAATTGA	AAAAAGATGT	GAACAGTGAA	TCAATCAAAA	ATTATCTTTA	950
	TAAAAACTCT	GATTTACAGA	TTTCATATAA	TTTCAACATG	GTCGCTATTA	1000
	GTGATGGTCG	TCCAAAATTG	ATGGGTATTC	GTCAAATTAT	AGATAGTTAT	1050
25	TTGAATCATC	AAATTGAGGT	TGTTGCAAAT	AGAACGAAGT	TTGAATTAGA	1100
	TAATGCTGAA	AAACGTATGC	ATATCGTTGA	AGGTTTGATT	AAAGCGTTGT	1150
	CAATTTTAGA	TAAAGTAATT	GAATTGATTC	GTAGCTCTAA	AAACAAGCGT	1200
	GACGCTAAAG	AAAACCTTAT	CGAAGTATTC	GAGTTCACAG	AAGAACAGGC	1250
	TGAAGCAATT	GTAATGTTAC	AGTTATATCG	TTTAACAAAC	ACTGACATAG	1300
30	TTGCGCTTGA	AGGTGAACAT	AAAGAACTTG	AAGCATTAAT	CAAACAATTA	1350
	CGTCATATTC	TTGATAACCA	TGATGCATTA	TTGAATGTCA	TAAAAGAAGA	1400
	ATTGAATGAA	ATTAAAAAGA	AATTCAAATC	TGAACGACTG	TCTTTAATTG	1450
	AAGCAGAAAT	TGAAGAAATT	AAAATTGACA	AAGAAGTTAT	GGTGCCTAGT	1500
	GAAGAAGTTA	TTTTAAGTAT	GACACGTCAT	GGATATATTA	AACGTACTTC	1550
35	TATTCGTAGC	TTTAATGCTA	GCGGTGTTGA	GGATATTGGT	TTAAAAGATG	1600
	GTGACAGTTT	ACTTAAACAT	CAAGAAGTAA	ATACGCAAGA	TACCGTACTA	1650
	GTATTTACAA	ATAAAGGTCG	TTATCTATTT	ATACCGGTTC	ATAAATTAGC	1700
	AGATATTCGT	TGGAAAGAAT	TGGGGCAACA	TGTATCACAA	ATAGTTCCTA	1750
	TCGAAGAAGA	TGAAGTGGTT	ATTAATGTCT	TTAATGAAAA	GGACTTTAAT	1800
40	ACAGATGCAT	TTTATGTTTT	TGCGACTCAA	AATGGCATGA	TTAAGAAAAG	1850
	TACAGTGCCT	CTATTTAAAA	CAACGCGTTT	TAATAAACCT	TTAATTGCTA	1900
	CTAAAGTTAA	AGAAAATGAT	GATTTGATTA	GTGTTATGCG	CTTTGAAAAA	1950
	GATCAATTAA	TTACCGTCAT	TACTAATAAA	GGTATGTCAT	TAACGTATAA	2000
	TACAAGTGAA	CTATCAGATA	CCGGATTAAAG	GGCAGCTGGT	GTAAATCAA	2050
45	TAAATCTTAA	AGCTGAAGAT	TTCGTTGTTA	TGACAGAAGG	TGTTTCTGAA	2100
	AATGATACTA	TATTGATGGC	CACACAACGC	GGCTCGTTAA	AACGTATTAG	2150
	TTTTAAAATC	TTACAAGTTG	CTAAAAGAGC	ACAACGTGGA	ATAACTTTAT	2200
	TAAAAGAATT	AAAGAAAAAT	CCACATCGTA	TTGTAGCTGC	ACATGTAGTG	2250
	ACAGGTGAAC	ATAGTCAATA	TACATTATAT	TCAAAATCAA	ATGAAGAACA	2300
50	TGGTTTAATT	AATGATATTC	ATAAATCTGA	ACAATATACA	AATGGCTCAT	2350
	TCATTGTAGA	TACAGATGAT	TTTGGTGAAG	TAATAGACAT	GTATATTAGC	2400
	TAA					2403

2) INFORMATION FOR SEQ ID NO: 1322

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322

RTIGAIAAYI SIGTIGAYGA RG

22

15

2) INFORMATION FOR SEQ ID NO: 1323

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323

ACIAWRSAIG GIGGIACICA YG

22

30

2) INFORMATION FOR SEQ ID NO: 1324

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324

45 CCICCGCIS WRTCICCYTC

20

50 2) INFORMATION FOR SEQ ID NO: 1325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325

RTTCATYTCI CCIARICCYT T

21

10

2) INFORMATION FOR SEQ ID NO: 1326

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326

TGATTCAATA CAGGTTTTAG AG

22

25

2) INFORMATION FOR SEQ ID NO: 1327

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327

40

CTAGATTTCC TCCTCATCAA AT

22

2) INFORMATION FOR SEQ ID NO: 1328

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1992 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: RN4220

(C) ACCESSION NUMBER: D67075

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328

	ATGAATAAAC	AAAATAATTA	TTCAGATGAT	TCAATACAGG	TTT TAGAGGG	50
	GTTAGAAGCA	GTT CGTAAAA	GACCTGGTAT	GTATATTGGA	TCAACTGATA	100
10	AACGGGGATT	ACATCATCTA	GTATATGAAA	TTGTCGATAA	CTCCGTCGAT	150
	GAAGTATTGA	ATGGTTACGG	TAACGAAATA	GATGTAACAA	TTAATAAAGA	200
	TGGTAGTATT	TCTATAGAAG	ATAATGGACG	TGGTATGCCA	ACAGGTATAC	250
	ATAAATCAGG	TAAACCGACA	GTCGAAGTTA	TCTTTACTGT	TTTACATGCA	300
	GGAGGTAAAT	TTGGACAAGG	CGGCTATAAA	ACTTCAGGTG	GTCTTCACGG	350
15	TGTTGGTGCT	TCAGTTGTAA	ATGCATTGAG	TGAATGGCTT	GAAGTTGAAA	400
	TCCATCGAGA	TGGTAATATA	TATCATCAAA	GTTTTAAAAA	CGGTGGTTCG	450
	CCATCTTCTG	GTTTAGTGAA	AAAAGGTAAA	ACTAAGAAAA	CAGGTACCAA	500
	AGTAACATTT	AAACCTGATG	ACACAATTTT	TAAAGCATCT	ACATCATTTA	550
	ATTTTGATGT	TTTAAGTGAA	CGACTACAAG	AGTCTGCGTT	CTTATTGAAA	600
20	AATTTAAAAA	TAACGCTTAA	TGATTTACGC	AGTGGTAAAG	AGCGTCAAGA	650
	GCATTACCAT	TATGAAGAAG	GAATCAAAGA	GTTTGTTAGT	TATGTCAATG	700
	AAGGAAAAGA	AGTTTTGCAT	GACGTGGCTA	CATTTTCAGG	TGAAGCAAAT	750
	GGTATAGAGG	TAGACGTAGC	TTTCCAATAT	AATGATCAAT	ATTCAGAAAG	800
	TATTTTAAGT	TTTGTAATA	ATGTACGTAC	TAAAGATGGT	GGTACACATG	850
25	AAGTTGGTTT	TAAAACAGCA	ATGACACGTG	TATTTAATGA	TTATGCACGT	900
	CGTATTAATG	AACTTAAAAC	AAAAGATAAA	AACTTAGATG	GTAATGATAT	950
	TCGTGAAGGT	TTAACAGCTG	TTGTGTCTGT	TCGTATTCCA	GAAGAATTAT	1000
	TGCAATTTGA	AGGACAAACG	AAATCTAAAT	TGGGTACTTC	TGAAGCTAGA	1050
	AGTGCTGTTG	ATTCAGTTGT	TGCAGACAAA	TTGCCATTCT	ATTTAGAAGA	1100
30	AAAAGGACAA	TTGTCTAAAT	CACTTGTGAA	AAAAGCGATT	AAAGCACAAAC	1150
	AAGCAAGGGA	AGCTGCACGT	AAAGCTCGTG	AAGATGCTCG	TTCAGGTAAG	1200
	AAAAACAAGC	GTAAAGACAC	TTTGCTATCT	GGTAAATTAA	CACCTGCACA	1250
	AAGTAAAAAC	ACTGAAAAAA	ATGAATTGTA	TTTAGTCGAA	GGTGATTCTG	1300
	CGGGAGGTTC	AGCAAAACTT	GGACGAGACC	GCAAATTCCA	AGCGATATTA	1350
35	CCATTACGTG	GTAAGGTAAT	TAATACAGAG	AAAGCACGTC	TAGAAGATAT	1400
	TTTTTAAAAAT	GAAGAAATTA	ATACAATTAT	CCACACAATC	GGGGCAGGCG	1450
	TTGGTACTGA	CTTTAAAATT	GAAGATAGTA	ATTATAATCG	TGTAATTATT	1500
	ATGACTGATG	CTGATACTGA	TGGTGCGCAT	ATTCAAGTGC	TATTGTTAAC	1550
	ATTCTTCTTC	AAATATATGA	AACCGCTTGT	TCAAGCAGGT	CGTGTATTTA	1600
40	TTGCTTTACC	TCCACTTTAT	AAATTGGAAA	AAGGTAAAGG	CAAAACAAAG	1650
	CGAGTTGAAT	ACGCTTGGAC	AGACGAAGAG	CTTAATAAAT	TGCAAAAAGA	1700
	ACTTGGTAAA	GGCTTCACGT	TACAACGTTA	CAAAGGTTTG	GGTGAAATGA	1750
	ACCCTGAGCA	ATTATGGGAA	ACGACGATGA	ACCCAGAAAC	ACGAACTTTA	1800
	ATTCGTGTAC	AAGTTGAAGA	TGAAGTGCGT	TCATCTAAAC	GTGTAACAAC	1850
45	ATTAATGGGT	GACAAAGTAC	AACCTAGACG	TGAATGGATT	GAAAAGCATG	1900
	TTGAGTTTGG	TATGCAAGAG	GACCAAAGTA	TTTTAGATAA	TTCTGAAGTA	1950
	CAAGTGCTTG	AAAATGATCA	ATTTGATGAG	GAGGAAATCT	AG	1992

50

2) INFORMATION FOR SEQ ID NO: 1329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329

10 TGTAGAGCGC GGTATCATCA AAGTA

25

2) INFORMATION FOR SEQ ID NO: 1330

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330

25

AGATTCGAAC TTGGTGTGCG GG

22

30 2) INFORMATION FOR SEQ ID NO: 1331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331

40

GCCCTTGAGG TACAGAATGG TAATGAAGTT

30

45

2) INFORMATION FOR SEQ ID NO: 1332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332

5 GACCGCGGCG CAGACCATCA

20

2) INFORMATION FOR SEQ ID NO: 1333

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333

20

TCATGGTGAC TTATCTATTT ATG

23

25 2) INFORMATION FOR SEQ ID NO: 1334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334

CATCTATTTA TAAAGCAATG GTA

23

40

2) INFORMATION FOR SEQ ID NO: 1335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335

CTATTTATGG AGCAATGGT

19

2) INFORMATION FOR SEQ ID NO: 1336

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336

TGGAGACTAC TCAGTGT

17

15

2) INFORMATION FOR SEQ ID NO: 1337

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337

TGGAGACTTC TCAGTGT

17

30

2) INFORMATION FOR SEQ ID NO: 1338

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338

45 GTGTACGGAG CAATG

15

50 2) INFORMATION FOR SEQ ID NO: 1339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339

CCAGCGGAAA TCGGT

15

10

2) INFORMATION FOR SEQ ID NO: 1340

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340

GAACAAGGTA TGACACCGGA TAAAT

25

25

2) INFORMATION FOR SEQ ID NO: 1341

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341

40 GATAACTGAA ATCCTGAGCC ATACG

25

2) INFORMATION FOR SEQ ID NO: 1342

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342

GATGTTATTG GTCAATATCA TCCA

24

5

2) INFORMATION FOR SEQ ID NO: 1343

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343

AAGAAACTGT CTCTTTATTA ATATCACGT

29

20

2) INFORMATION FOR SEQ ID NO: 1344

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344

35 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1345

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345

50

CCCGCCGAGC ATTTCAACTA TTG

23

2) INFORMATION FOR SEQ ID NO: 1346

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346

GATGTTACGC AGCAGGGCAG TC

22

15

2) INFORMATION FOR SEQ ID NO: 1347

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347

ACCAAGCAGG TTCGCAGTCA AGTA

24

30

2) INFORMATION FOR SEQ ID NO: 1348

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: Unidentified bacterium
(C) ACCESSION NUMBER: X04555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348

50 ATGCGCTCAC GCAACTGGTC CAGAACCTTG ACCGAACGCA GCGGTGGTAA 50
CGGCGCAGTG GCGGTTTTCA TGGCTTGTTA TGACTGTTTT TTTGTACAGT 100
CTATGCCTCG GGCATCCAAG CAGCAAGCGC GTTACGCCGT GGGTCGATGT 150
TTGATGTTAT GGAGCAGCAA CGATGTTACG CAGCAGGGCA GTCGCCCTAA 200
AACAAAGTTA GGCCGCATGG ACACAACGCA GGTCACATTG ATACACAAAA 250

	TTCTAGCTGC	GGCAGATGAG	CGAAATCTGC	CGCTCTGGAT	CGGTGGGGGC	300
	TGGGCGATCG	ATGCACGGCT	AGGGCGTGTA	ACACGCAAGC	ACGATGATAT	350
	TGATCTGACG	TTTCCCGGCG	AGAGGCGCGG	CGAGCTCGAG	GCAATAGTTG	400
	AAATGCTCGG	CGGGCGCGTC	ATGGAGGAGT	TGGACTATGG	ATTCTTAGCG	450
5	GAGATCGGGG	ATGAGTTACT	TGACTGCGAA	CCTGCTTGGT	GGGCAGACGA	500
	AGCGTATGAA	ATCGCGGAGG	CTCCGCAGGG	CTCGTGCCCA	GAGGCGGCTG	550
	AGGGCGTCAT	CGCCGGGCGG	CCAGTCCGTT	GTAACAGCTG	GGAGGCGATC	600
	ATCTGGGATT	ACTTTTACTA	TGCCGATGAA	GTACCACCAG	TGGACTGGCC	650
	TACAAAGCAC	ATAGAGTCCT	ACAGGCTCGC	ATGCACCTCA	CTCGGGGCGG	700
10	AAAAGGTTGA	GGTCTTGCGT	GCCGCTTTCA	GGTCGCGATA	TGCGGCCTAA	750

2) INFORMATION FOR SEQ ID NO: 1349

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349

25

CAGCCGACCA ATGAGTATCT TGCC

24

30 2) INFORMATION FOR SEQ ID NO: 1350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350

40

TAATCAGGGC AGTTGCGACT CCTA

24

45

2) INFORMATION FOR SEQ ID NO: 1351

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: Stone 130
(C) ACCESSION NUMBER: L06157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351

10	ATGTTATGGA GCAGCAACGA TGTTACGCAG CAGGGCAGTC GCCCTAAAAC	50
	AAAGTTAGGT GGCTCAATGA GCATCATTGC AACCGTCAAG ATCGGCCCTG	100
	ACGAAATTTC AGCCATGAGG GCTGTGCTCG ATCTCTTCGG CAAAGAGTTT	150
	GAGGACATTC CAACCTACTC TGATCGCCAG CCGACCAATG AGTATCTTGC	200
	CAATCTTCTG CACAGCGAGA CGTTCATCGC GCTCGCTGCT TTTGACCGCG	250
15	GAACAGCAAT AGGTGGGCTC GCCGCCTACG TTCTACCCAA GTTCGAGCAA	300
	GCGCGAAGCG AGATCTACAT TTATGACTTG GCAGTCGCTT CCAGCCATCG	350
	AAGGCTAGGA GTCGCAACTG CCCTGATTAG CCACCTGAAG CGTGTGGCGG	400
	TTGAACTTGG CGCGTATGTA ATCTATGTGC AAGCAGACTA CGGTGACGAT	450
	CCGGCAGTCG CTCTCTACAC AAAGCTTGGA GTTCGGGAAG ACGTCATGCA	500
20	CTTCGACATT GATCCAAGAA CCGCCACCTA A	531

2) INFORMATION FOR SEQ ID NO: 1352

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352

35

CCACGCTGAC AGAGCCGCAC CG

22

40 2) INFORMATION FOR SEQ ID NO: 1353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353

GGCCAGCTCC CATCGGACCC TG

22

2) INFORMATION FOR SEQ ID NO: 1354

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354

CACGCTGACA GAGCCGCACC G

21

15

2) INFORMATION FOR SEQ ID NO: 1355

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355

ATGCCGTTGC TGTCGAAATC CTCG

24

30

2) INFORMATION FOR SEQ ID NO: 1356

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M97172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356

ATGAACACGA TCGAATCGAT CACGGCGGAC CTGCACGGAC TGGGCGTCCG 50
 50 GCCCGGCGAC CTGATCATGG TCCATGCATC GCTGAAAGCC GTCGGCCCCG 100
 TCGAGGGAGG TGCGGCCTCG GTGGTGTCTGG CCCTTCGCGC CGCGGTCTGG 150
 TCCGCAGGGA CCCTGATGGG TTATGCCTCA TGGGACCGCT CGCCCTATGA 200
 GGAGACGCTG AACGGCGCGC GGATGGACGA AGAACTGCGC CGCCGGTGGC 250

	CACCCTTCGA	TCTGGCCACA	TCCGGTACCT	ATCCCGGCTT	CGGCCTGCTC	300
	AACCGGTTTC	TGCTTGAGGC	GCCCGACGCA	CGGCGCAGCG	CGCATCCCGA	350
	CGCCTCCATG	GTCGCGGTCG	GCCCCCTTGC	CGCCACGCTG	ACAGAGCCGC	400
	ACCGGCTTGG	GCAGGCGCTG	GGCGAAGGCT	CGCCGCTGGA	GCGCTTCGTC	450
5	GGGCATGGCG	GAAAGGTCCT	GCTTCTGGGA	GCGCCGCTCG	ACTCCGTCAC	500
	CGTGCTGCAT	TACGCCGAGG	CCATCGCCCC	CATCCCGAAC	AAACGCCGCG	550
	TGACCTATGA	AATGCCGATG	CTCGGCCCGG	ATGGCAGGGT	CCGATGGGAG	600
	CTGGCCGAGG	ATTTGACAG	CAACGGCATT	CTCGATTGCT	TCGCGGTCGA	650
	TGGGAAGCCG	GATGCCGTCG	AGACGATCGC	CAAGGCTTAT	GTCGAACCTGG	700
10	GCCGGCATCG	GGAAGGCATC	GTCGGTCGCG	CACCCTCCTA	TCTGTTTGAA	750
	GCGCAGGATA	TCGTCTCGTT	CGGCGTCACC	TATCTCGAAC	AGCATTTTCGG	800
	CGCGCCCTGA					810

15

2) INFORMATION FOR SEQ ID NO: 1357

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357

GCCCATCCAT TTGCCTTTGC

20

30

2) INFORMATION FOR SEQ ID NO: 1358

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358

GCGTACCAAC TTGCCATCCT GAAG

24

45

2) INFORMATION FOR SEQ ID NO: 1359

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359

TGCCCCTGCC ACCTCACTC

19

10

2) INFORMATION FOR SEQ ID NO: 1360

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360

CGTACCAACT TGCCATCCTG AAGA

24

25

2) INFORMATION FOR SEQ ID NO: 1361

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 786 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X01385

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361

	GTGCAATACG AATGGCGAAA AGCCGAGCTC ATCGGTCAGC TTCTCAACCT	50
	TGGGGTTACC CCCGGCGGTG TGCTGCTGGT CCACAGCTCC TTCCGTAGCG	100
45	TCCGGCCCCT CGAAGATGGG CCACTTGGAC TGATCGAGGC CCTGCGTGCT	150
	GCGCTGGGTC CGGGAGGGAC GCTCGTCATG CCCTCGTGGT CAGGTCTGGA	200
	CGACGAGCCG TTCGATCCTG CCACGTCGCC CGTTACACCG GACCTTGGAG	250
	TTGTCTCTGA CACATTCTGG CGCCTGCCAA ATGTAAAGCG CAGCGCCCAT	300
	CCATTTGCCT TTGCGGCAGC GGGGCCACAG GCAGAGCAGA TCATCTCTGA	350
50	TCCATTGCC CTGCCACCTC ACTCGCCTGC AAGCCCGGTC GCCCGTGTCC	400
	ATGAACTCGA TGGGCAGGTA CTTCTCCTCG GCGTGGGACA CGATGCCAAC	450
	ACGACGCTGC ATCTTGCCGA GTTGATGGCA AAGGTTCCCT ATGGGGTGCC	500
	GAGACACTGC ACCATTCTTC AGGATGGCAA GTTGGTACGC GTCGATTATC	550

TCGAGAATGA CCACTGCTGT GAGCGCTTTG CCTTGGCGGA CAGGTGGCTC 600
AAGGAGAAGA GCCTTCAGAA GGAAGGTCCA GTCGGTCATG CCTTTGCTCG 650
GTTGATCCGC TCCCGCGACA TTGTGGCGAC AGCCCTGGGT CAACTGGGCC 700
GAGATCCGTT GATCTTCCTG CATCCGCCAG AGGGCGGGAT GCGAAGAATG 750
5 CGATGCCGCT CGCCAGTCGA TTGGCTGAGC TCATGA 786

2) INFORMATION FOR SEQ ID NO: 1362

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362

20

CGCCGCCATC GCCCAAAGCT GG

22

25 2) INFORMATION FOR SEQ ID NO: 1363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363

CGGCATAATG GAGCGCGGTG ACTG

24

40

2) INFORMATION FOR SEQ ID NO: 1364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364

TTTCTCGCCC ACGCAGGAAA AATC

24

2) INFORMATION FOR SEQ ID NO: 1365

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365

CATCCTCGAC GAATATGCCG CG

22

15

2) INFORMATION FOR SEQ ID NO: 1366

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
(C) ACCESSION NUMBER: M88012

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366

	ATGACTGATC	CCCGCAAAAA	CGGCGATTTG	CACGAACCCG	CGACGGCACC	50
	CGCGACGCCC	TGGTCCAAAA	GCGAGCTGGT	CCGGCAATTG	CGCGACCTCG	100
35	GCGTGCGCTC	AGGCGATATG	GTGATGCCGC	ATGTGTCGTT	GCGCGCCGTC	150
	GGGCCGCTGG	CGGACGGACC	GCAGACACTT	GTCGATGCGC	TGATCGAGGC	200
	CGTCGGCCCC	ACCGGGAATA	TTCTCGCCTT	CGTCTCGTGG	CGCGATTTCG	250
	CCTATGAACA	GACGCTGGGT	CATGATGCGC	CGCCCGCCGC	CATCGCCCAA	300
	AGCTGGCCTG	CGTTCGACCC	CGACCATGCG	CCCGCCTACC	CCGGCTTTGG	350
40	CGCGATCAAC	GAATTTATCC	GAACCTATCC	GGGGTGTCGG	CGCACGGCCC	400
	ATCCCGACGC	ATCGATGGCG	GCGATCGGGC	CCGATGCGGC	GTGGCTGGTG	450
	GCGCCGCACG	AGATGGGCGC	CGCTTATGGC	CCCCGCTCGC	CGATCGCGCG	500
	TTTTCTCGCC	CACGCAGGAA	AAATCCTGTC	GATCGGCGCC	GGGCCCCGAT	550
	CAGTCACCGC	GCTCCATTAT	GCCGAAGCGG	TGGCGCGGAT	CGAGGGCAAG	600
45	CGCCGCGTCA	CTTATTTCGAT	GCCCTTACTG	CGCGAAGGCA	AGCGCGTCTG	650
	GGTCACCACG	TCCGACTGGG	ATTCGAACGG	CATCCTCGAC	GAATATGCCG	700
	CGCCCGACGG	CCCCGACGCG	GTCGAACGGA	TCGCCCGCGA	CTATCTCGCC	750
	CGCACCAGGG	TTGCGCAAGG	CCCGGTCGGC	GGCGCGCAAT	CCCGGCTGAT	800
	CGACGCGGCC	GATATCGTTT	CCTTCGGCAT	CGAATGGCTC	GAGGCGCGCC	850
50	ACGCCGCGCC	AGCGGCGGCA	GCGCTGAAGC	CGAAACAACG	CCGCGACTGA	900

2) INFORMATION FOR SEQ ID NO: 1367

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367

CAAATATACT AACAGAAGCG TTCA

24

15

2) INFORMATION FOR SEQ ID NO: 1368

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368

AGGATCTTGC CAATACCTTT AT

22

30

2) INFORMATION FOR SEQ ID NO: 1369

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369

45 AAACCTTTGT TTCGGTCTGC TAAT

24

2) INFORMATION FOR SEQ ID NO: 1370

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370

AAGCGATTCC AATAATACCT TGCT

24

10

2) INFORMATION FOR SEQ ID NO: 1371

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 558 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter diversus*
- (C) ACCESSION NUMBER: M18967

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371

	ATGAATTATC AAATTGTGAA TATTGCGGAA TGCAGCAATT ATCAGTTAGA	50
	AGCAGCAAAT ATACTAACAG AAGCGTTCAA TGATCTTGGT AACAATTCAT	100
30	GGCCAGATAT GACGAGTGCA ACAAAGAAG TAAAAGAATG TATTGAGAGT	150
	CCAAACCTTT GTTTCGGTCT GCTAATAAAT AACTCCTTAG TTGGCTGGAT	200
	AGGCTTAAGG CCAATGTACA AGGAAACCTG GGAATTGCAT CCATTGGTTG	250
	TCAGACCAGA TTATCAAAAT AAAGGTATTG GCAAGATCCT GCTTAAGGAA	300
	TTAGAAAACA GAGCTAGAGA GCAAGGTATT ATTGGAATCG CTTTAGGAAC	350
35	AGATGATGAA TACTATAGAA CAAGTCTCTC TTTAATAACT ATAACAGAAG	400
	ATAATATATT TGATTCAATA AAAAATATTA AAAATATTAA TAAACATCCA	450
	TATGAGTTTT ATCAGAAGAA TGGTTATTAT ATTGTTGGAA TAATTCCAAA	500
	TGCCAATGGT AAAAACAAAC CAGATATTTG GATGTGGAAA AGTTTAATCA	550
	AAGAGTAA	558

40

2) INFORMATION FOR SEQ ID NO: 1372

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372

GCTTTCGTTG CCTTTGCCGA GGTC

24

5

2) INFORMATION FOR SEQ ID NO: 1373

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373

CACCCCTGTT GCTTCGCCCA CTC

23

20

2) INFORMATION FOR SEQ ID NO: 1374

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374

AGATATTGGC TCGCCGCAC CACA

24

35

2) INFORMATION FOR SEQ ID NO: 1375

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375

50 CCCTGTTGCT TCGCCCACTC CTG

23

2) INFORMATION FOR SEQ ID NO: 1376

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 441 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M94066

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376

	ATGATCGTCA	TCTGCGACCA	CGACAACCTC	GACGCCTGGC	TGGCGCTGCG	50
	CACCGCGCTG	TGGCCCTCCG	GCTCGCCTGA	AGATCACCGC	GCGGAAATGC	100
	GCGAGATATT	GGCTTCGCCG	CACCACACCG	CGTTTATGGC	GCGGGGGCTG	150
20	GACGGCGCTT	TCGTTGCCTT	TGCCGAGGTC	GCGCTGCGCT	ACGATTACGT	200
	CAACGGCTGC	GAATCGTCGC	CGGTGGCGTT	TTTGGAAGGA	ATTTATACCG	250
	CCGAACGCGC	CCGCCGCCAG	GGCTGGGCCG	CGCGCCTGAT	CGCGCAGGTG	300
	CAGGAGTGGG	CGAAGCAACA	GGGGTGCAGC	GAGCTGGCGT	CGGATACCGA	350
	TATCGCCAAT	CTGGACTCCC	AGCGCCTGCA	TGCGGCGCTG	GGCTTTGCCG	400
25	AAACGGAGCG	AGTAGTGTTT	TACCGCAAAA	CGCTGGGCTG	A	441

2) INFORMATION FOR SEQ ID NO: 1377

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377

40

GCCGTGGGTC GATGTTTGAT GTTA

24

45 2) INFORMATION FOR SEQ ID NO: 1378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378

GCTCGATGAC GCCAACTACC TCTG

24

5

2) INFORMATION FOR SEQ ID NO: 1379

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379

20 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1380

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380

35

CGCTCGATGA CGCCAACTAC CTCT

24

40 2) INFORMATION FOR SEQ ID NO: 1381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X02340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381

	GTGGTAACGG	CGCAGTGGCG	GTTTTTCATGG	CTTCTTGTTA	TGACATGTTT	50
	TTTTGGGGTA	CAGTCTATGC	CTCGGGCATC	CAAGCAGCAA	GCGCGTTACG	100
5	CCGTGGGTCG	ATGTTTGATG	TTATGGAGCA	GCAACGATGT	TACGCAGCAG	150
	GGCAGTCGCC	CTAAAACAAA	GTTAAACATC	ATGAGGGAAG	CGGTGATCGC	200
	CGAAGTATCG	ACTCAACTAT	CAGAGGTAAGT	TGGCGTCATC	GAGCGCCATC	250
	TCGAACCGAC	GTTGCTGGCC	GTACATTTGT	ACGGCTCCGC	AGTGGATGGC	300
	GGCCTGAAGC	CACACAGTGA	TATTGATTTG	CTGGTTACGG	TGACCGTAAG	350
10	GCTTGATGAA	ACAACGCGGC	GAGCTTTGAT	CAACGACCTT	TTGGAAACTT	400
	CGGCTTCCCC	TGGAGAGAGC	GAGATTCTCC	GCGCTGTAGA	AGTCACCATT	450
	GTTGTGCACG	ACGACATCAT	TCCGTGGCGT	TATCCAGCTA	AGCGCGAACT	500
	GCAATTTGGA	GAATGGCAGC	GCAATGACAT	TCTTGCAAGT	ATCTTCGAGC	550
	CAGCCACGAT	CGACATTGAT	CTGGCTATCT	TGCTGACAAA	AGCAAGAGAA	600
15	CATAGCGTTG	CCTTGGTAGG	TCCAGCGGCG	GAGGAACTCT	TTGATCCGGT	650
	TCCTGAACAG	GATCTATTTG	AGGCGCTAAA	TGAAACCTTA	ACGCTATGGA	700
	ACTCGCCGCC	CGACTGGGCT	GGCGATGAGC	GAAATGTAGT	GCTTACGTTG	750
	TCCCGCATTT	GGTACAGCGC	AGTAACCGGC	AAAATCGCGC	CGAAGGATGT	800
	CGCTGCCGAC	TGGGCAATGG	AGCGCCTGCC	GGCCCAGTAT	CAGCCCGTCA	850
20	TACTTGAAGC	TAGACAGGCT	TATCTTGGAC	AAGAAGAAGA	TCGCTTGGCC	900
	TCGCGCGCAG	ATCAGTTGGA	AGAATTTGTC	CACTACGTGA	AAGGCGAGAT	950
	CACCAAGGTA	GTCGGCAAAT	AA			972

25

2) INFORMATION FOR SEQ ID NO: 1382

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382

TAGATATGAT AGGCGGTAAA AAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1383

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383

CCCAAATTCG AGTAAGAGGT ATT

23

5 2) INFORMATION FOR SEQ ID NO: 1384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384

GATATGATAG GCGGTAAAAA GC

22

20

2) INFORMATION FOR SEQ ID NO: 1385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385

TCCCAAATTC GAGTAAGAGG TA

22

35

2) INFORMATION FOR SEQ ID NO: 1386

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 477 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01282

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386

ATGAAAGAAA GATATGGAAC AGTATATAAA GGCTCTCAGA GGCTCATAGA

50

CGAGGAAAGT GGAGAAGTAA TAGAGGTAGA TAAGCTATAC CGTAAACAAA 100
 CGTCTGGTAA CTTTGTAATA GCGTATATCG TCCAATTAAT AAGTATGTTA 150
 GATATGATAG GCGGTAAAAA GCTCAAGATT GTTAATTATA TATTAGATAA 200
 TGTACATCTA AGTAATAACA CAATGATAGC AACTGTTAGA GAAATAGCAG 250
 5 AAGGAACAAA TACAAGCACG AAAACCGTAA ATACAACGCT TAAAATCTTA 300
 GAAGAAGGAA ATATCATTAA AAGAAGAACT GGAGCATTA TGTAAACCC 350
 AGAGCTACTC ATGAGAGGCG ATGACCAAAA AAAAAATAC CTCTTACTCG 400
 AATTTGGGAA CTTTGAGCAA GAGGACGACC AAAAGCAAGA AAATGCTTTA 450
 TCAGAATATT ATTCTTTCAA GGAGTAG 477
 10

2) INFORMATION FOR SEQ ID NO: 1387

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387

25 TTATGCCTCT TCCGACCATC AAGC 24

2) INFORMATION FOR SEQ ID NO: 1388

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388

40 TACGCTCGTC ATCAAATCA CTCG 24

45 2) INFORMATION FOR SEQ ID NO: 1389

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389

GAATAACGGT TTGGTTGATG CGAG

24

5

2) INFORMATION FOR SEQ ID NO: 1390

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390

20 ATGGCAAGAT CCTGGTATCG GTCT

24

2) INFORMATION FOR SEQ ID NO: 1391

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: J01839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391

40	ATGAGCCATA TTCAACGGGA AACGTCTTGC TCGAGGCCGC GATTAAATTC	50
	CAACATGGAT GCTGATTTAT ATGGGTATAA ATGGGCTCGC GATAATGTCG	100
	GGCAATCAGG TGCGACAATC TATCGATTGT ATGGGAAGCC CGATGCGCCA	150
	GAGTTGTTTC TGAAACATGG CAAAGGTAGC GTTGCCAATG ATGTTACAGA	200
	TGAGATGGTC AGACTAAACT GGCTGACGGA ATTTATGCCT CTTCCGACCA	250
45	TCAAGCATTT TATCCGTACT CCTGATGATG CATGGTACT CACCACTGCG	300
	ATCCCCGGGA AAACAGCATT CCAGGTATTA GAAGAATATC CTGATTCAGG	350
	TGAAAATATT GTTGATGCGC TGGCAGTGTT CCTGCGCCGG TTGCATTCGA	400
	TTCCTGTTTG TAATTGTCCT TTTAACAGCG ATCGCGTATT TCGTCTCGCT	450
	CAGGCGCAAT CACGAATGAA TAACGGTTTG GTTGATGCGA GTGATTTTGA	500
50	TGACGAGCGT AATGGCTGGC CTGTTGAACA AGTCTGGAAA GAAATGCATA	550
	AGCTTTTGCC ATTCTCACCG GATTCAGTCG TCACTCATGG TGATTTCTCA	600
	CTTGATAACC TTATTTTGA CGAGGGGAAA TTAATAGGTT GTATTGATGT	650
	TGGACGAGTC GGAATCGCAG ACCGATACCA GGATCTTGCC ATCCTATGGA	700

ACTGCCTCGG TGAGTTTTCT CCTTCATTAC AGAAACGGCT TTTTCAAAAA 750
TATGGTATTG ATAATCCTGA TATGAATAAA TTGCAGTTTC ATTTGATGCT 800
CGATGAGTTT TTCTAA 816

5

2) INFORMATION FOR SEQ ID NO: 1392

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392

20 TGGGTGGAGA GGCTATTCGG CTAT 24

2) INFORMATION FOR SEQ ID NO: 1393

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393

35 CAGTCCCTTC CCGCTTCAGT GAC 23

2) INFORMATION FOR SEQ ID NO: 1394

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394

GACGTTGTCA CTGAAGCGGG AAGG 24

2) INFORMATION FOR SEQ ID NO: 1395

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1395

CTTGGTGGTC GAATGGGCAG GTAG

24

15

2) INFORMATION FOR SEQ ID NO: 1396

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: V00618

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396

ATGATTGAAC AAGATGGATT GCACGCAGGT TCTCCGGCCG CTTGGGTGGA 50
GAGGCTATTC GGCTATGACT GGGCACAACA GACAATCGGC TGCTCTGATG 100
35 CCGCCGTGTT CCGGCTGTCA GCGCAGGGGC GCCCGGTTCT TTTTGTCAAG 150
ACCGACCTGT CCGGTGCCCT GAATGAACTG CAGGACGAGG CAGCGCGGCT 200
ATCGTGGCTG GCCACGACGG GCGTTCCTTG CGCAGCTGTG CTCGACGTTG 250
TCACTGAAGC GGGAAGGGAC TGGCTGCTAT TGGGCGAAGT GCCGGGGCAG 300
GATCTCCTGT CATCTCACCT TGCTCCTGCC GAGAAAGTAT CCATCATGGC 350
40 TGATGCAATG CGGCGGCTGC ATACGCTTGA TCCGGCTACC TGCCCATTCG 400
ACCACCAAGC GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC 450
GGTCTTGTCG ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC 500
AGCCGAACTG TTCGCCAGGC TCAAGGCGCG CATGCCCGAC GGCGAGGATC 550
TCGTCGTGAC CCATGGCGAT GCCTGCTTGC CGAATATCAT GGTGGAAAAT 600
45 GGCCGCTTTT CTGGATTTCAT CGACTGTGGC CGGCTGGGTG TGGCGGACCG 650
CTATCAGGAC ATAGCGTTGG CTACCCGTGA TATTGCTGAA GAGCTTGGCG 700
GCGAATGGGC TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT 750
TCGCAGCGCA TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGA 795

50

2) INFORMATION FOR SEQ ID NO: 1397

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397
10 GTGGGAGAAA ATGAAAACCT AT 22

15 2) INFORMATION FOR SEQ ID NO: 1398

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398
 ATGGAGTGAA AGAGCCTGAT 20

30 2) INFORMATION FOR SEQ ID NO: 1399

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399
 ACCTATGATG TGGAACGGGA AAAG 24

45 2) INFORMATION FOR SEQ ID NO: 1400

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400

5

CGATGGAGTG AAAGAGCCTG ATG

23

10 2) INFORMATION FOR SEQ ID NO: 1401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
(C) ACCESSION NUMBER: V01547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401

25

	ATGGCTAAAA	TGAGAATATC	ACCGGAATTG	AAAAAACTGA	TCGAAAAATA	50
	CCGCTGCGTA	AAAGATACGG	AAGGAATGTC	TCCTGCTAAG	GTATATAAGC	100
	TGGTGGGAGA	AAATGAAAAC	CTATATTTAA	AAATGACGGA	CAGCCGGTAT	150
	AAAGGGACCA	CCTATGATGT	GGAACGGGAA	AAGGACATGA	TGCTATGGCT	200
30	GGAAGGAAAG	CTGCCTGTTC	CAAAGGTCCT	GCACTTTGAA	CGGCATGATG	250
	GCTGGAGCAA	TCTGCTCATG	AGTGAGGCCG	ATGGCGTCCT	TTGCTCGGAA	300
	GAGTATGAAG	ATGAACAAAG	CCCTGAAAAG	ATTATCGAGC	TGTATGCGGA	350
	GTGCATCAGG	CTCTTTCACT	CCATCGACAT	ATCGGATTGT	CCCTATACGA	400
	ATAGCTTAGA	CAGCCGCTTA	GCCGAATTGG	ATTACTTACT	GAATAACGAT	450
35	CTGGCCGATG	TGGATTGCGA	AAACTGGGAA	GAAGACACTC	CATTTAAAGA	500
	TCCGCGCGAG	CTGTATGATT	TTTTAAAGAC	GGAAAAGCCC	GAAGAGGAAC	550
	TTGTCTTTTC	CCACGGCGAC	CTGGGAGACA	GCAACATCTT	TGTGAAAGAT	600
	GGCAAAGTAA	GTGGCTTTAT	TGATCTTGGG	AGAAGCGGCA	GGGCGGACAA	650
	GTGGTATGAC	ATTGCCTTCT	GCGTCCGGTC	GATCAGGGAG	GATATCGGGG	700
40	AAGAACAGTA	TGTCGAGCTA	TTTTTTGACT	TACTGGGGAT	CAAGCCTGAT	750
	TGGGAGAAAA	TAAAATATTA	TATTTTACTG	GATGAATTGT	TTTAG	795

45 2) INFORMATION FOR SEQ ID NO: 1402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402

TATTCAACAA TTTATCGGAA ACAG

24

5

2) INFORMATION FOR SEQ ID NO: 1403

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403

20 TCAGAGAGCC AACTCAACAT TTT

23

2) INFORMATION FOR SEQ ID NO: 1404

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404

35

AAACAGCGTT TTAGAGCCAA ATAA

24

40 2) INFORMATION FOR SEQ ID NO: 1405

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405

TTCTCAGAGA GCCAACTCAA CATT

24

2) INFORMATION FOR SEQ ID NO: 1406

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: BM2580
- (C) ACCESSION NUMBER: X07753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406

	ATGGAATTGC	CCAATATTAT	TCAACAATTT	ATCGGAAACA	GCGTTTTAGA	50
	GCCAAATAAA	ATTGGTCAGT	CGCCATCGGA	TGTTTATTCT	TTTAATCGAA	100
20	ATAATGAAAC	TTTTTTTCTT	AAGCGATCTA	GCACTTTATA	TACAGAGACC	150
	ACATACAGTG	TCTCTCGTGA	AGCGAAAATG	TTGAGTTGGC	TCTCTGAGAA	200
	ATTAAAGGTG	CCTGAACTCA	TCATGACTTT	TCAGGATGAG	CAGTTTGAAT	250
	TCATGATCAC	TAAAGCGATC	AATGCAAAAC	CAATTTTCAGC	GCTTTTTTTA	300
	ACAGACCAAG	AATTGCTTGC	TATCTATAAG	GAGGCACTCA	ATCTGTTAAA	350
25	TTCAATTGCT	ATTATTGATT	GTCCATTTAT	TTCAAACATT	GATCATCGGT	400
	TAAAAGAGTC	AAAATTTTTT	ATTGATAACC	AACTCCTTGA	CGATATAGAT	450
	CAAGATGATT	TTGACACTGA	ATTATGGGGA	GACCATAAAA	CTTACCTAAG	500
	TCTATGGAAT	GAGTTAACCG	AGACTCGTGT	TGAAGAAAGA	TTGGTTTTTT	550
	CTCATGGCGA	TATCACGGAT	AGTAATATTT	TTATAGATAA	ATTCAATGAA	600
30	ATTTATTTTT	TAGATCTTGG	TCGTGCTGGG	TTAGCAGATG	AATTTGTAGA	650
	TATATCCTTT	GTTGAACGTT	GCCTAAGAGA	GGATGCATCG	GAGGAAACTG	700
	CGAAAATATT	TTTAAAGCAT	TTAAAAAATG	ATAGACCTGA	CAAAAGGAAT	750
	TATTTTTTAA	AACTTGATGA	ATTGAATTGA			780

35

2) INFORMATION FOR SEQ ID NO: 1407

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407

CCCTGTAATA GAAAAGCAAG TAGG

50

24

2) INFORMATION FOR SEQ ID NO: 1408

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408

TTGTCGTATC CCTCAAATCA CC 22

15

2) INFORMATION FOR SEQ ID NO: 1409

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409

TGGGATTACA ATGGCAATCA GCG 23

30

2) INFORMATION FOR SEQ ID NO: 1410

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410

GGGGAATAGG TCACAAGATC TGCTT 25

45

2) INFORMATION FOR SEQ ID NO: 1411

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 912 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(C) ACCESSION NUMBER: S46063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411

```

10  ATGCTTTTAT ATAAAATGTG TGACAATCAA AATTATGGGG TTA CTTACAT      50
    GAAGTTTTTA TTGGCATT TT CGCTTTTAAT ACCATCCGTG GTTTTTTGCAA    100
    GTAGTTCAAA GTTTCAGCAA GTTGAACAAG ACGTTAAGGC AATTGAAGTT    150
    TCTCTTTCTG CTCGTATAGG TGTTTCCGTT CTTGATACTC AAAATGGAGA    200
15  ATATTGGGAT TACAATGGCA ATCAGCGCTT CCCGTTAACA AGTACTTTTA    250
    AAACAATAGC TTGCGCTAAA TTACTATATG ATGCTGAGCA AGGAAAAGTT    300
    AATCCCAATA GTACAGTCGA GATTAAGAAA GCAGATCTTG TGACCTATTC    350
    CCCTGTAATA GAAAAGCAAG TAGGGCAGGC AATCACACTC GATGATGCGT    400
    GCTTCGCAAC TATGACTACA AGTGATAATA CTGCGGCAAA TATCATCCTA    450
20  AGTGCTGTAG GTGGCCCCAA AGGCGTTACT GATTTTTTTAA GACAAATTGG    500
    GGACAAAGAG ACTCGTCTAG ACCGTATTGA GCCTGATTTA AATGAAGGTA    550
    AGCTCGGTGA TTTGAGGGAT ACGACAATC CTAAGGCAAT AGCCAGTACT    600
    TTGAATAAAC TTTTATTTGG TTCCGCGCTA TCTGAAATGA ACCAGAAAAA    650
    ATTAGAGTCT TGGATGGTGA ACAATCAAGT CACTGGTAAT TTACTACGTT    700
25  CAGTATTGCC GGCGGGATGG AACATTGCGG ATCGCTCAGG TGCTGGCGGA    750
    TTTGGTGCTC GGAGTATTAC AGCAGTTGTG TGGAGTGAGC ATCAAGCCCC    800
    AATTATTGTG AGCATCTATC TAGCTCAAAC ACAGGCTTCA ATGGCAGAGC    850
    GAAATGATGC GATTGT TAAA ATTGGTCATT CAATTTTGA CGTTTATACA    900
    TCACAGTCGC GC                                         912
30

```

2) INFORMATION FOR SEQ ID NO: 1412

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412

45 GAGAAAACGC TCCAGCAGGG C

21

2) INFORMATION FOR SEQ ID NO: 1413

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413

CATGAGGCTT TCACTGCGGG G

21

10

2) INFORMATION FOR SEQ ID NO: 1414

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414

TATCGTTAAT CGCACCATCA C

21

25

2) INFORMATION FOR SEQ ID NO: 1415

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415

40

ATGCAGTAAT GCGGCTTTAT C

21

2) INFORMATION FOR SEQ ID NO: 1416

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(B) STRAIN: HEL-1

(C) ACCESSION NUMBER: X91840

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416

	ATGATGAAAA	AATCGTTATG	CTGCGCTCTG	CTGCTGACAG	CCTCTTTCTC	50
	CACATTTGCT	GCCGCAAAAA	CAGAACAACA	GATTGCCGAT	ATCGTTAATC	100
10	GCACCATCAC	CCCGTTGATG	CAGGAGCAGG	CTATTCCGGG	TATGGCCGTT	150
	GCCGTTATCT	ACCAGGGAAA	ACCCTATTAT	TTCACCTGGG	GTAAAGCCGA	200
	TATCGCCAAT	AACCACCCAG	TCACGCAGCA	AACGCTGTTT	GAGCTAGGAT	250
	CGGTTAGTAA	GACGTTTAAC	GGCGTGTTGG	GCGGCGATGC	TATCGCCCGC	300
	GGCGAAATTA	AGCTCAGCGA	TCCGGTCACG	AAATACTGGC	CAGAACTGAC	350
15	AGGCAAACAG	TGGCAGGGTA	TCCGCCTGCT	GCACTTAGCC	ACCTATACGG	400
	CAGGCGGCCT	ACCGCTGCAG	ATCCCCGATG	ACGTTAGGGA	TAAAGCCGCA	450
	TTACTGCATT	TTTATCAAAA	CTGGCAGCCG	CAATGGACTC	CGGGCGCTAA	500
	GCGACTTTAC	GCTAACTCCA	GCATTGGTCT	GTTTGGCGCG	CTGGCGGTGA	550
	AACCCTCAGG	AATGAGTTAC	GAAGAGGCAA	TGACCAGACG	CGTCCTGCAA	600
20	CCATTAAAAC	TGGCGCATAC	CTGGATTACG	GTTCCGCAGA	ACGAACAAAA	650
	AGATTATGCC	TGGGGCTATC	GCGAAGGGAA	GCCCGTACAC	GTTTCTCCGG	700
	GACAACTTGA	CGCCGAAGCC	TATGGCGTGA	AATCCAGCGT	TATTGATATG	750
	GCCCGCTGGG	TTCAGGCCAA	CATGGATGCC	AGCCACGTTC	AGGAGAAAAC	800
	GCTCCAGCAG	GGCATTGCGC	TTGCGCAGTC	TCGCTACTGG	CGTATTGGCG	850
25	ATATGTACCA	GGGATTAGGC	TGGGAGATGC	TGAACTGGCC	GCTGAAAGCT	900
	GATTCGATCA	TCAACGGCAG	CGACAGCAAA	GTGGCATTGG	CAGCGCTTCC	950
	CGCCGTTGAG	GTAAACCCGC	CCGCCCCCGC	AGTGAAAGCC	TCATGGGTGC	1000
	ATAAAACGGG	CTCCACTGGT	GGATTTGGCA	GCTACGTAGC	CTTCGTTCCA	1050
	GAAAAAACC	TTGGCATCGT	GATGCTGGCA	AACAAAAGCT	ATCCTAACCC	1100
30	TGTCCGTGTC	GAGGCGGCCT	GGCGCATTCT	TGAAAAGCTG	CAATAA	1146

2) INFORMATION FOR SEQ ID NO: 1417

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417

45

TGGTTAACTA YAATCCSATT GCGGA

25

50 2) INFORMATION FOR SEQ ID NO: 1418

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418

10 ATGCTTTACC CAGCGTCAGA TT 22

2) INFORMATION FOR SEQ ID NO: 1419

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419

25 CGATGAATAA GCTGATTTCT CACG 24

2) INFORMATION FOR SEQ ID NO: 1420

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420

40 TGCTTTACCC AGCGTCAGAT TACG 24

45 2) INFORMATION FOR SEQ ID NO: 1421

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421

AATTAGAGCG GCAGTCGGGA GGAA

24

5

2) INFORMATION FOR SEQ ID NO: 1422

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422

20 GAAATCAGCT TATTCATCGC CACG

24

2) INFORMATION FOR SEQ ID NO: 1423

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: GRI-1
- (C) ACCESSION NUMBER: X92506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423

40

ATGGTTAAAA	AATCACTGCG	TCAGTTCACG	CTGATGGCGA	CGGCAACCGT	50
CACGCTGTTG	TTAGGAAGTG	TGCCGCTGTA	TGCGCAAACG	GCGGACGTAC	100
AGCAAAAAC	TGCCGAATTA	GAGCGGCAGT	CGGGAGGAAG	ACTGGGTGTG	150
GCATTGATTA	ACACAGCAGA	TAATTCGCAA	ATACTTTATC	GTGCTGATGA	200
45 GCGCTTTGCG	ATGTGCAGCA	CCAGTAAAGT	GATGGCCGTG	GCCGCGGTGC	250
TGAAGAAAAG	TGAAAGCGAA	CCGAATCTGT	TAAATCAGCG	AGTTGAGATC	300
AAAAAATCTG	ACTTGGTTAA	CTATAATCCG	ATTGCGGAAA	AGCACGTCGA	350
TGGGACGATG	TCACTGGCTG	AGCTTAGCGC	GGCCGCGCTA	CAGTACAGCG	400
ATAACGTGGC	GATGAATAAG	CTGATTTCTC	ACGTTGGCGG	CCCGGCTAGC	450
50 GTCACCGCGT	TCGCCCAGCA	GCTGGGAGAC	GAAACGTTCC	GTCTCGACCG	500
TACCGAGCCG	ACGTTAAACA	CCGCCATTCC	GGGCGATCCG	CGTGATACCA	550
CTTCACCTCG	GGCAATGGCG	CAAACCTCTG	GTAATCTGAC	GCTGGGTAAA	600
GCATTGGGTG	ACAGCCAACG	GGCGCAGCTG	GTGACATGGA	TGAAAGGCAA	650

TACCACCGGT GCAGCGAGCA TTCAGGCTGG ACTGCCTGCT TCCTGGGTTG 700
 TGGGGGATAA AACCGGCAGC GGTGACTATG GCACCACCAA CGATATCGCG 750
 GTGATCTGGC CAAAAGATCG TGCGCCGCTG ATTCTGGTCA CTTACTTCAC 800
 CCAGCCTCAA CCTAAGGCAG AAAGCCGTCG CGATGTATTA GCGTCGGCGG 850
 5 CTAAAATCGT CACCAACGGT TTGTAA 876

2) INFORMATION FOR SEQ ID NO: 1424

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424

20

GTTAACGGTG ATGGCGACGC TAC

23

25 2) INFORMATION FOR SEQ ID NO: 1425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425

GAATTATCGG CGGTGTTAAT CAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426

CACGCTCAAT ACCGCCATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1427

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427

TTATCGCCCA CTACCCATGA TTTC

24

15

2) INFORMATION FOR SEQ ID NO: 1428

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 876 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
(B) STRAIN: CAS-5
30 (C) ACCESSION NUMBER: X92507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428

	ATGATGACTC	AGAGCATTCG	CCGCTCAATG	TTAACGGTGA	TGGCGACGCT	50
35	ACCCCTGCTA	TTTAGCAGCG	CAACGCTGCA	TGCGCAGGCG	AACAGCGTGC	100
	AACAGCAGCT	GGAAGCCCTG	GAGAAAAGTT	CGGGAGGTCG	GCTTGGCGTT	150
	GCGCTGATTA	ACACCGCCGA	TAATTCGCAG	ATTCTCTACC	GTGCCGATGA	200
	ACGTTTGTGCG	ATGTGCAGTA	CCAGTAAGGT	GATGGCGGCC	GCGGCGGTGC	250
	TTAAACAGAG	CGAGAGCGAT	AAGCACCTGC	TAAATCAGCG	CGTTGAAATC	300
40	AAGAAGAGCG	ACCTGGTTAA	CTACAATCCC	ATTGCGGAGA	AACACGTTAA	350
	CGGCACGATG	ACGCTGGCTG	AGCTTGGCGC	AGCGGCGCTG	CAGTATAGCG	400
	ACAATACTGC	CATGAATAAG	CTGATTGCCC	ATCTGGGTGG	TCCCGATAAA	450
	GTGACGGCGT	TTGCTCGCTC	GTTGGGTGAT	GAGACCTTCC	GTCTGGACAG	500
	AACCGAGCCC	ACGCTCAATA	CCGCCATTCC	AGGCGACCCG	CGTGATACCA	550
45	CCACGCCGCT	CGCGATGGCG	CAGACCCTGA	AAAATCTGAC	GCTGGGTAAA	600
	GCGCTGGCGG	AAACTCAGCG	GGCACAGTTG	GTGACGTGGC	TTAAGGGCAA	650
	TACTACCGGT	AGCGCGAGCA	TTCGGGCGGG	TCTGCCGAAA	TCATGGGTAG	700
	TGGGCGATAA	AACCGGCAGC	GGAGATTATG	GCACCACCAA	CGATATCGCG	750
	GTTATCTGGC	CGGAAAACCA	CGCACCGCTG	GTTCTGGTGA	CCTACTTTAC	800
50	CCAACCGGAG	CAGAAGGCGG	AAAGCCGTCG	GGATATTCTG	GCTGCGGCGG	850
	CGAAAATCGT	AACCCACGGT	TTCTGA			876

2) INFORMATION FOR SEQ ID NO: 1429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429

TTTACGGCTA AAGATACTGA AAAGT

25

2) INFORMATION FOR SEQ ID NO: 1430

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430

GTTTAATAAA ACAACCACCG AATAAT

26

2) INFORMATION FOR SEQ ID NO: 1431

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431

TAATTGACAC TCCATTTACG GCTAA

25

2) INFORMATION FOR SEQ ID NO: 1432

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432

ACCGAATAAT ATTTTCCTTT CAGGCA

26

10

2) INFORMATION FOR SEQ ID NO: 1433

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 741 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: AJ223604

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433

	ATGAGCAAGT	TATCTGTATT	CTTTATATTT	TTGTTTTGCA	GCATTGCTAC	50
	CGCAGCAGAG	TCTTTGCCAG	ATTTAAAAAT	TGAAAAGCTT	GATGAAGGCG	100
30	TTTATGTTCA	TACTTCGTTT	GAAGAAGTTA	ACGGGTGGGG	CGTTGTTTCT	150
	AAACATGGTT	TGGTGGTTCT	TGTAAATGCT	GAGGCTTACC	TAATTGACAC	200
	TCCATTTACG	GCTAAAGATA	CTGAAAAGTT	AGTCACTTGG	TTTGTGGAGC	250
	GTGGCTATAA	AATAAAAGGC	AGCATTTTCT	CTCATTTTCA	TAGCGACAGC	300
	ACGGGCGGAA	TAGAGTGGCT	TAATTCTCGA	TCTATCCCCA	CGTATGCATC	350
35	TGAATTAACA	AATGAAGTGC	TTAAAAAAGA	CGGTAAGGTT	CAAGCCACAA	400
	ATTCATTTAG	CGGAGTTAAC	TATTGGCTAG	TTAAAAATAA	AATTGAAGTT	450
	TTTTATCCAG	GCCCGGGACA	CACTCCAGAT	AACGTAGTGG	TTTGGTTGCC	500
	TGAAAGGAAA	ATATTATTCG	GTGGTTGTTT	TATTAAACCG	TACGGTTTAG	550
	GCAATTTGGG	TGACGCAAAT	ATAGAAGCTT	GGCCAAAGTC	CGCCAAATTA	600
40	TTAAAGTCCA	AATATGGTAA	GGCAAACTG	GTTGTTCCAA	GTCACAGTGA	650
	AGTTGGAGAC	GCATCACTCT	TGAAACTTAC	ATTAGAGCAG	GCGGTTAAAG	700
	GGTTAAACGA	AAGTAAAAAA	CCATCAAAAC	CAAGCAACTA	A	741

45

2) INFORMATION FOR SEQ ID NO: 1434

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434

5 CACAATCAAG ACCAAGATTT GCGAT

25

2) INFORMATION FOR SEQ ID NO: 1435

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435

20

GAAAGGGCAG CTCGTTACGA TAGAG

25

25 2) INFORMATION FOR SEQ ID NO: 1436

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436

CAGCATCAAC ATTTAAGATC CCCA

24

40

2) INFORMATION FOR SEQ ID NO: 1437

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437

CTCCACTTGA TTAAGTGC GG AAATTC

26

2) INFORMATION FOR SEQ ID NO: 1438

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: X06046

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438

ATGGCAATCC GAATCTTCGC GATACTTTTC TCCATTTTTT CTCTTGCCAC 50
 TTTCGCGCAT GCGCAAGAAG GCACGCTAGA ACGTTCTGAC TGGAGGAAGT 100
 TTTTCAGCGA ATTTCAAGCC AAAGGCACGA TAGTTGTGGC AGACGAACGC 150
 20 CAAGCGGATC GTGCCATGTT GGTTTTTTGAT CCTGTGCGAT CGAAGAAACG 200
 CTACTCGCCT GCATCGACAT TCAAGATACC TCATACACTT TTTGCACTTG 250
 ATGCAGGCGC TGTTCGTGAT GAGTTCCAGA TTTTTCGATG GGACGGCGTT 300
 AACAGGGGCT TTGCAGGCCA CAATCAAGAC CAAGATTTGC GATCAGCAAT 350
 GCGGAATTCT ACTGTTTGGG TGTATGAGCT ATTTGCAAAG GAAATTGGTG 400
 25 ATGACAAAGC TCGGCGCTAT TTGAAGAAAA TCGACTATGG CAACGCCGAT 450
 CCTTCGACAA GTAATGGCGA TTACTGGATA GAAGGCAGCC TTGCAATCTC 500
 GGCGCAGGAG CAAATTGCAT TTCTCAGGAA GCTCTATCGT AACGAGCTGC 550
 CCTTTCGGGT AGAACATCAG CGCTTGGTCA AGGATCTCAT GATTGTGGAA 600
 GCCGGTCGCA ACTGGATACT GCGTGCAAAG ACGGGCTGGG AAGGCCGTAT 650
 30 GGGTTGGTGG GTAGGATGGG TTGAGTGGCC GACTGGCTCC GTATTCTTCG 700
 CACTGAATAT TGATACGCCA AACAGAATGG ATGATCTTTT CAAGAGGGAG 750
 GCAATCGTGC GGGCAATCCT TCGCTCTATT GAAGCGTTAC CGCCCAACCC 800
 GGCAGTCAAC TCGGACGCTG CGCGATAA 828

35

2) INFORMATION FOR SEQ ID NO: 1439

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: J03427

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439

ATGAAAACAT TTGCCGCATA TGTAATTATC GCGTGTCTTT CGAGTACGGC 50

ATTAGCTGGT TCAATTACAG AAAATACGTC TTGGAACAAA GAGTTCTCTG 100
CCGAAGCCGT CAATGGTGTC TTCGTGCTTT GTAAAAGTAG CAGTAAATCC 150
TGCGCTACCA ATGACTTAGC TCGTGCATCA AAGGAATATC TTCCAGCATC 200
AACATTTAAG ATCCCCAACG CAATTATCGG CCTAGAAACT GGTGTCATAA 250
5 AGAATGAGCA TCAGGTTTTT AAATGGGACG GAAAGCCAAG AGCCATGAAG 300
CAATGGGAAA GAGACTTGAC CTTAAGAGGG GCAATACAAG TTTCAGCTGT 350
TCCCGTATTT CAACAAATCG CCAGAGAAGT TGGCGAAGTA AGAATGCAGA 400
AATACCTTAA AAAATTTTCC TATGGCAACC AGAATATCAG TGGTGGCATT 450
GACAAATTCT GGTGGAAGG CCAGCTTAGA ATTTCCGCAG TTAATCAAGT 500
10 GGAGTTTCTA GAGTCTCTAT ATTTAAATAA ATTGTCAGCA TCTAAAGAAA 550
ACCAGCTAAT AGTAAAAGAG GCTTTGGTAA CGGAGGCGGC ACCTGAATAT 600
CTAGTGCATT CAAAACTGG TTTTCTGGT GTGGGAAGT AGTCAAATCC 650
TGGTGTGCA TGGTGGGTTG GGTGGGTTGA GAAGGAGACA GAGGTTTACT 700
TTTTCGCCTT TAACATGGAT ATAGACAACG AAAGTAAGTT GCCGCTAAGA 750
15 AAATCCATTC CCACCAAAT CATGGAAAGT GAGGGCATCA TTGGTGGCTA 800
A 801

20 2) INFORMATION FOR SEQ ID NO: 1440

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
25 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440

AGACCGTTAT CGTAAACAGG GCTAAG

26

35

2) INFORMATION FOR SEQ ID NO: 1441

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441

TTTTTTGCTC AACTTTTTTC AGGATC

26

50

2) INFORMATION FOR SEQ ID NO: 1442

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 927 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: RNL-1
(C) ACCESSION NUMBER: Z21957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442

15 ATGAATGTCA TTATAAAAGC TGTAGTTACT GCCTCGACGC TACTGATGGT 50
ATCTTTTAGT TCATTCGAAA CCTCAGCGCA ATCCCCACTG TTAAAAGAGC 100
AAATTGAATC CATAGTCATT GGAAAAAAG CCACTGTAGG CGTTGCAGTG 150
TGGGGGCCTG ACGATCTGGA ACCTTTACTG ATTAATCCTT TTGAAAAATT 200
20 CCCAATGCAA AGTGTATTTA AATTGCATTT AGCTATGTTG GTACTGCATC 250
AGGTTGATCA GGGAAAGTTG GATTTAAATC AGACCGTTAT CGTAAACAGG 300
GCTAAGGTTT TACAGAATAC CTGGGCTCCG ATAATGAAAG CGTATCAGGG 350
AGACGAGTTT AGTGTTCCAG TGCAGCAACT GCTGCAATAC TCGGTCTCGC 400
ACAGCGATAA CGTGGCCTGT GATTTGTTAT TTGAACTGGT TGGTGGACCA 450
25 GCTGCTTTGC ATGACTATAT CCAGTCTATG GGTATAAAGG AGACCGCTGT 500
GGTCGCAAAT GAAGCGCAGA TGCACGCCGA TGATCAGGTG CAGTATCAAA 550
ACTGGACCTC GATGAAAGGT GCTGCAGAGA TCCTGAAAAA GTTTGAGCAA 600
AAAACACAGC TGTCTGAAAC CTCGCAGGCT TTGTTATGGA AGTGGATGGT 650
CGAAACCACC ACAGGACCAG AGCGGTTAAA AGGTTTGTGA CCAGCTGGTA 700
30 CTGTGGTCGC ACATAAAACT GGTACTTCGG GTATCAAAGC CGGAAAAACT 750
GCGGCCACTA ATGATTTAGG TATCATTCTG TTGCCTGATG GACGGCCCTT 800
GCTGGTTGCT GTTTTGTGA AAGACTCAGC CGAGTCAAGC CGAACCAATG 850
AAGCTATCAT TGCGCAGGTT GCTCAGACTG CGTATCAATT TGAATTGAAA 900
AAGCTTTCTG CCCTAAGCCC AAATTAA 927
35

2) INFORMATION FOR SEQ ID NO: 1443

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443

50 CTTCTGCTCT GCTGATGCTT GGC

23

2) INFORMATION FOR SEQ ID NO: 1444

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444

GGCGACCAGG TATTTTGTA TACTGC

26

15

2) INFORMATION FOR SEQ ID NO: 1445

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 927 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
(B) STRAIN: JMC
30 (C) ACCESSION NUMBER: X93314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445

	ATGAATGTCA	TCACAAAATG	TGTTTTTCACC	GCTTCTGCTC	TGCTGATGCT	50
35	TGGCTTAAGT	TCATTTGTAG	TATCAGCCCA	ATCCCCTTTG	TTAAAAGAGC	100
	AGATTGAAAC	CATAGTGACG	GGTAAAAAGG	CCACTGTAGG	TGTAGCAGTG	150
	TGGGGGCCTG	ACGATCTGGA	ACCTTTGTTG	CTGAATCCAT	TTGAAAAGTT	200
	TCCGATGCAA	AGTGTGTTTA	AACTGCATTT	AGCTATGTTA	GTTCTGCATC	250
	AGGTCGATCA	GGGGAAACTG	GATTTAAATC	AGTCTGTTAC	TGTTAATCGT	300
40	GCTGCAGTAT	TACAAAATAC	CTGGTCGCCA	ATGATGAAAG	ATCATCAGGG	350
	CGATGAATTT	ACTGTTGCAG	TACAGCAGTT	ACTGCAGTAT	TCGGTGTCAC	400
	ACAGCGACAA	TGTGGCCTGC	GATTTGTTAT	TTGAACTGGT	GGGCGGGCCG	450
	CAAGCTTTGC	ATGCTTATAT	CCAGTCTTTA	GGCGTTAAAG	AAGCTGCCGT	500
	GGTAGCAAAT	GAAGCGCAAA	TGCATGCGGA	TGATCAGGTG	CAATATCAAA	550
45	ACTGGACGTC	GATGAAAGCC	GCAGCACAA	TTCTGCAAAA	GTTTGAACAG	600
	AAAAAGCAGT	TGTCTGAAAC	CTCTCAGGCC	TTGTTATGGA	AATGGATGGT	650
	TGAAACCACC	ACAGGACCAC	AGCGGTATAA	AGGCTTGTTA	CCTGCTGGTA	700
	CTATAGTGGC	GCATAAAACC	GGTACTTCGG	GCGTCAGAGC	AGGAAAAACT	750
	GCGGCGACTA	ATGATGCGGG	CGTCATTATG	TTGCCTGATG	GACGGCCTTT	800
50	ATTGGTGGCG	GTATTTGTCA	AGGATTCGGC	TGAATCAGAA	CGAACCAATG	850
	AAGCTATTAT	TGCGCAGGTT	GCGCAAGCGG	CTTATCAGTT	TGAGCTGAAA	900
	AAACTCTCTG	CAGTGAGTCC	GGATTGA			927

2) INFORMATION FOR SEQ ID NO: 1446

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446

GGCCTGYGAT TTGTTATTTG AACTGGT

27

15

2) INFORMATION FOR SEQ ID NO: 1447

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447

CGCTSTGGTC CTGTGGTGGT TTC

23

30

2) INFORMATION FOR SEQ ID NO: 1448

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448

45 GATCAGGTGC ARTATCAAAA CTGGAC

26

2) INFORMATION FOR SEQ ID NO: 1449

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449

AGCWGGTAAC AAYCCTTTTA ACCGCT

26

10

2) INFORMATION FOR SEQ ID NO: 1450

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450

ACCACTGGGA ATACACTTGT AATGGC

26

25

2) INFORMATION FOR SEQ ID NO: 1451

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451

40

ATCTACCTGG TCAATCATTG CTCGT

26

2) INFORMATION FOR SEQ ID NO: 1452

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: BM10393
 (C) ACCESSION NUMBER: AF045472

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452

	ATGACATTAT	CAATAATTGT	CGCTCACGAT	AAACAAAGAG	TCATTGGGTA	50
	CCAAAATCAA	TTACCTTGGC	ACTTACCAA	TGATTTAAAG	CATATTAAAC	100
10	AACTGACCAC	TGGGAATACA	CTTGTAATGG	CACGGAAAAC	TTTTAATTCT	150
	ATAGGGAAGC	CATTGCCAAA	TAGACGTAAC	GTCGTACTCA	CTAACCAAGC	200
	TTCATTTTAC	CATGAAGGGG	TAGATGTTAT	AAACTCTCTT	GATGAAATTA	250
	AAGAGTTATC	TGGTCATGTT	TTTATATTTG	GAGGACAAAC	GTTATACGAA	300
	GCAATGATTG	ACCAGGTAGA	TGATATGTAT	ATCACAGTAA	TAGATGGAAA	350
15	GTTTCAAGGA	GACACATTCT	TTCCACCATA	CACATTCGAA	AACTGGGAAG	400
	TCGAATCTTC	AGTAGAAGGT	CAACTAGATG	AAAAAAATAC	TATACCGCAT	450
	ACATTCTTAC	ATTTAGTGCG	TAGAAAAGGG	AAATAG		486

20

2) INFORMATION FOR SEQ ID NO: 1453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453

ATCGAAGAAT GGAGTTATCG GRAATG 26

35

2) INFORMATION FOR SEQ ID NO: 1454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454

CCTAAAYTR CTGGGGATTT CWGGA 25

50

2) INFORMATION FOR SEQ ID NO: 1455

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455

CAGGTGGTGG GGAGATATAC AAAA 24

15

2) INFORMATION FOR SEQ ID NO: 1456

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456

TATGTTAGAS RCGAAGTCTT GGKTAA 26

30

2) INFORMATION FOR SEQ ID NO: 1457

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457

CAAAGGTGAA CAGCTCCTGT TT 22

45

2) INFORMATION FOR SEQ ID NO: 1458

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458

TCCGTTATTT TCTTTAGGTT GGTAAA

27

10

2) INFORMATION FOR SEQ ID NO: 1459

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1459

AAGGTGAACA GCTCCTGTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1460

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460

GATCACTACG TTCTCATTGT CA

22

40

2) INFORMATION FOR SEQ ID NO: 1461

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: AJ238350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461

5 GTGAAACTAT CACTAATGGT AGCTATATCG AAGAATGGAG TTATCGGGAA 50
TGGCCCTGAT ATTCCATGGA GTGCCAAAGG TGAACAGCTC CTGTTTAAAG 100
CTATTACCTA TAACCAATGG CTGTTGGTTG GACGCAAGAC TTTTGAATCA 150
ATGGGAGCAT TACCCAACCG AAAGTATGCG GTCGTAACAC GTCCAAGTTT 200
10 TACATCTGAC AATGAGAACG TAGTGATCTT TCCATCAATT AAAGATGCTT 250
TAACCAACCT AAAGAAAATA ACGGATCATG TCATTGTTTC AGGTGGTGGG 300
GAGATATACA AAAGCCTGAT CGATCAAGTA GATACACTAC ATATATCTAC 350
AATAGACATC GAGCCGGAAG GTGATGTTTA CTTTCCTGAA ATCCCCAGCA 400
ATTTTAGGCC AGTTTTTACC CAAGACTTCG CCTCTAACAT AAATTATAGT 450
15 TACCAAATCT GGCAAAAGGG TTAA 474

2) INFORMATION FOR SEQ ID NO: 1462

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

25

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462

30

GCACTCCCYA ATAGGAAATA CGC

23

35 2) INFORMATION FOR SEQ ID NO: 1463

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

40

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463

AGTGTTGCTC AAAAACAAC TCG

23

50

2) INFORMATION FOR SEQ ID NO: 1464

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464

10 ACGTTYGAAT CTATGGGMGC ACT

23

2) INFORMATION FOR SEQ ID NO: 1465

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465

25

GTCGATAAGT GGAGCGTAGA GGC

23

30 2) INFORMATION FOR SEQ ID NO: 1466

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466

40

AAGCATTGAC CTACAATCAG TGT

23

45

2) INFORMATION FOR SEQ ID NO: 1467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467

5 AATACAATA CATTGTCATC ATTTGAT

27

2) INFORMATION FOR SEQ ID NO: 1468

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468

20

CGTTACCCGC TCAGGTTGGA CATCAA

26

25 2) INFORMATION FOR SEQ ID NO: 1469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1469

CATCCCCCTC TGGCTCGATG TCG

23

40

2) INFORMATION FOR SEQ ID NO: 1470

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: Z50804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470

	TTGAAAGTAT	CATTGATAGC	TGCGAAACGA	AAAAACGGCG	TGATTGGTTG	50
5	CGGTCCAGAC	ATACCGTGGT	CCGCGAAAGG	GGAGCAGCTA	CTTTTAAAG	100
	CATTGACCTA	CAATCAGTGT	CTTCTGGTGG	GTCGCAAGAC	GTTTGAATCT	150
	ATGGGCGCAC	TCCCCAATAG	GAAATACGCG	GTCGTTACCC	GCTCAGGTTG	200
	GACATCAAAT	GATGACAATG	TAGTTGTATT	TCAGTCAATC	GAAGAGGCCA	250
	TGGACAGGCT	AGCTGAATTC	ACCGGTCACG	TTATAGTGTC	TGGTGGCGGA	300
10	GAAATTTACC	GAGAAACATT	ACCCATGGCC	TCTACGCTCC	ACTTATCGAC	350
	GATCGACATC	GAGCCAGAGG	GGGATGTTTT	CTTCCCGAGT	ATTCCAAATA	400
	CCTTCGAAGT	TGTTTTTGAG	CAACACTTTA	CTTCAAACAT	TAAC TATTGC	450
	TATCAAATTT	GGAAAAAGGG	TAA			474

15

2) INFORMATION FOR SEQ ID NO: 1471

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471

30 GATAATGACA ACGTAATAGT ATTCCC 26

2) INFORMATION FOR SEQ ID NO: 1472

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472

45 GCTCAATATC AATCGTCGAT ATA 23

2) INFORMATION FOR SEQ ID NO: 1473

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473

TTAAAGCCTT GACGTACAAC CAGTGG

26

10

2) INFORMATION FOR SEQ ID NO: 1474

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474

TGGGCAATGT TTCTCTGTAA ATCTCC

26

25

2) INFORMATION FOR SEQ ID NO: 1475

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X12868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475

	GTGAAAGTAT	CATTAATGGC	TGCAAAAGCG	AAAAACGGAG	TGATTGGTTG	50
45	CGGTCCACAC	ATACCCTGGT	CCGCGAAAGG	AGAGCAGCTA	CTCTTTAAAG	100
	CCTTGACGTA	CAACCAAGTG	CTTTTGGTGG	GCCGCAAGAC	GTTCTGAATCT	150
	ATGGGAGCAC	TCCCTAATAG	GAAATACGCG	GTCGTTACTC	GCTCAGCCTG	200
	GACGGCCGAT	AATGACAACG	TAATAGTATT	CCCGTCGATC	GAAGAGGCCA	250
	TGTACGGGCT	GGCTGAACTC	ACCGATCACG	TTATAGTGTC	TGGTGGCGGG	300
50	GAGATTTACA	GAGAAACATT	GCCCATGGCC	TCTACGCTCC	ATATATCGAC	350
	GATTGATATT	GAGCCGGAAG	GAGATGTTTT	CTTTCCGAAT	ATTCCCAATA	400
	CCTTCGAAGT	TGTTTTTGAG	CAACACTTTA	GCTCAAACAT	TAACCTATTGC	450
	TATCAAATTT	GGCAAAAGGG	TTAA			474

2) INFORMATION FOR SEQ ID NO: 1476

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476

GGCGAGCAGC TCCTATTCAA AG

22

15

2) INFORMATION FOR SEQ ID NO: 1477

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477

TAGGTAAGCT AATGCCGATT CAACA

25

30

2) INFORMATION FOR SEQ ID NO: 1478

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478

45 GAGAATGGAG TAATTGGCTC TGGATT

26

2) INFORMATION FOR SEQ ID NO: 1479

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479

GCGAAATACA CAACATCAGG GTCAT

25

10

2) INFORMATION FOR SEQ ID NO: 1480

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 474 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
- (B) STRAIN: J120
- (C) ACCESSION NUMBER: Z86002

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480

30	ATGAAAATAT CTCTTATGGC AGCTGTTTCC GAGAATGGAG TAATTGGCTC	50
	TGGATTGGAT ATACCTTGGC ATGTACAAGG CGAGCAGCTC CTATTCAAAG	100
	CCATGACTTA CAATCAATGG CTTCTAGTTG GTCGTAAAAC CTTCGACTCA	150
	ATGGGTAAAC TTCCGAATAG AAAATATGCA GTGGTTACTC GTTCTAAAAT	200
	TATCTCGAAT GACCCTGATG TTGTGTATTT CGCAAGTGTT GAATCGGCAT	250
	TAGCTTACCT AAACAATGCG ACAGCACATA TCTTTGTTTC TGGTGGTGGT	300
35	GAAATATATA AAGCTTTAAT CGATCAAGCA GATGTTATCC ATCTTTCAGT	350
	GATTCACAAG CATATCTCTG GCGATGTGTT TTTTCCTCCA GTTCCACAGG	400
	GCTTCAAGCA AACATTTGAG CAAAGTTTCA GTTCAAATAT TGATTACACG	450
	TACCAAATTT GGGCAAAGGG CTAA	474

40

2) INFORMATION FOR SEQ ID NO: 1481

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481

RTTACAGATC ATKTATATGT CTCT

24

5 2) INFORMATION FOR SEQ ID NO: 1482

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482

TAATTTATAT TAGACAWAAA AAACGTG

26

20

2) INFORMATION FOR SEQ ID NO: 1483

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483

CARYGTCAGA AAATGGCGTA ATC

23

35

2) INFORMATION FOR SEQ ID NO: 1484

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1484

TKCAAAGCRW TTTCTATTGA AGGAAA

26

50

2) INFORMATION FOR SEQ ID NO: 1485

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485
- AAAATGGCGT AATCGGTAAT GGC 23
- 15 2) INFORMATION FOR SEQ ID NO: 1486
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486
- CATTGAGCT TGAAATTCCT TTCCTC 26
- 30 2) INFORMATION FOR SEQ ID NO: 1487
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487
- AATCGAAAAT ATGCAGTAGT GTCGAG 26
- 45 2) INFORMATION FOR SEQ ID NO: 1488
- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488

AGACTATTGT AGATTGACC GCCA

24

10

2) INFORMATION FOR SEQ ID NO: 1489

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: VA292

(C) ACCESSION NUMBER: U31119

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489

30

TTGAAAATTT	CATTGATTTC	TGCAACGTCA	GAAAATGGCG	TAATCGGTAA	50
TGGCCCTGAT	ATCCCATGGT	CAGCAAAAGG	TGAGCAGTTA	CTCTTTAAAG	100
CGCTCACATA	TAATCAGTGG	CTCCTTGTTG	GAAGGAAAAC	ATTTGACTCT	150
ATGGGTGTTC	TTCCAAATCG	AAAATATGCA	GTAGTGTCGA	GGAAAGGAAT	200
TTCAAGCTCA	AATGAAAATG	TATTAGTCTT	TCCTTCAATA	GAAATCGCTT	250
TGCAAGAACT	ATCGAAAATT	ACAGATCATT	TATATGTCTC	TGGTGGCGGT	300
CAAATCTACA	ATAGTCTTAT	TGAAAAGCA	GATATAATTC	ATTTGTCTAC	350
35 TGTTACGTT	GAGGTGAAG	GTGATATCAA	TTTTCCTAAA	ATTCCAGAGA	400
ATTTCAATTT	GGTTTTTGAG	CAGTTTTTTT	TGTCTAATAT	AAATTACACA	450
TATCAGATTT	GGAAAAAAGG	CTAA			474

40

2) INFORMATION FOR SEQ ID NO: 1490

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490

GACCTATGAG AGCTTGCCCG TCAAA

25

2) INFORMATION FOR SEQ ID NO: 1491

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491

TCGCCTTCGT ACAGTCGCTT AACAAA

26

15

2) INFORMATION FOR SEQ ID NO: 1492

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492

CATTTTAGCT GCCACCGCCA ATGGTT

26

30

2) INFORMATION FOR SEQ ID NO: 1493

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493

45 GCGTCGCTGA CGTTGTTAC GAAGA

25

2) INFORMATION FOR SEQ ID NO: 1494

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(B) STRAIN: BL26A
(C) ACCESSION NUMBER: U10186

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494

	ATGATCGAGC	TTCATGCCAT	TTTAGCTGCC	ACCGCCAATG	GTTGCATTGG	50
	GAAGGACAAC	GCACTTCCCT	GGCCACCACT	AAAAGGCGAT	CTGGCCAGAT	100
15	TCAAAAAATT	GACCATGGGG	AAGGTGGTCA	TTATGGGGCG	CAAGACCTAT	150
	GAGAGCTTGC	CCGTCAAATT	AGAAGGTCGC	ACCTGCATCG	TTATGACGCG	200
	CCAAGCGCTG	GAGCTTCCGG	GTGTTCGTGA	CGCTAACGGC	GCTATCTTCG	250
	TGAACAACGT	CAGCGACGCC	ATGCGGTTTCG	CTCAAGAAGA	GAGCGTGGGC	300
	GATGTGGCCT	ACGTCATTGG	TGGCGCTGAG	ATATTCAAGC	GACTTGCCTT	350
20	GATGATCACG	CAGATTGAAT	TGACCTTTGT	TAAGCGACTG	TACGAAGGCG	400
	ACACCTACGT	TGATCTGGCC	GAAATGGTCA	AAGACTACGA	GCAGAATGGC	450
	ATGGAAGAAC	ATGACCTTCA	CACTTACTTC	ACTTACCGTA	AAAAGGAGCT	500
	TACAGAATGA					510

25

2) INFORMATION FOR SEQ ID NO: 1495

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495

40

TCTCTAAACA TGATTGTCGC TGTC

24

2) INFORMATION FOR SEQ ID NO: 1496

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496

CAGTGAGGCA AAAGTTTTTC TACC

24

5

2) INFORMATION FOR SEQ ID NO: 1497

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1497

CGGACGACTT CATGTGGTAG TCAGT

25

20

2) INFORMATION FOR SEQ ID NO: 1498

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498

TTTGTTTTCA GTAATGGTCG GGACCT

26

35

2) INFORMATION FOR SEQ ID NO: 1499

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 534 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X57730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499

	ATGGCTTCTC	TAAACATGAT	TGTCGCTGTC	AATAAGACAG	GAGGTATCGG	50
	ATTTGAAAAT	CAGATTCCGT	GGCATGAACC	AGAAGATTTA	AAACACTTCA	100
	AAGCTGTTAC	AATGAACTCA	GTTTTGATTA	TGGGTAGAAA	AACTTTTGCC	150
	TCAGTGCCTA	AAGTGCTGCC	CGGACGACTT	CATGTGGTAG	TCAGTAAAAC	200
5	AGTACCACCC	ACCCAGAACA	CTGATCAAGT	TGTGTATGTA	AGTACATACC	250
	AGATCGCAGT	AAGAACTGCA	AGCTTGTTGG	TTGACAAACC	AGAGTATTCT	300
	CAAATTTTGT	TAATTGGTGG	GAAGAGTGCG	TACGAGAACT	TAGCTGCCTA	350
	CGTGGACAAA	CTCTACTTAA	CTAGAGTACA	GCTCAACACA	CAACAAGACA	400
	CTGAACTGGA	TTTATCCCTA	TTCAAGTCAT	GGAAACTCGT	ATCTGAGGTC	450
10	CCGACCATTA	CTGAAAACAA	AACAAAACCT	ATTTTCCAAA	TTTGGATTAA	500
	CCCTAACCCCT	ATTAGTGAGG	AACCCACATG	TTAG		534

15 2) INFORMATION FOR SEQ ID NO: 1500

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500

ATCGGGTTAT TGGCAATGGT CCTA

24

30

2) INFORMATION FOR SEQ ID NO: 1501

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501

GCGGTAGTTA GCTTGGCGTG AGATT

25

45

2) INFORMATION FOR SEQ ID NO: 1502

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502

5

GCGGGCGGAG CTGAGATATA CA

22

10 2) INFORMATION FOR SEQ ID NO: 1503

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503

AACGGAGTGG GTGTACGGAA TTACAG

26

25

2) INFORMATION FOR SEQ ID NO: 1504

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 498 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: TKS84
(C) ACCESSION NUMBER: Z21672

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504

	ATGAACTCGG	AATCAGTACG	CATTTATCTC	GTTGCTGCGA	TGGGAGCCAA	50
	TCGGGTATT	GGCAATGGTC	CTAATATCCC	CTGGAAAATT	CCGGGTGAGC	100
45	AGAAGATTTT	TCGCAGACTC	ACTGAGGGAA	AAGTCGTTGT	CATGGGGCGA	150
	AAGACCTTTG	AGTCTATCGG	CAAGCCTCTA	CCGAACCGTC	ACACATTGGT	200
	AATCTCACGC	CAAGCTAACT	ACCGCGCCAC	TGGCTGCGTA	GTTGTTTCAA	250
	CGCTGTCGCA	CGCTATCGCT	TTGGCATCCG	AACTCGGCAA	TGAACTCTAC	300
	GTCGCGGGCG	GAGCTGAGAT	ATACACTCTG	GCACTACCTC	ACGCCCACGG	350
50	CGTGTTTCTA	TCTGAGGTAC	ATCAAACCTT	CGAGGGTGAC	GCCTTCTTCC	400
	CAATGCTCAA	CGAAACAGAA	TTCGAGCTTG	TCTCAACCGA	AACCATTCAA	450
	GCTGTAATTC	CGTACACCCA	CTCCGTTTAT	GCGCGTCGAA	ACGGCTAA	498

2) INFORMATION FOR SEQ ID NO: 1505

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505

ATTTTTCGCA GGCTCACCGA GAGC

24

15

2) INFORMATION FOR SEQ ID NO: 1506

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506

CGGATGAGAC AACCTCGAAT TCTGCTG

27

30

2) INFORMATION FOR SEQ ID NO: 1507

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 498 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: RA33.2
 (C) ACCESSION NUMBER: Z50802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507

50 ATGAACCCGG AATCGGTCCG CATTTATCTG GTCGCTGCCA TGGGTGCCAA 50
 TCGGGTTATT GGCAATGGTC CCGATATCCC CTGGAAAATC CCAGGTGAGC 100
 AGAAGATTTT TCGCAGGCTC ACCGAGAGCA AAGTGGTCGT TATGGGCCGC 150
 AAGACATTTG AGTCCATAGG CAAGCCCTTA CCAAACCGCC ACACAGTGGT 200

	GCTCTCGCGC	CAAGCTGGTT	ATAGCGCTCC	TGGTTGTGCA	GTTGTTTCAA	250
	CGCTGTCACA	CGTATCGCCA	TCGACAGCCG	AACACGGCAA	AGAACTCTAC	300
	GTAGCGCGCG	GAGCCGAGGT	ATATGCGCTG	GCGCTACCGC	ATGCCAACGG	350
	CGTCTTTCTA	TCTGAGGTAC	ATCAAACCTT	TGAGGGTGAC	GCCTTCTTCC	400
5	CAGTGCTTAA	CGCAGCAGAA	TTCGAGGTTG	TCTCATCCGA	AACCATTCAA	450
	GGCACAATCA	CGTACACGCA	CTCCGTCTAT	GCGCGTCGTA	ACGGCTAA	498

10 2) INFORMATION FOR SEQ ID NO: 1508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508

AGAATGTATT GGTATTTCCA TCTATCG

27

25

2) INFORMATION FOR SEQ ID NO: 1509

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509

CAATGTCGAT TGTGAAATA TGTAATA

26

40

2) INFORMATION FOR SEQ ID NO: 1510

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510

TGGAGTGCCA AAGGGGAACA AT

5 2) INFORMATION FOR SEQ ID NO: 1511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511

CAGACACAAT CACATGATCC GTTATCG

27

20

2) INFORMATION FOR SEQ ID NO: 1512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: UI14
 (C) ACCESSION NUMBER: Z83331

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512

	GTGAAACTAT CACTAATGGC AGCAATTTTCG AAGAATGGAG TTATCGGAAA	50
	TGGCCCAGAT ATTCCATGGA GTGCCAAAGG GGAACAATTA CTCTTCAAAG	100
40	CGATTACCTA TAATCAGTGG CTTTTGGTAG GCCGAAAGAC TTTCGAGTCA	150
	ATGGGGGCTT TACCCAACCG AAAATATGCC GTTGTAAGCTC GTTCAAGCTT	200
	CACTTCCAGT GATGAGAATG TATTGGTATT TCCATCTATC GATGAAGCGC	250
	TAAATCATCT GAAGACGATA ACGGATCATG TGATTGTGTC TGGTGGTGGT	300
	GAAATATACA AAAGCCTGAT CGATAAAGTT GATACTTTAC ATATTTCAAC	350
45	AATCGACATT GAGCCAGAAG GTGATGTCTA TTTTCCAGAA ATCCCCAGTA	400
	GTTTTAGGCC AGTTTTTAGC CAAGACTTCG TGTCTAACAT AAATTATAGT	450
	TACCAAATCT GGCAAAAGGG TTAA	474

50

2) INFORMATION FOR SEQ ID NO: 1513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513

10 TTCAAGCTCA AATGAAAACG TCC

23

2) INFORMATION FOR SEQ ID NO: 1514

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514

25

GAAATTCTCA GGCATTATAG GGAAT

25

30 2) INFORMATION FOR SEQ ID NO: 1515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515

GTGGTCAGTA AAAGGTGAGC AAC

23

45

2) INFORMATION FOR SEQ ID NO: 1516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

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MISSING AT THE TIME OF PUBLICATION

CTATGTCTCA	AGGCCGTGCA	ACATACTCTA	TGGAATTTGC	TAAATATGCT	50
GAAACTCCAC	GTAACGTGGC	TGAAGGCATC	ATTTCTAAAT	TTCAGTCTGG	100
CGGTAAAAAA	GGTGACGACG	AGTAA			125

5

2) INFORMATION FOR SEQ ID NO: 1519

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
- (B) STRAIN: CDCF 3697

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519

TCTTTCGATT	ACTATAAGCC	CAAAC TAATT	CATAGTTAAA	AACCAAGTGC	50
TCATGCAGTG	ATCCTGCATG	AGTAGTTTAA	AAAGGAAGAT	CTC	93

25

2) INFORMATION FOR SEQ ID NO: 1520

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
- (B) STRAIN: CDCF 3697

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520

45	ATGGCTAAGG	CTAAGTTTGA	ACGTAATAAG	CCACACGTTA	ACGTGGGCAC	50
	AATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACAGCT	GCAATTGCAA	100
	CTGTATGTGC	GAAGAAATTC	GGTGGCGAAG	CGAAAGACTA	CGCTGCAATT	150
	GACTCTGCAC	CAGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACTTCACA	200
	CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTA	GACTGCCCGG	250
50	GCCACGCCGA	TTATGT TAAA	AACATGATTA	CTGGTGCTGC	TCAGATGGAC	300
	GGCGCGATCC	TTGTATGTGC	TGCGACTGAT	GGTCCAATGC	CACAGACTCG	350
	TGAACACATC	CTTCTTTCTC	GTCAGGTTGG	TGTACCTTAC	ATTCTTGTAT	400
	TCCTTAACAA	GTGTGACCTT	GTTGATGATG	AAGAACTTCT	TGAGCTAGTG	450

5 GAAATGGAAG TTCGTGAACT TCTTTCTACT TATGACTTCC CAGGTGATGA 500
CACTCCAGTT ATCCGTGGTT CAGCTCTTCT TGCACTTAAC GGTGACGCTG 550
GTCAGTATGG CGAAGAAGCA GTTGTTGCGC TTGTTGACGC ACTTGACACT 600
TACATTCCAG AGCCAGTACG TGCAATCGAC CAAGCATTCT TAATGCCAAT 650
CGAAGACGTA TTCTCTATTT CTGGTCGTGG TACAGTAGTA ACTGGCCGTG 700
TAGAAACTGG TATTGTGAAA GTAGGCGAAT CAGTTGAAAT CGTTGGTATC 750
CGTGATACTC AAGTAACTAC AGTTACTGGC GTAGAAATGT TCCGTAAATT 800
GCTTGACGAA GGTCGTGCGG GCGAGAACTG TGGTGTTCTT CTACGTGGTA 850
CTAAGCGTGA AGACGTACAA CGTGGTCAAG TACTTGCTAA ACCAGGTGCA 900
10 ATCAAGCCAC AACTAAATT CGATGCAGAA GTATACGTAC TTTCTAAAGA 950
AGAAGGTGGT CGTCACACTC CATTCTTAA CGGTACCGT CCACAGTTCT 1000
ACTTCCGTAC AACTGACGTA ACTGGCGCGA TCAAATTACA AGATGGCGTT 1050
GAAATGGTTA TGCCTGGTGA CAACGTAGAA ATGTCAGTAG AATTAATCCA 1100
CCCAAT 1106
15

2) INFORMATION FOR SEQ ID NO: 1521

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*
30 (B) STRAIN: ATCC 9006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521

ACAAACTCAA GGTCGTGCAT CTTACTCAAT GGAACCGTTA AAATATGCTG 50
35 AAGCTCCAAC AAGTGTTGCG GCTGCAGTAA TTGAAGCGCG TAAAAAATAA 100

2) INFORMATION FOR SEQ ID NO: 1522

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: *Haemophilus influenzae*
(B) STRAIN: ATCC 9006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522

TTTTTGTAAG CCAGCGGTGT AAAATATGAT TGTTTTATAC CGCACTTCTT 50
AGGAAACATT AGAA 64

5

2) INFORMATION FOR SEQ ID NO: 1523

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*
(B) STRAIN: ATCC 9006

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523

ATGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTAA ACGTGGGTAC 50
AATCGGCCAC GTTGACCACG GTAAAACAAC TTTAACAGCA GCAATTACAA 100
25 CCGTATTAGC AAAACACTAC GGTGGTGCAG CGCGTGCATT TGACCAAATC 150
GATAACGCGC CAGAAGAAAA AGCGCGTGGT ATTACCATCA ACACTTCACA 200
TGTTGAATAC GATACACCAA CTCGCCACTA TGCACACGTA GACTGTCCAG 250
GACACGCCGA CTATGTTAAA AACATGATTA CCGGTGCGGC GCAAATGGAT 300
GGTGCTATTT TAGTAGTAGC AGCAACAGAT GGTCCTATGC CACAAACTCG 350
30 TGAACATATC TTATTAGGTC GCCAAGTAGG TGTTCATAC ATCATCGTAT 400
TCTTAAACAA ATGCGACATG GTAGATGATG AAGAGTTATT AGAATTAGTA 450
GAAATGGAAG TCGGTGAAC TCTATCTCAA TATGACTTCC CAGGTGACGA 500
TACACCAATC GTACGTGGTT CAGCATTACA AGCATTGAAC GGCGTAGCAG 550
AATGGGAAGA AAAAATCCTT GAATTAGCTG GTCACCTAGA TACTTACATC 600
35 CCAGAACCAG AACGTGCGAT TGACCAACCG TTCCTTCTTC CAATTGAAGA 650
CGTATTCTCA ATTTTCAGGTC GTGGTACAGT AGTAACTGGT CGTGTAGAAC 700
GTGGTATCAT CCGTACTGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT 750
ACAGCGAAAA CTACTGTAAC AGGTGTTGAA ATGTTCCGTA AATTACTTGA 800
CGAAGGTCGT GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC 850
40 GTGAAGAAAT CGAACGTGGT CAAGTATTAG CGAAACCAGG TTCAATCACA 900
CCACACACTG ATTTTGAATC AGAAGTATAC GTATTATCAA AAGATGAAGG 950
TGGTCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAA TTCTATTTCC 1000
GTACAACAGA CGTAACTGGT ACAATTGAAT TACCAGAAGG CGTGGAAATG 1050
GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCCA 1098

45

2) INFORMATION FOR SEQ ID NO: 1524

- 50 (i) SEQUENCE CHARACTERISTICS:,
(A) LENGTH: 77 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524

10

CAATGGAGTT CTTGAAGTAC AACGAAGCGC CTAGCAACGT CGCTCAGGCT
ATTATCGAAG CTCGTAAAGC GAAATAA

50

77

15

2) INFORMATION FOR SEQ ID NO: 1525

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 bases

20

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525

GATCCTTTCG AGTTCAATTT AGTTTACGCT CCCTCTGTGA GAGGGAGCGA
TATTAAGGAA TATAGTC

50

67

35

2) INFORMATION FOR SEQ ID NO: 1526

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 1112 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526

GTGTCTAAAG AAAAATTTGA ACGTTCAAAA CCGCACGTTA ACGTTGGTAC

50

	TATCGGCCAC	GTTGACCACG	GTAAAACAAC	TCTGACTGCT	GCAATCACTA	100
	CAGTTTTAGC	TAAAACTTAC	GGTGGTGCTG	CTCGTGCATT	CGACCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCGCGTGGT	ATCACCATCT	CTACTTCACA	200
	CGTAGAATAC	GATACTCCAA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
5	GTCACGCCGA	CTATGTTAAA	AACATGATCA	CTGGTGCTGC	GCAAATGGAC	300
	GGCGCTATTC	TGGTAGTAGC	AGCAACTGAT	GGTCCAATGC	CACAAACTCG	350
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTC	CAGGTGATGA	500
10	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCTTATATC	600
	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATCGAAGA	650
	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	TATCAAAGAA	750
15	ACCACCAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	800
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACAAAAC	850
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CAAAACCAGG	CTCAATCAAC	900
	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAC	ACACCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
20	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	1050
	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGAACTGA	TCCACCCAAT	1100
	CGCAATGGAC	GA				1112

25

2) INFORMATION FOR SEQ ID NO: 1527

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527

	ATCAACGAAG	CTATCGAGGT	TTATTTTGAG	GTTGAGGGCA	AGAAAAATAG	50
	ATTGATCCTG	GAGGTCGCGG	CTCACTTGGG	TGATAACCGC	GTCAGAACGA	100
	TCGCTATGGA	TATGAGTGAG	GGGCTTACTC	GCGGGCTTGA	AGCTACCGCT	150
45	CTTGGTGCGC	CTATTAGTGT	GCCGGTTGGC	GAGAAGGTTT	TGGGAAGAAT	200
	TTTTAACGTC	GTCGGCGATC	TCATCGACGA	GGGCGAGGGC	GTAAATTTTG	250
	ATAAACATTG	GTCTATCCAC	CGCGATCCGC	CACCATTTGA	AGAACAAAGC	300
	ACGAAAAGTG	AAATTTTTGA	AACCGGTATA	AAGGTTGTGG	ATCTTCTTGC	350
	GCCTTACGCA	AAGGGCGGTA	AGGTCGGACT	ATTTGGCGGT	GCAGGTGTCG	400
50	GTAAACGGT	CATCATCATG	GAGCTCATCC	ACAATGTTCG	CTTCAAACAC	450
	AGCGGATACT	CTGTATTTGC	AGGTGTTGGC	GAGAGGACGC	GCGAAGGAAA	500
	CGACCTTTAT	CACGAGATGA	AAGAAAGTAA	CGTTTTGGAT	AAAGTCGCCT	550
	TGTGCTACGG	ACAGATGAAC	GAGCCGCCAG	GGGCGAGAAA	TCGTATCGCA	600

CTGACTGGTC	TAACGATGGC	TGAGTATTTC	CGCGATGAGA	TGGGACTTGA	650
TGTGCTTATG	TTTATCGACA	ACATCTTCCG	CTTCTCTCAA	TCTGGTGCAG	700
AGATGTCGGC	ACTCCTCGGA	CGTATCCCAT	CAGCCGTTGG	TTACCAGCCG	750
ACGCTGGCAA	GCGAGATGGG	TAAATTTCAA	GAAAGGATCA	CATCGACTAA	800

5

2) INFORMATION FOR SEQ ID NO: 1528

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528

20 AACTTGAGCG ATTTTCGGAT ACCCTG

26

2) INFORMATION FOR SEQ ID NO: 1529

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529

35

TTGCCGATGA AATAACCGCC GACT

24

40 2) INFORMATION FOR SEQ ID NO: 1530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: M11277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530

	ATGCGATTGG	TTTGGAAATG	TGGGGCGATT	CAGGCATCCC	GGTTATCTGA	50
	ATGGCTCAAC	TCAACAGCCG	GTGCTCATGA	ACTTGAGCGA	TTTTCGGATA	100
5	CCCTGACCTT	TTCTGTGTAT	GGCTCAGTGC	TGATCTGGCT	GAAATCATAT	150
	CTCCGCGAAT	CAGGAAGAAA	ACTGCAGTTA	GTCGGAATCG	CCTTACCCAA	200
	CACCCTGAAC	CCAAGGGACG	ACCTAGCGCA	ATTGGCCGAA	ATTATCCAGC	250
	TCATCGATCA	CCTCATGAAA	CCGCACGTTG	ATATGTTGAC	TCACTTGTTG	300
	GCGTCCATTG	ATGGCCAGTC	GGCGGTTATT	TCATCGGCAA	AATGGGGGGA	350
10	GCTAGAAACG	GCTCGGCAGG	AGAAAGCTAT	CTCAGGGGTA	ACCAGATTGA	400
	AGCTCCGCTT	GGCGTCGCTT	GCCCCGTCC	TGAAAAACA	CGTCAACAGC	450
	GATTTGTTCC	GAAAAGCCTC	TGATCGAATA	GAGTCGATAG	AGTATACGTT	500
	GGAAACCTTG	CGTATAATGA	AAACTTTCTT	CGATGGTACC	TCTCTTGAGG	550
	GAGATACTTC	CGTACGTGAC	TCGTATATGG	CGGGCGTAGT	AGATGGAATG	600
15	GTTCGAGCGA	ATCCGGATGT	GAAGATAATT	CTGCTGGCGC	ACAACAATCA	650
	TCTACAAAAA	ACTCCAGTCT	CCTTTTTCAGG	CGAGCTTACG	GCTGTTCCCA	700
	TGGGGCAGCA	CCTCGCAGAG	AGGGTGAATT	ACCGTGCGAT	TGCATTCAAC	750
	CATCTTGGAC	CCACCGTGCC	GGAAATGCAT	TTCCCATCGC	CAAAAAGTCC	800
	TCTTGATTTC	TCTGTTGTGA	CCACGCCTGC	CGATGCAATC	CGTGAGGATA	850
20	GTATGGAACA	GTATGTCATC	GACGCCTGTG	GTACGGAGAA	TTCATGTCTG	900
	ACATTGACAG	ATGCCCCCAT	GGAAGCAAAG	CGAATGCCGT	CTCAAAGCGC	950
	CTCTGTAGAA	ACGAAATTGA	GCGAGGCATT	TGATGCCATC	GTCTGTGTTA	1000
	CAAGCGCCGG	CAAGGACAGC	CTGGTTGCCC	TATAG		1035

25

2) INFORMATION FOR SEQ ID NO: 1531

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531

40 TCTTTTGTGTT ACGACATACG CTTTT

25

2) INFORMATION FOR SEQ ID NO: 1532

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532

AGTGCTTCTT TATCCGCTGT TCTA

24

5

2) INFORMATION FOR SEQ ID NO: 1533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533

CAGCGGATAA AGAAGCACTA CACATT

26

20

2) INFORMATION FOR SEQ ID NO: 1534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534

CCTCCTGAAA TAAAGCCCGA CAT

23

35

2) INFORMATION FOR SEQ ID NO: 1535

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: A15097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535

	ATGAGGTTTCG	AAGAATGGGT	CAAAGATAAG	CATATTCCTT	NCAAACNGAA	50
	TCACCCTGAT	GATAATTACG	ATGATTTTAA	GCCATTAAGA	AANATAATTG	100
	GAGATACCCG	AGTTGTAGCA	TTAGGTGAAA	ATTCTCATTT	CATAAAAGAA	150
	TTCTTTTTGT	TACGACATAC	GCTTTTGCGT	TTTTTTATCG	AAGATCTAGG	200
5	TTTTACTACG	TTTGCTTTTG	AATTTGGTTT	TGCTGAGGGT	CAAATCATCA	250
	ATAACTGGAT	ACATGGACAA	GGAAGTACG	ATGAAATAGG	CAGATTCTTA	300
	AAACACTTCT	ATTATCCAGA	AGAGCTCAAA	ACCACATTTT	TATGGCTAAG	350
	GGAGTACAAT	AAAGCAGCAA	AAGAAAAAAT	CACATTTCTT	GGCATTGATA	400
	TACCCAGAAA	TGGAGGTTCA	TACTTACCAA	ATATGGAGAT	AGTGCATGAC	450
10	TTTTTTTAGAA	CAGCGGATAA	AGAAGCACTA	CACATTATCG	ATGATGCATT	500
	TAATATTGCA	AAAAAGATTG	ATTACTTCTC	CACATCACAG	GCAGCCTTAA	550
	ATTTACATGA	GCTAACAGAT	TCTGAGAAAT	GCCGTTTAAC	TAGCCAATTA	600
	GCTCGAGTAA	AAGTTCGCCT	TGAAGCTATG	GCTCCAATTC	ACATTGAAAA	650
	ATATGGGATT	GATAAATATG	AGACAATTCT	GCATTATGCC	AACGGTATGA	700
15	TATACTTGGA	CTATAACATT	CAAGCTATGT	CGGGCTTTAT	TTCAGGAGGC	750
	GGAATGCAGG	GCGATATGGG	TGCAAAAGAC	AAATACATGG	CAGATTCTGT	800
	GCTGTGGCAT	TTAAAAAACC	CACAAAGTGA	GCAGAAAGTG	ATAGTAGTAG	850
	CACATAATGC	ACATATTCAA	AAAACACCCA	TTCTGTATGA	TGGATTTCTA	900
	AGTTGCCTAC	CAATGGGCCA	AAGACTTAAA	AATGCCATTG	GTGATGATTA	950
20	TATGTCTTTA	GGTATTACTT	CTTATAGTGG	GCATACTGCA	GCCCTCTATC	1000
	CGGAAGTTGA	TACAAAATAT	GGTTTTCGAG	TTGATAACTT	CCAACTGCAG	1050
	GAACCAAATG	AAGGTTCTGT	CGAGAAAGCT	ATTTCTGGTT	GTGGAGTTAC	1100
	TAATTCTTTT	GTCTTTTTTA	GAAATATTCC	TGAAGATTTA	CAATCCATCC	1150
	CGAACATGAT	TCGATTTGAN	TCTATTTACA	TGAAAGCAGA	ACTCGAGAAA	1200
25	GCTTTCGATG	GAATATTTCA	AATTGAAAAG	TCATCTGTAT	CTGAGGTCGT	1250
	TTATGAATAA					1260

30 2) INFORMATION FOR SEQ ID NO: 1536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536

AGATGTATTA ACTGGAAAAC AACAA

25

45

2) INFORMATION FOR SEQ ID NO: 1537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537

5 CTTTGTAATT AGTTTCTGAA AACCA

25

2) INFORMATION FOR SEQ ID NO: 1538

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538

20

TTAGAAGATA TAGGATACAA AATAGAAG

28

25 2) INFORMATION FOR SEQ ID NO: 1539

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539

GAATGAAAAA GAAGTTGAGC TT

22

40

2) INFORMATION FOR SEQ ID NO: 1540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

(C) ACCESSION NUMBER: M14039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540

	ATGAAAAATA	ATAATGTAAC	AGAAAAAGAA	TTATTTTATA	TTT TAGATTT	50
5	ATTTGAACAC	ATGAAAGTAA	CTTATTGGTT	AGATGGTGGC	TGGGGGGTAG	100
	ATGTATTAAC	TGGAAAACAA	CAAAGAGAAC	ACAGAGATAT	AGATATAGAT	150
	TTTGACGCTC	AACACACTCA	AAAAGTTATA	CAAAAATTAG	AAGATATAGG	200
	ATACAAAATA	GAAGTTCATT	GGATGCCTTC	ACGTATGGAA	CTTAAGCATG	250
	AAGAATATGG	GTATTTAGAT	ATTCATCCTA	TAAATCTAAA	TGATGATGGA	300
10	TCAATTACCC	AAGCAAACCC	AGAAGGTGGT	AATTATGTTT	TCCAAAATGA	350
	CTGGTTTTCA	GAAACTAATT	ACAAAGATCG	AAAAATACCA	TGTATTTCAA	400
	AAGAAGCTCA	ACTTCTTTTT	CATTCTGGTT	ATGATTTAAC	AGAAACAGAC	450
	CATTTTGATA	TAAAAAATTT	AAAATCAATA	ACATAA		486

15

2) INFORMATION FOR SEQ ID NO: 1541

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541

	TGATAATCTT	ATACGTGGGG	AATTT	25
30				

2) INFORMATION FOR SEQ ID NO: 1542

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542

45	ATAATTTTCT	AATTGCCCTG	TTTCAT	26
----	------------	------------	--------	----

2) INFORMATION FOR SEQ ID NO: 1543

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543

GGGCAATTAG AAAATTATTT ATCAGA

26

10

2) INFORMATION FOR SEQ ID NO: 1544

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544

TTTTACTCAT GTTTAGCCAA TTATCA

26

25

2) INFORMATION FOR SEQ ID NO: 1545

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Enterococcus faecium*
(C) ACCESSION NUMBER: AF110130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545

	ATGTTAAAAC	AAAAAGAATT	AATTGCAAAC	GTAAAGAATC	TTACTGAGTC	50
45	AGATGAACGA	ATTACAGCTT	GTATGATGTA	TGGATCGTTT	ACCAAAGGAG	100
	AAGGTGACCA	ATACTCTGAT	ATAGAGTTCT	ATATATTTTT	GAAACATAGT	150
	ATAACCTCGA	ACTTTGATTC	ATCCAACCTG	TTGTTTGACG	TAGCTCCGTA	200
	CTTGATGCTT	TATAAAAATG	AGTACGGAAC	AGAGGTAGTT	ATTTTTGATA	250
	ATCTTATACG	TGGGGAATTT	CATTCCTTT	CTGAAAAGA	TATGAACATA	300
50	ATCCCCTCGT	TTAAAGATTC	AGGTTATATT	CCTGATACGA	AGGCTATGCT	350
	TATTTACGAT	GAAACAGGGC	AATTAGAAAA	TTATTTATCA	GAGATAAGTG	400
	GTGCAAGACC	AAATAGACTT	ACTGAAGAAA	ATGCTAATTT	TTTGTTGTGT	450
	AATTTCTCTA	ATCTATGGTT	GATGGGAATC	AACGTTCTAA	AAAGAGGAGA	500

ATATGCTCGT TCATTAGAAC TCTTATCACA ACTTCAAAAA AATACACTAC 550
AACTTATACG TATGGCAGAA AAAAATGCTG ATAATTGGCT AAACATGAGT 600
AAAAACCTTG AAAAAGAAAT TAGCCTTGAA AATTATAAAA AATTTGCAAA 650
GACCACTGCT CGATTAGATA AGGTAGAATT ATTTGAAGCC TATAAAAATT 700
5 CTTTGCTATT AGTTATGGAT TTGCAAAGTC ACCTTATTGA ACAATACAAC 750
TTAAAAGTTA CACATGACAT TTTAGAAAGA TTGTTGAATT ACATTAGTGA 800
ATAG 804

10

2) INFORMATION FOR SEQ ID NO: 1546

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546

CAAGAAGGAA TGGCTGTACT AC

22

25

2) INFORMATION FOR SEQ ID NO: 1547

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
30 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1547

TAATTCCCAA ATAACCCTAA TAATAGA

27

40

2) INFORMATION FOR SEQ ID NO: 1548

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1218 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(C) ACCESSION NUMBER: U70055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548

5
ATGGAAAAAT ACAACAATTG GAAACTTAAG TTTTATACAA TATGGGCAGG 50
GCAAGCAGTA TCATTAATCA CTAGTGCCAT CTTGCAAATG GCGATTATTT 100
TTTACCTTAC AGAAAAAACT GGATCCGCGA TGGTCTTGTC TATGGCTTCA 150
CTATTAGGTT TTTTACCCTA TGCGGTCTTT GGACCTGCAA TTGGTGTGCT 200
10 AGTGGATCGT CATGATAGGA AGAAGATAAT GATTGGTGCT GATTTAATTA 250
TCGCAGCAGC TGGTTCGGTG CTTACTATTG TTGCATTCTA TATGGAGCTA 300
CCTGTCTGGA TGGTTATGAT AGTATTGTTT ATCCGTAGCA TTGGAACAGC 350
TTTTACACACC CCGGCTCTCA ATGCGGTTAC GCCACTTTTA GTACCAGAAG 400
AACAGCTTAC GAAATGTGCA GGCTATAGTC AGTCTTTGCA GTCTATAAGC 450
15 TATATTGTTA GTCCGGCGGT TGCAGCACTC TTATACTCCG TTTGGGAACT 500
AAATGCTATT ATTGCCATCG ATGTATTGGG TGCTGTGATT GCATCTATTA 550
CGGTAGCAAT TGTACGTATT CCTAAGCTGG GTGATCGCGT GCAAAGTTTG 600
GACCCAAATT TCATAAGAGA AATGCAAGAA GGAATGGCTG TACTACGGCA 650
AAATAAAGGA TTATTTGCTT TATTACTCGT TGGAACATTA TATATGTTTG 700
20 TTTATATGCC AATTAATGCA CTATTCCCTT TAATTAGCAT GGATTACTTT 750
AATGGAACAC CTGTGCATAT TTCTATTACG GAAATTTCTT TTGCATCTGG 800
AATGTTGATA GGGGGTCTAT TATTAGGGTT ATTTGGGAAT TACCAAAGC 850
GAATCTTATT AATAACGGCA TCCATTTTTA TGATGGGGAT AAGCTTAACC 900
ATTTCAGGAT TACTTCCCCA AAGTGGATTT TTCATTTTTG TAGTCTGCTG 950
25 TGCAATAATG GGGCTTTCTG TTCCGTTTTA CAGCGGTGTG CAAACAGCTC 1000
TTTTTCAGGA GAAATTAAG CCTGAATATT TAGGACGTGT ATTTTCTTTA 1050
ACTGGAAGTA TCATGTCTCT TGCTATGCCA ATTGGATTAA TTCTTTCTGC 1100
ACTCTTTGCT GATAGAATCG GTGTAAATCA TTGGTTTTTA CTATCAGGTA 1150
CTTTAATTAT TTGCATTGCA ATAGTTTGCC CAATGATAAA TGAGATTAGA 1200
30 AAATTAGATT TAAAATAA 1218

2) INFORMATION FOR SEQ ID NO: 1549

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549

45

GCTTATTATT AGGAAGATTA GGGGGC

26

50 2) INFORMATION FOR SEQ ID NO: 1550

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

800

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550

TAGCAAGTGA CATGATACTT CCGA

24

10

2) INFORMATION FOR SEQ ID NO: 1551

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (C) ACCESSION NUMBER: U83667

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551

	ATGGAAAAAT	ACAACAATTG	GAAACGAAAA	TTTTATGCAA	TATGGGCAGG	50
30	GCAAGCAGTA	TCATTAATCA	CTAGTGCCAT	CCTGCAAATG	GCGATTATTT	100
	TTTACCTTAC	AGAAAAAACA	GGATCTGCGA	TGGTCTTGTC	TATGGCTTCA	150
	TTAGTAGGTT	TTTTACCCTA	TGCGATTTTG	GGACCTGCCA	TTGGTGTGCT	200
	AGTGGATCGT	CATGATAGGA	AGAAGATAAT	GATTGGTGCC	GATTTAATTA	250
	TCGCAGCAGC	TGGTGCAGTG	CTTGCTATTG	TTGCATTCTG	TATGGAGCTA	300
35	CCTGTCTGGA	TGATTATGAT	AGTATTGTTT	ATCCGTAGCA	TTGGAACAGC	350
	TTTTCATACC	CCAGCACTCA	ATGCGGTTAC	ACCACTTTTA	GTACCAGAAG	400
	AACAGCTAAC	GAAATGCGCA	GGCTATAGTC	AGTCTTTGCA	GTCTATAAGC	450
	TATATTGTTA	GTCCGGCAGT	TGCAGCACTC	TTATACTCCG	TTTGGGATTT	500
	AAATGCTATT	ATTGCCATCG	ACGTATTGGG	TGCTGTGATT	GCATCTATTA	550
40	CGGTAGCAAT	TGTACGTATA	CCTAAGCTGG	GTAATCAAGT	GCAAAGTTTA	600
	GAACCAAATT	TCATAAGGGA	GATGAAAGAA	GGAGTTGTGG	TTCTGAGACA	650
	AAACAAAGGA	TTGTTTGCCT	TATTACTCTT	AGGAACACTA	TATACTTTTG	700
	TTTATATGCC	AATCAATGCA	CTATTTCCCT	TAATAAGCAT	GGAACACTTT	750
	AATGGAACGC	CTGTGCATAT	TTCTATTACG	GAAATTTCCCT	TTGCATTTGG	800
45	GATGCTAGCA	GGAGGCTTAT	TATTAGGAAG	ATTAGGGGGC	TTCGAAAAGC	850
	ATGTATTACT	AATAACAAGT	TCATTTTTTA	TAATGGGGAC	CAGTTTAGCC	900
	GTTTCGGGAA	TACTTCCTCC	AAATGGATTT	GTAATATTCG	TAGTTTGCTG	950
	TGCAATAATG	GGGCTTTCGG	TGCCATTTTA	TAGCGGTGTG	CAAACAGCTC	1000
	TTTTTCAGGA	GAAAATTAAG	CCTGAATATT	TAGGACGTGT	ATTTTCTTTG	1050
50	ATCGGAAGTA	TCATGTCACT	TGCTATGCCA	ATTGGGTAA	TTCTTTCTGG	1100
	ATTCTTTGCT	GATAAAATCG	GTGTAAATCA	TTGGTTTTTA	CTATCAGGTA	1150
	TTTAAATTAT	TGGCATTGCT	ATAGTTTGCC	AAATGATAAC	TGAGGTTAGA	1200
	AAATTAGATT	TAAAATAA				1218

2) INFORMATION FOR SEQ ID NO: 1552

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552

GGCAAGCAGT ATCATTAATC ACTA

24

15

2) INFORMATION FOR SEQ ID NO: 1553

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553

CAATGCTACG GATAACAAT ACTATC

26

30

2) INFORMATION FOR SEQ ID NO: 1554

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554

45 AGAAAATTAA GCCTGAATAT TTAGGAC

27

2) INFORMATION FOR SEQ ID NO: 1555

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555

TAGTAAAAAC CAATGATTTA CACCG

25

10

2) INFORMATION FOR SEQ ID NO: 1556

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556

ACTGTACGCA CTTGCAGCCC GACAT

25

25

2) INFORMATION FOR SEQ ID NO: 1557

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557

40 GAACGGCAGG CGATTCTTGA GCAT

24

2) INFORMATION FOR SEQ ID NO: 1558

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558

GTGGTGGTGC ATGGCGATCT CT

22

5

2) INFORMATION FOR SEQ ID NO: 1559

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559

GCCGCAGCGA GGTACTCTTC GTTA

24

20

2) INFORMATION FOR SEQ ID NO: 1560

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: D16251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560

	ATGACCGTAG	TCACGACCGC	CGATACCTCC	CAACTGTACG	CACTTGCAGC	50
40	CCGACATGGG	CTCAAGCTCC	ATGGCCCGCT	GACTGTCAAT	GAGCTTGGGC	100
	TCGACTATAG	GATCGTGATC	GCCACCGTCG	ACGATGGACG	TCGGTGGGTG	150
	CTGCGCATCC	CGCGCCGAGC	CGAGGTAAGC	GCGAAGGTCG	AACCAGAGGC	200
	GCGGGTGCTG	GCAATGCTCA	AGAATCGCCT	GCCGTTTCGC	GTGCCGGACT	250
	GGCGCGTGGC	CAACGCCGAG	CTCGTTGCCT	ATCCCATGCT	CGAAGACTCG	300
45	ACTGCGATGG	TCATCCAGCC	TGGTTCGTCC	ACGCCCGACT	GGGTCGTGCC	350
	GCAGGACTCG	GAGGTCTTCG	CGGAGAGCTT	CGCGACCGCG	CTCGCCGCCC	400
	TGCATGCCGT	CCCCATTTCC	GCCGCCGTGG	ATGCGGGGAT	GCTCATCCGT	450
	ACACCGACGC	AGGCCCGTCA	GAAGGTGGCC	GACGACGTTG	ACCGCGTCCG	500
	ACGCGAGTTC	GTGGTGAACG	ACAAGCGCCT	CCACCGGTGG	CAGCGCTGGC	550
50	TCGACGACGA	TTCGTCGTGG	CCAGATTTCT	CCGTGGTGGT	GCATGGCGAT	600
	CTCTACGTGG	GCCATGTGCT	CATCGACAAC	ACGGAGCGCG	TCAGCGGGAT	650
	GATCGACTGG	AGCGAGGCC	GCGTTGATGA	CCCTGCCATC	GACATGGCCG	700
	CGCACCTTAT	GGTCTTTGGT	GAAGAGGGGC	TCGCGAAGCT	CCTCCTCACG	750

TATGAAGCGG	CCGGTGGCCG	GGTGTGGCCG	CGGCTCGCCC	ACCACATCGC	800
GGAGCGCCTT	GCGTTCGGGG	CGGTCACCTA	CGCACTCTTC	GCCCTCGACT	850
CGGGTAACGA	AGAGTACCTC	GCTGCGGCGA	AGGCGCAGCT	CGCCGCAGCG	900
GAATGA					906

5

2) INFORMATION FOR SEQ ID NO: 1561

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 20 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1561

GATCATGGTA	AAACTACATT	GACTGCTGCT	ATCACCAAAG	TTTtagccga	50
25 ACAAGGTGGT	GCCAACTTCT	TGGATTAYGG	TTCTATTGAT	AGAGCTCCAG	100
AAGAAAGAGC	TAGAGGTATC	ACTATTTCCA	CTGCCCACGT	TGAATACGAA	150
ACCAAGAACA	GACACTATGC	CCACGTTGAT	TGTCCAGGAC	ACGCTGATTA	200
TATCAAAAAT	ATGATTACTG	GTGCCGCTCA	AATGGATGGT	GCTATCATTG	250
TTGTTGCTGC	CACTGATGGT	CAAATGCCTC	AAACCAGAGA	ACATTTGTTA	300
30 TTGGCCAGAC	AAGTTGGTGT	TCAAGACTTG	GTTGTGTTTG	TCAACAAAGT	350
CGATACTATT	GATGACCCTG	AAATGTTGGA	ATTAGTCGAA	ATGGAAATGA	400
GAGAATTGTT	ATCCACCTAC	GGTTTTGATG	GTGACAACAC	TCCAGTTATT	450
ATGGGATCTG	CTTTAATGGC	TTTGGAAGAC	AAGAAACCAG	AAATTGGTAA	500
GGAAGCTATC	TTGAAATTGT	TAGATGCTGT	CGATGAACAC	ATTCCAACCTC	550
35 CATCAAGAGA	CTTGGAACAA	CCATTTTTGT	TACCAGTTGA	AGACGTGTTC	600
TCCATCTCCG	GTAGAGGAAC	TGTTGTCACT	GGTAGAGTTG	AAAGAGGTGT	650
TTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTT	GACAAACCTT	700
ACAAGACTAC	TGTTACCGGT	ATTGAAATGT	TCAAAAAGA	ATTAGACTCT	750
GCTATGGCTG	GTGACAACCTG	TGGTGTTTTG	TTAAGAGGTG	TTAAAAGAGA	800
40 TGAAATCAAG	AGAGGTATGG	TTTTGGCCAA	ACCAGGTACT	GCCACTTCTC	850
ACAAGAAGTT	CTTGGCTTCC	TTGTATATTT	TGACTTCCGA	AGAAGGTGGY	900
CGTTCCACTC	CATTTGGTGA	AGGTTACAAG	CCTCAATGCT	TCTTCAGAAC	950
TAACGATGTC	ACTACCACAT	TTTCATTCCC	AGAAGGAGAA	GGTGTTGACC	1000
ATTCTCAAAT	GATCATGCCA	GGTGACAACA	TTGAAATGGT	TGGTGAAT	1048

45

2) INFORMATION FOR SEQ ID NO: 1562

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

805

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562

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10  TGATCACGGT AAAACCACAT TAACTGCTGC CATTACCAAA GTATTAGCTG      50
    AACAAGGTGG TGCCAAC TTT TTGGATTACG GTTCCATTGA TAGAGCTCCA      100
    GAAGAAAGAG CCAGAGGTAT CACTATTTCC ACTGCCCACG TTGAATACGA      150
    AACCAAGAAC AGACACTATG CCCACGTTGA TTGTCCAGGA CACGCTGATT      200
15  ATATCAAAAA CATGATTACT GGTGCTGCTC AAATGGATGG TGCTATCATT      250
    GTTGTGCTG CTACTGACGG TCAAATGCCA CAAACCAGAG AACATTTATT      300
    GTTGGCAAGA CAAGTTGGTG TTCAAGACTT GGTGTCTTT GTCAACAAAG      350
    TTGATACTAT TGATGACCCT GAGATGTTGG AATTAGTCGA AATGGAAATG      400
    AGAGAATTGT TGTCCACCTA CGGTTTTGAT GGTGACAACA CTCCTGTTAT      450
20  TATGGGATCT GCTTTAATGG CCTTGGAAGG CAAAAACCA GAAATTGGTA      500
    AGGAAGCTAT TTTGAGATTG TTAGATGCTG TCGATGAACA CATTCCAAC T      550
    CCATCAAGAG ACTTGGAACA ACCATTTTTG TTGCCAGTTG AAGACGTGTT      600
    CTCCATCTCT GGTAGAGGAA CTGTTGTCAC CGGTAGAGTT GAAAGAGGTG      650
    TCTTGAAGAA GGGTGAAGAA ATCGAAATTG TTGGTGGTTT TGACAAACCA      700
25  TACAAGACCA CTGTTACTGG TATTGAAATG TTCAAAAAGG AATTAGATTC      750
    TGCTATAGCT GGTGACAAC TGTGGTGT TTT GTTGAGAGGT GTTAAAAGAG      800
    ATGAAATCAA GAGAGGTATG GTTTTGGCCA AGCCAGGTAC TGCTACTTCT      850
    CACAAGAAAT TTTTAGCATC TTTGTATATT TTGACTTCAG AAGAAGGTGG      900
    TCGTTCCACT CCATTGAGG AAGGTTACAA GCCTCAATGT TTCTTCAGAA      950
30  CTAATGACGT CACTACCACA TTTTCATTCC CAGAAGGAGA AGGTGTTGAC     1000
    CACTCCCAA TGGTCATGCC AGGTGATAAC ATTGAAATGG TTGGTGAATT     1050
    GATCAAATCA TGTCCATTGG AAGT                                     1074

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35

2) INFORMATION FOR SEQ ID NO: 1563

(i) SEQUENCE CHARACTERISTICS:

```

40  (A) LENGTH: 1033 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida famata*

(B) STRAIN: ATCC 62894

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563

```

    GATCACGGGA AGACTACTTT GACCGCTGCC ATCACCAAAG TTTTAGCCGA      50
    AAAAGGTGGT GCTAACTTCT TGGACTACGG TTCTATCGAT AAAGCTCCAG      100

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	AAGAAAGAGC	CAGAGGTATT	ACTATTTCTG	CTGCCCATGT	TGAATACGAA	150
	ACTGACAAGA	GACACTATGC	CCATGTTGAT	TGTCCAGGTC	ACGCAGATTA	200
	TATCAAGAAT	ATGATTACTG	GTGCTGCTCA	AATGGATGGT	GCCATTATTG	250
	TTGTTGCTGC	TTCCGATGGT	CAAATGCCTC	AAACCAGAGA	ACATTTGTTA	300
5	TTGGCCAGAC	AAGTTGGTGT	TCAACACTTG	GTTGTTTTTCG	TCAACAAGGT	350
	CGACACCATT	GACGATCCAG	AAATGTTGGA	ATTGGTTGAA	ATGGAAATGA	400
	GAGATTTGTT	AACTACTTAC	GGTTTTGATG	GTGATAACAC	CCCAGTTATC	450
	ATGGGATCTG	CTTTGTGTGC	TTTGGAATCC	AGAGAACCAG	AAATTGGTCA	500
	AAAAGCCATT	GAAAAATTGT	TAGATGCCGT	CGATGAATAC	ATTCCAACCC	550
10	CAGTCAGAGA	CTTGGAACAA	CCATTCTTGA	TGCCAGTTGA	AGAAGTTTTC	600
	TCCATTTCCG	GTAGAGGTAC	CGTTGTTGCT	GGTAGAGTCG	AAAGAGGTAC	650
	CTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTC	GACAAGCCAT	700
	TCAAGGCCAC	TGTTACTGGT	ATTGAAATGT	TCAAGAAGGA	ATTGGACTCC	750
	GCTCTTGCTG	GTGACAACCTG	TGGTATCTTG	TTGAGAGGTG	TCAAGAGAGA	800
15	CGAAGTTAAG	AGAGGTATGG	TCTTGACCAA	GCCAAACACC	GTCACTTCCC	850
	ACAAGAAGAT	CTTGCCCTCG	TTGTATATCT	TGACCAAGGA	AGAAGGTGGT	900
	AGACACTCTC	CATTTGGAGC	CAACTACAAG	CCCCAATTGT	TCATGAGAAC	950
	CACCGATGTT	ACCGGTACCA	TGACCTTCCC	AGAAGGTGCC	GACCAATCTG	1000
	CCATGGTCAT	GCCAGGTGAC	AACGTTGAAA	TGC		1033
20						

2) INFORMATION FOR SEQ ID NO: 1564

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 35 (B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564

	GATCACGGTA	AGACTACATT	GACAGCTGCT	ATCACCAAGA	CATTGGCCAA	50
40	GAACGGTGGT	GCTGATTTCT	TGGACTACTC	TTCCATTGAC	AAAGCTCCAG	100
	AGGAGAGAGC	CCGTGGTATC	ACTATCTCTA	CTGCCCATGT	CGAGTACGAG	150
	ACCGCCAAGA	GACATTACTC	CCACGTCGAC	TGTCCAGGTC	ACGCCGACTA	200
	CATCAAGAAC	ATGATTACTG	GTGCTGCCCA	AATGGACGGT	GCTATCATCG	250
	TTGTCGCCGC	CACCGATGGT	CAAATGCCAC	AAACTAGAGA	GCATTTGCTG	300
45	TTGGCCAGAC	AAGTCGGTGT	TCAACGTATC	GTTGTCTTTG	TCAACAAGGT	350
	GGACACCATC	GATGACCCTG	AAATGTTGGA	ATTAGTGGAA	ATGGAAATGA	400
	GAGAATTGTT	GAACGAATAC	GGTTTTGACG	GTGACAATGC	CCCTATCATT	450
	ATGGGTTCCG	CTTTGTGTGC	CCTAGAAGGT	CGTCAACCTG	AAATTGGTGA	500
	GCAAGCTATC	ATGAAACTAT	TGGACGCTGT	TGATGAATAC	ATTCCAACCC	550
50	CAGAAAGAGA	CTTGAACAAG	CCATTCTTGA	TGCCTGTTGA	AGACATCTTC	600
	TCCATCTCTG	GTAGAGGTAC	CGTCGTCACT	GGACGTGTCG	AAAGAGGTAA	650
	CTTGAAGAAG	GGTGAAGAAG	TTGAAATTGT	TGGTCACAAC	ACTACCCCAT	700
	TGAAGACCAC	CGTTACTGGT	ATCGAAATGT	TCAGAAAGGA	ATTGGACCAA	750

GCTATGGCTG GTGACAACGC CGGTATCCTA TTGAGAGGTA TCAGAAGAGA 800
 CCAATTGAAG AGAGGTATGG TCATGGCCAA GCCAGGTACC GTCAAGGCTC 850
 ACACCAAGAT TTTGGCTTCT TTGTACATCT TGTCTAAGGA AGAAGGTGGT 900
 AGACATTCTG GTTTCGGTGA AAACCTACAGA CCTCAGATGT TTATCAGAAC 950
 5 CGCAGATGTC ACTGTTGTGA TGAAGTTCCC AGAATCTGTG GAAGACCACT 1000
 CTATGCAAGT TATGCCAGGT GACAACGTCG AAATGGTCTG TGAAC TAGTC 1050
 CACCCA 1056

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2) INFORMATION FOR SEQ ID NO: 1565

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1061 bases
 - 15 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida guilliermondii*
 - (B) STRAIN: ATCC 6260

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565

GATCATGGTA AGACCACTTT GACCGCTGCT ATCACCAAGG TTTTGTCTGGA 50
 AAAAGGAGGT GCTAATTTCT TGGATTACGG CTCCATCGAC AGAGCTCCAG 100
 AAGAGAGAGC CAGAGGTATC ACCATTTCCA CTGCCCATGT TGAGTACCAA 150
 30 ACTGATAAGA GACATTATGC CCACGTTGAC TGTCCAGGTC ACGCCGATTA 200
 CATTAAGAAT ATGATTACTG GTGCCGCCCA GATGGACGGT GCCATTATTG 250
 TTGTTGCTGC CACTGACGGT CAAATGCCTC AGACCAGAGA GCACTTGTTG 300
 TTGGCCAGAC AAGTTGGTGT GCAACACTTG GTAGTTTTTTG TGAACAAGGT 350
 GGACACCATT GACGATCCCG AGATGTTGGA ATTGGTCGAG ATGGAAATGA 400
 35 GAGAATTGTT GAGTCAGTAC GGTTTCGATG GTGACAACAC CCCAGTTATC 450
 ATGGGATCTG CTTTGTGTGC TTTGGAAAGT AAGCAGCCAG AAATTGGTGT 500
 GCAAGCCATT GAAAAATTGT TGGACGCTGT CGATGAGCAC ATTCCTACTC 550
 CTACCCGTGA CTTGGAACAG CCATTCTTGT TGCCTGTTGA AGATGTGTTC 600
 TCCATTTCTG GTAGAGGAAC TGTGGTTACT GGTAGAGTCG AAAGAGGTTC 650
 40 GTTGAAGAAG GGTGAGGAAA TCGAGATTGT TGGTGACTTT GACAAGCCAT 700
 TCAAGACCAC TGTGACTGGA ATTGAAATGT TCAAGAAGGA ATTGGATGCT 750
 GCTATGGCTG GTGACAATGC TGGTATCTTG TTGAGAGGTG TCAAGAGAGA 800
 CGATGTCAAG AGAGGTATGG TTTTGGCCAA GCCTTCCACC GTCATTCTC 850
 ACAAGAAGGT GTTGGCTTCC TTGTACATCT TGAGTAAGGA AGAAGGTGGC 900
 45 CGTCACTCTC CTTTGGTGA GAACCTACAAG CCTCAATTGT TCATCAGAAC 950
 TACTGACGTT ACCGGTACTT TAAGATTCCC AGCCGGCGAG GGTGTCGACC 1000
 ACTCGCAAAT GGTTATGCCA GGTGACAATG TTGAGATGGA AATTGAGCTT 1050
 GTGAGAAAGA C 1061

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2) INFORMATION FOR SEQ ID NO: 1566

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566

15	GATCACGGTA	AGACTACCTT	GACTGCTGCT	ATCACCAAGG	TTTTGGCTTC	50
	TAAGGGTGGT	GCTAGCTTCT	TGGACTATGG	TTCCATTGAC	AGAGCCCCAG	100
	AGGAGAGAGC	TAGAGGTATT	ACTATTTCTA	CTGCCCCACGT	TGAGTACCAA	150
	ACCGAAAAGA	GACACTACGC	CCACGTCGAC	TGTCCAGGTC	ACGCTGATTA	200
	CATTAAGAAT	ATGATTACTG	GTGCCGCCCA	GATGGACGGT	GCTATCATTG	250
20	TTGTTGCTGC	TTCTGATGGT	CAGATGCCTC	AGACCAGAGA	GCACCTTTTG	300
	TTGGCCAGAC	AGGTTGGTGT	TCAGAACTTG	GTTGTTTTTCG	TTAACAAGGT	350
	TGACACCATT	GACGACCCTG	AAATGTTGGA	ATTGGTTGAG	ATGGAAATGA	400
	GAGAATTGTT	GACTACTTAC	GGTTTTGACG	GTGATGAGAC	TCCTGTTATC	450
	ATGGGTTCTG	CTTTGTGCGC	TTTGGAAGAG	AAGCAACCAG	AGATTGGTGA	500
25	GCAGGCTATC	ATGAAGTTGT	TGGACGCTGT	CGATGAGTAC	ATTCCAACCC	550
	CACAGCGTGA	CTTGGAGCAG	CCATTCTTGA	TGCCTGTTGA	GGATGTTTTTC	600
	TCCATTTCTG	GTAGAGGTAC	TGTCGTTACT	GGTAGAGTTG	AGAGAGGTTTC	650
	TTTGAAGAAG	GGTGAGGAAA	TCGAGATTGT	CGGTGACTTC	GCCAAGACTT	700
	TCAAGGCTAC	CGTTACTGGT	ATTGAGATGT	TCAAGAAGGA	ATTGGATGCT	750
30	GCTATGGCTG	GTGACAACGC	CGGTATCTTG	TTGAGAGGTG	TCAAGAGAGA	800
	TGAGATCTCC	CGTGGTGATG	TCTTGGCCAA	GCCAGGTACT	GTTACTCCAC	850
	ACAAGAAGAT	CTTGGCTTCT	TTGTACGTTT	TGACCAAGGA	AGAAGGTGGT	900
	CGTCACAACC	CATTCGCTGA	GAACTACAAG	CCACAGTTGT	TCCTCAGAAC	950
	CACCAACGTC	ACTGGTACCA	TGAGATTCCC	AGAAGGTGAA	GATGTTGACC	1000
35	ACTCTGCCAT	GGTTAACCCA	GGTGACAACG	TTGAGATGGA	AATCGAGTTG	1050
	GGTAGAAAGG	CCCCACTTGA	GTT			1073

40 2) INFORMATION FOR SEQ ID NO: 1567

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567

	CATGGTAAGA	CCACTTTGAC	TGCTGCCATC	ACCAAGACTC	TAGCTGAACG	50
	TGGTGGTGCT	GACTTTTTTG	ACTACTCTTC	TATTGACAAG	GCTCCAGAAG	100
5	AAAGAGCYAG	AGGTATCACT	ATTTCTACTG	CTCATGTTGA	ATACGAGACT	150
	GAAAAGAGAC	ATTACTCCCA	CGTTGACTGT	CCAGGTCACG	CTGATTACAT	200
	CAAGAACATG	ATTACTGGTG	CTGCTCAAAT	GGACGGTGCT	ATTATTGTTG	250
	TTGCTGCTAC	TGATGGTCAA	ATGCCTCAAA	CCAGAGAGCA	TTTGTTGTTG	300
	GCCAGACAAG	TTGGTGTCCA	ACACATTGTT	GTTTTTCGTTA	ACAAGGTTGA	350
10	CACCATCGAT	GATCCAGAAA	TGTTGGAATT	GGTTGAAATG	GAAATGAGAG	400
	AATTRTTGAC	TCAATATGGC	TTTGACGGTG	ACAACACTCC	AGTGATCATG	450
	GGTTCTGCTT	TGTGTGCCTT	GGAAGGTAAG	CAACCAGAAA	TTGGTGAGCA	500
	AGCCATCATG	AAGTTGTTGG	ACGCTGTTGA	CGAATACATC	CCAACCCCAG	550
	CCCGTGACTT	GGAAAVCCA	TTCTTGATGC	CTGTTGAAGA	TATCTTCTCC	600
15	ATTTCCGGTA	GAGGTACTGT	CGTCACTGGT	AGAGTTGAAC	GTGGTAACTT	650
	GAAGAAGGGT	GAAGAAATCG	AAATTGTTGG	TCACAACACC	ACTCCTTTCA	700
	AGACTACTGT	TACTGGTATT	GAAATGTTCA	GAAAGGAATT	GGACCAAGCC	750
	ATGGCTGGTG	ACAACGCTGG	TGTCCTTTTG	AGAGGTGTCA	GAAGAGACCA	800
	ATTGAAGAGA	GGTATGGTTT	TGGCTAAGCC	AGGTACTGTT	AAGGCCCA	850
20	CCAAGTTCTT	GGCTTCCTTG	TACATTTTGA	CCAAGGAAGA	AGGTGGTAGA	900
	CACTCCGGTT	TCGGTGAAAA	CTACAGACCA	CAAATCTACG	TCAGAACTGC	950
	TGACGTTACC	GTDGTCTTGA	AGTTCCCAGA	ATCTGTTGAA	GACCATTCCA	1000
	TGCAAGTCAT	GCCAGGTGAC	AATGTCGAAA	TGGAGTGTGA	ATTGGTTCAC	1050
	CCAACCTCCAT	TG				1062

2) INFORMATION FOR SEQ ID NO: 1568

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
 40 (B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568

	CGGAAAGACC	ACCTTGACCG	CCGCCATTAC	CAAGGTTTTG	GCTGACAAGG	50
45	GTGGCGCCAA	CTTCTTGAC	TACGGTGCCA	TTGACAAGGC	TCCTGAAGAA	100
	AGAGCACGTG	GTATCACCAT	TTCCACTGCC	CACGTTGAAT	ACGAGACCGA	150
	CAACAGACAC	TACGCCACG	TTGACTGTCC	AGGTCACGCC	GATTACATCA	200
	AGAACATGAT	CACGGGTGCC	GCTCAAATGG	ACGGTGCCAT	TATTGTTGTT	250
	GCAGCCACCG	ACGGCCAAAT	GCCTCAAACC	AGAGAGCACT	TGTTGTTGGC	300
50	CAGACAAGTT	GGTGTGCAAC	ACTTGTTGTT	TTTCGTGAAC	AAGGTTGATA	350
	CCATCGACGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGAGAA	400
	TTGTTGACTC	AATACGGATT	TGACGGCGAT	GAAACCCCTG	TTGTTATGGG	450
	CTCTGCTCTT	TGCGCTTTGG	AAGGTAGAGA	ACCAGAGATT	GGTGAGCAAG	500

	CCATCACCAA	GTTGTTGGAG	GCTGTTGACG	AGTACATCCC	AACCCCACAA	550
	CGTGACTTGG	AACAACCATT	CTTGATGCCT	GTTGAAGATG	TTTTCTCCAT	600
	TTCTGGTAGA	GGTACTGTTG	TCACTGGTAG	AGTGGAGAGA	GGTTCCTTGA	650
	AGAAGGGTGA	GGAGATCGAG	ATTGTTGGTG	ACTTTGACAA	GCCTTTCAAG	700
5	ACTACTGTTA	CTGGTATTGA	GATGTTCAAG	AAGGAATTGG	ACGCTGCTAT	750
	GGCTGGTGAC	AATGCTGGTA	TCTTGTTGAG	AGGTGTCAAG	AGAGAACAAG	800
	TTTCCCGTGG	TATGGTTTTG	GCCAAGCCAG	GCACTGTGAC	CTCGCACAAG	850
	AAGGTTTTTG	CTTCTTTGTA	CATTTTGTCT	AAGGAAGAAG	GTGGTCGTCA	900
	CTCTCCATTT	GGCGAGAACT	ACAAGCCTCA	ATTGTTTCCTT	AGAACTACCG	950
10	ATGTCACTGG	TACTTTGAGA	TTCCCAGCAG	GTGAGGACGT	TGACCACTCC	1000
	GCTATGGTTT	CTCCAGGTGA	CAATGTCTGAG	ATGGAAATCG	AGTTGGTCAG	1050
	AAAGACTCCT	CT				1062

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2) INFORMATION FOR SEQ ID NO: 1569

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 990 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
(B) STRAIN: ATCC 2504

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569

	TCACCAAGAC	TTTGGCTGAA	CGTGGTGGTG	CTGATTTCTT	GGACTACTCT	50
35	TCCATTGACA	AGGCTCCAGA	AGAAAGAGCR	AGAGGTATCA	CTATTTCTAC	100
	TGCACATGTT	GAATATGAAA	CTGACAAGAG	ACATTACTCT	CACGTCGACT	150
	GTCCAGGTCA	TGCTGATTAC	ATCAAGAATA	TGATTACTGG	TGCTGCCCAA	200
	ATGGATGGTG	CTATCATTGT	TGTTGCTGCT	ACAGATGGTC	AAATGCCTCA	250
	AACCAGAGAA	CATTTGTTGT	TGGCTAGACA	AGTTGGTGTT	CAACAYATCG	300
40	TTGTTTTTCGT	TAACAAGGTT	GACACTATCG	ATGACCCTGA	AATGTTAGAA	350
	TTGGTTGAAA	TGGAAATGAG	AGAATTATTG	ACCCAATACG	GTTTCGATGG	400
	TGACAACACT	CCAGTCATCA	TGGGTCTCTG	TTTGTGTGCT	TTAGAAGGTA	450
	AGCAACCAGA	AATTGGTGAA	CAAGCAATCA	TGAAGTTATT	GGACGCTGTT	500
	GACGAATACA	TCCCAACTCC	AGCTCGTGAT	TTGGAAAAGC	CTTTCTTGAT	550
45	GCCTGTTGAA	GATATCTTCT	CCATCTCCGG	TAGAGGTACC	GTCGTAAC TG	600
	GTAGAGTTGA	ACGTGGTAAC	TTGAAKAAGG	GTRAAGAAAT	CGAAATCGTT	650
	GGTCACAACA	CCACTCCATT	CAAGACCACT	GTTACTGGTA	TTGAAATGTT	700
	CAGAAAGGAA	TTGGACCAAG	CTATGGCTGG	TGATAACGCT	GGTGTCWTGT	750
	TGAGAGGTGT	CAGAAGAGAC	CAATTAAAGA	GAGGTATGGT	CTTGGCCAAG	800
50	CCAGGTACTG	TCAAGGCTCA	CACCRAATTC	TTGGCCTCTT	TGTATATCTT	850
	GACCAAGGAA	GAAGGTGGTA	GACATTCCGG	TTTCGGTGAA	AATTACAGAC	900
	CTCAAATCTA	CGTTAGAACT	GCTGATGTCA	CCGTTGTTTT	GAAGTTCCCA	950
	GAAGCTGTTG	AAGATCACTC	TATGCAAGTC	ATGCCAGGTG		990

2) INFORMATION FOR SEQ ID NO: 1570

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1184 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida tropicalis*
- (B) STRAIN: ATCC 750
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570

	GATCATGGTA	AAACCACTTT	GACTGCTGCC	ATTACTAAAG	TCTTGGCTGA	50
	TAAAGGTCAA	GCTAACTTCT	TAGATTACGG	TTCTATTGAT	AGAGCTCCAG	100
	AAGAAAGAGC	CAGAGGTATC	ACCATCTCTA	CTGCCCACGT	TGAATATGAA	150
20	ACCGAAAAAA	GACATTACGC	CCATGTTGAG	TATGTATACT	TTTTTTTGTT	200
	GTGTAATTGT	TTTAAAGATT	TTCTTTAAAG	CTGAAGAAGT	CAAATCAGTT	250
	CTTTGATAAC	TTCTATTAAA	AAAAGGGAAA	AATTAACAAG	ATATACTAAC	300
	ACTATAACAG	TTGTCCTGGA	CATCAAGATT	ATATCAAGAA	TATGATTACC	350
	GGTGCCGCTC	AAATGGATGG	TGCTATTATT	GTTGTTGCTG	CCACTGATGG	400
25	TCAAATGCCA	CAAACCAGAG	AACATTTGTT	GTTGGCTAGA	CAAGTCGGTG	450
	TTCAAGATTT	GGTTGTCTTT	GTTAACAAG	TCGACACTAT	TGATGACCCA	500
	GAAATGTTGG	AATTGGTTGA	AATGGAAATG	AGAGAATTAT	TGACTACTTA	550
	CGGTTTTGAT	GGTGATAACA	CTCCTGTTAT	CATGGGTTCT	GCTTTGATGG	600
	CCTTGCAAGG	TAAACAACCA	GAAATTGGTG	AACAAGCTAT	CATGAAATTG	650
30	ATGGACGCTA	TTGATGAACA	CATTCCAACC	CCAACCAGAG	ACTTGGAACA	700
	ATCTTTCTTG	ATGCCAGTTG	AAGATGTTTT	CTCCATTCT	GGTAGAGGTA	750
	CTGTTGTTAC	TGGTAGAGTC	GAAAGAGGTG	TCTTAAAGAA	GGGTGAAGAA	800
	ATTGAAATTG	TTGGTGGTTT	CGAAAAACCA	TTCAAGACCA	CTGTTACTGG	850
	TATTGAAATG	TTCAAGAAAG	AATTAGATGC	TGCTATGGCT	GGTGACAAC	900
35	GTGGTGTCTT	GTTGAGAGGT	GTCAAGAGAG	ACGAAATCAA	GAGAGGTATG	950
	GTTTTGGCTA	AACCAGGTAC	TGCTACTTCC	CACAAGAAAT	TCTTGGCTTC	1000
	CATGTATATC	TTAACTGCTG	AAGAAGGTGG	TCGTTCCACT	CCATTCGGTG	1050
	AAGGTTACAA	GCCACAATGT	TTCTTCAGAA	CTAACGATGT	TACCACTTCC	1100
	TTCTCTTTCC	CAGAAGGTGA	AGGTGTTGAC	CACTCCCAA	TGGTTATGCC	1150
40	AGGTGACAAC	ATTGAAATGG	TCGGTGAATT	GATT		1184

2) INFORMATION FOR SEQ ID NO: 1571

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1071 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida viswanathii*

(B) STRAIN: ATCC 28269

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571

	CGATCACGGT	AAGACCACCT	TGACCGCCGC	CATCACCAAG	GTCTTGGCCG	50
	ACAAGGGTCA	GGCTAACTTC	TTGGACTACG	GATCCATTGA	CAGAGCCCCT	100
	GAAGAAAGAG	CAAGAGGTAT	CACTATCTCC	ACTGCCACG	TTGAATACGA	150
10	GACTGATAAG	AGACACTATG	CCCACGTTGA	TTGCCCCGGC	CATCAAGATT	200
	ATATCAAGAA	TATGATCACT	GGTGCTGCCC	AAATGGACGG	TGCTATCATT	250
	GTTGTTGCTG	CTACTGACGG	TCAGATGCCA	CAAACCAGAG	AACACTTGTT	300
	GTTGGCTAGA	CAAGTTGGTG	TCCAAGACTT	GGTTGTTTTT	GTTAACAAGG	350
	TTGACACTAT	CGATGACCCA	GAAATGTTGG	AATTGGTTGA	AATGGAAATG	400
15	AGAGAATTAT	TATCTTCTTA	YGGCTTTGAC	GGTGACAACA	CCCCAGTTGT	450
	CATGGGTTCC	GCTTTGATGG	CTTTGCAAGG	TAAGCAACCA	GAAATTGGTG	500
	AACAAGCTAT	TATTAAGTTG	ATGGACGCTA	TTGATGAACA	CATYCCAACC	550
	CCAACCAGAG	ACTTGGAACA	ACCATTCTTG	TTGCCAGTTG	AAGATGTCTT	600
	TTCTATTTCC	GGTAGAGGTA	CCGTCGTCAC	TGGTAGAGTC	GAAAGAGGTG	650
20	TCTTGAAGAA	GGGTGAAGAA	ATTGAAATTG	TCGGTAACTT	TGAAAAGCCA	700
	TTCAAGACCA	CCGTTACTGG	TATTGAAATG	TTCAAGAAGG	AATTGGATGC	750
	TGCTATGGCT	GGTGACAACT	GTGGTGTCTT	GTTGAGAGGT	GTCAAGAGAG	800
	ACGAAATCAG	CAGAGGTATG	GTTTTGGCCA	AGCCAGGTAC	CGTCACTTCC	850
	CACAAGAAGT	TCTTGGCCTC	CATGTACATC	TTGACTGGTG	AAGAAGGTGG	900
25	TCGTCGTACC	CCATTCGGTG	AAGGTTACAA	GCCACAATGT	TTCTTCAGAA	950
	CCAATGACAT	CACCACCACT	TTCACCTTCC	CAGAAGGTGA	AGGTGTCGAC	1000
	CACTCCCAA	TGGTTATGCC	AGGTGACAAC	ATCGAAATGG	TTGGTGAATT	1050
	GTACAAGGCT	TGTCCTTGGA	A			1071

30

2) INFORMATION FOR SEQ ID NO: 1572

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*

(B) STRAIN: ATCC 8750

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572

	TATCTTGGTT	WGCTCGGCCG	CTGACGGCCC	AATGCCTCAG	ACTCGCGAGC	50
	ACATCCTGCT	GAGCCGTCAG	GTTGGCGTTC	CTTACATCAT	CGTGTTCTTG	100
50	AACAAGGCCG	ACATGGTTGA	TGACGAAGAG	CTGATCGAAC	TGGTTGAAAT	150
	GGAAGTTCGC	GAGCTGTTGT	CCAAGTACGA	CTTCCCTGGC	GACGACACCC	200
	CGATCATCAA	GGGTTGCGCC	AAACTGGCTC	TGGAAGGCGA	CGAAGGCCCA	250
	CTGGGCAGCC	AAGCCGTTCT	GGCTCTGGCC	GAAGCGCTGG	ACAACCTACAT	300

	TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	G TTCCTGATG	CCTGTTGAAG	350
	ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
	CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
	CACGGTCAAG	ACCATTTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
	CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
	GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
10	GGTTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
	TCGCCATGGA	AGAAGGT				817

15 2) INFORMATION FOR SEQ ID NO: 1573

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 796 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella buccalis*
 (B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573

30	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTT	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAACTTCTTG	AGCAATACGA	ATTCTGAAGAG	GATACTCCAA	200
35	TCGTTTCGTGG	TTCTGCACTG	GGTGCAATTGA	ATGGTGTGTTGA	CAAGTGGGTT	250
	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAAACAG	GACGTATTGA	GACTGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450
40	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCACTTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
45	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GCGGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	G TAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

50 2) INFORMATION FOR SEQ ID NO: 1574

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574

	GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
	GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
15	TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
	ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
	TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
	GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTG	ATACATTCCA	300
	GAGCCAAAGC	GTGATATCGA	TGATCCATTG	CTATTACCAA	TCGAAGATAT	350
20	CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
	GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
	ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
	AGGTCGTGCA	GGTGATAACG	TTGGTGTCTT	ACTACGTGGT	ACCAAGCGTG	550
	ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
25	CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
	TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
	CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
	ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
30	TATGGCTGAA	GGCGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 1575

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
- (B) STRAIN: ATCC 33315

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575

	GGTAGTGTCT	GCAGCTGACG	GCCCAATGCC	ACAAACTCGT	GAACATATCC	50
50	TATTGTACAG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGACGATGA	AGAATTACTT	GAATTAGTTG	AAATGGAAGT	150
	ACGTGATCTA	TAACTGAAT	ACGACTTCCC	AGGTGATGAT	ACTCCTGTTA	200
	TTTCTGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	ATATGAACAA	250

	AAAGTCCTTAG	ACTTAATGGC	AGCTGTAGAT	GATTTTCATCC	CAACTCCTGA	300
	ACGTGACCAT	GACAAACCGT	TCATGATGCC	GATTGAAGAT	GTTTTCTCAA	350
	TCACTGGTCG	TGGAACGTG	GCTACAGGTC	GTGTTGAACG	TGGAACCTATT	400
	AAAGTCGGTG	ATGAAGTTGA	TATCATCGGT	ATTCATGAAA	ATGTTAAAAA	450
5	GACAACTGTT	ACGGGTGTAG	AAATGTTCCG	TAAATTGTTG	GATTACGCTG	500
	AAGCTGGCGA	TAACATCGGT	ACATTATTGC	GTGGTGTTTC	TCGTGATGAT	550
	ATCGAACGTG	GTCAAGTGTT	GGCTAAACCA	GGCACAATCA	CACCACATAC	600
	AAAATTCTCA	GCTGAAGTTT	ATGTATTAAC	AAAAGAAGAA	GGCGGACGTC	650
	ATACTCCATT	CTTCTCAAAC	TATCGCCCAC	AATTTTACTT	CCGTACAACT	700
10	GACATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	TGGTTATGCC	750
	AGGTGATAAC	GTAGCAATGG	AAGTTGAATT	AATTCACCCT	GTTGCTATTG	800
	AAA					803

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2) INFORMATION FOR SEQ ID NO: 1576

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*

(B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576

	TTAATGAAGC	AATTGTTGTA	AATTTTGAAA	GCGAAGGAAA	AAAACATAAA	50
	CTTGTTTTAG	AAGTAGCAGC	TCATTTAGGA	GATAATAGAG	TTAGAACTAT	100
	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	GGGCTTAAAA	GCTGAGGCTT	150
35	TAGGTGCTCC	TATTAGTGTT	CCTGTTGGTG	AGAAAGTTTT	AGGAAGAATT	200
	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	GGTGAAGAAA	TTTCTTTTGA	250
	TAAAAAATGG	GCAATTCATA	GAGATCCGCC	AGCTTTTGAA	GATCAAAGCA	300
	CAAAAAGTGA	GATTTTTTGAA	ACAGGGATTA	AAGTTGTAGA	TTTGCTTGCT	350
	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	TTTGGTGGTG	CAGGTGTTGG	400
40	TAAAACTGTT	ATTATTATGG	AGCTTATTCA	CAATGTTGCA	TTTAAGCATA	450
	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	AGAGAACTCG	TGAAGGAAAT	500
	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	GTTTTAGACA	AAGTTGCTCT	550
	ATGTTATGGA	CAAATGAATG	AACCACCAGG	AGCAAGAAAT	CGTATTGCTT	600
	TAACAGGTTT	AACAATGGCT	GAGTATTTTA	GAGATGAAAT	GGGTCTTGAT	650
45	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	TTTTCACAAT	CAGGTTCTGA	700
	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	AGCTGTGGGT	TATCAACCAA	750
	CCCTAGCAAG	TGAAATGGGT	AAATTCCAAG	AAAGAATTAC	TTCAACTAAA	800
	AAAGG					805

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2) INFORMATION FOR SEQ ID NO: 1577

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Campylobacter rectus*
 (B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577

15	ATTACCCAA	GATCAACGAA	GCCGTCGAAG	TAAATTTCTGA	GGTTGAGGGC	50
	AAGCAAAACA	GACTTGTGTT	AGAGGTTGCC	GCACACCTTG	GCGATAACCG	100
	CGTAAGAACG	ATCGCTATGG	ATATGAGCGA	AGGCTTAACC	AGAGGCCTTG	150
	AGGCTACGGC	TCTTGGCGCG	CCTATTAGCG	TTCCGGTCGG	CGAAAAAGTT	200
	TTGGGAAGGA	TTTTTAACGT	CGTCGGCGAT	CTGATCGACG	AGGGTGAAGG	250
20	CATAGAATTT	GATAAAAAAT	GGTCTATCCA	CCGCGATCCT	CCGCCGTTTG	300
	AAGAGCAAAG	CACGAAGAGT	GAAATTTTTG	AAACGGGTAT	AAAAGTGGTC	350
	GATCTTCTAG	CCCCTTATGC	AAAAGGCGGT	AAGGTCGGAT	TATTCGGCGG	400
	TGCCGGCGTC	GGTAAGACGG	TTATTATCAT	GGAGCTTATC	CACAACGTTG	450
	CATTTAAGCA	TAGCGGTTAT	TCCGTGTTTG	CCGGCGTGGG	CGAGCGAACC	500
25	CGCGAAGGAA	ACGACCTTTA	TCACGAGATG	AAAGAGAGTA	ACGTTTTGGA	550
	CAAAGTCGCC	TTGTGCTACG	GCCAGATGAA	CGAGCCGCCG	GGAGCAAGAA	600
	ACCGCATCGC	TCTAACAGGC	CTAACGATGG	CTGAATACTT	CCGCGACGAG	650
	ATGGGACTTG	ACGTTTTGAT	GTTTATAGAC	AACATCTTCC	GTTTCTCTCA	700
	GTCTGGCGCT	GAGATGTCGG	CGCTTCTTGG	ACGTATCCCG	TCAGCCGTTG	750
30	GTTATCAGCC	GACTTTGGCG	AGCGAAATGG	GCAAATTCCA	AGAGAGAATT	800
	ACATCAACC					809

35 2) INFORMATION FOR SEQ ID NO: 1578

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578

50	AATCGAAGTG	CAACGTTTCT	TGCGTGTACT	TGATGGTGCT	GTAAGTGTGT	50
	TGGACTCACA	ATCAGGTGTA	GAACCTCAAA	CAGAAACAGT	TTGGCGTCAA	100
	GCGACAGATT	ACCGCGTACC	GCGTGTGTGA	TTCTGTAAAC	AAATGGACAA	150

	AATTGGTGCA	GACTTCTTAT	ACTCTGTATC	AACTTTACAT	GATCGTTTAC	200
	AAGCAAATGC	TCACCCAATC	CAATTACCAA	TTGGTGCGGA	AGATGACTTT	250
	ACTGGTATTA	TCGACTTAGT	AAAAATGAAA	GCTGAAATCT	ACACAAATGA	300
	CTTAGGAACT	GAAATCCAAG	AGACTGAAAT	TCCTGAAGAA	TACGTAGAAT	350
5	TAGCTGAAGA	ATGGCGCGAA	AAATTAATTG	AAGCTGTTGC	TGATACTGAT	400
	GAAGAACTAA	TGATGAAATT	CTTGGAAGGT	GAAGAAATCA	CTGAAGAAGA	450
	ATTGAAAGCT	GGTATTCGTC	AAGCAACATT	GACTGTTGAC	TTTTTCCCTG	500
	TTCTTTGCGG	ATCTGCCTTT	AAAAACAAAG	GGGTTC AATT	GATGTTGGAT	550
	GCAGTCATCG	ACTACTTGCC	TTCACCACTT	GATGTTCCCTG	CGATTAAAGG	600
10	GATCAATCCT	AAAACAGACG	AAGAACTGA	TCGTCCGGCT	GACGATGAAG	650
	CACCATTTGC	TTCATTAGCA	TTTAAAGTAA	TGACTGACCC	ATTCTGTARGT	700
	CGTTTGACAT	TCTTYCGTGT	GTATTCARGT	ATCTTGAACT	CTGGATCATA	750
	CGTATTGAAT	GCTTCAAAAG	GCAAACGCGA	ACGTATCGGT	CGGATCCTAC	800
	AAATGCACGC	CAACACTCGT	GCTGAAATCC	AAACAGTATA	CTCAGGCGAT	850
15	ATCGCCGCTG	CTGTTGGTTT	GAAAGACACA	ACA ACTGGGG	ATCCACTATG	900
	TGATGAAAAA	TCCCCAGTAA	TCCTTGAATC	AATCGAATTC	CCAGAACCAG	950
	TTATCGAAGT	CGCTGTTGAG	CTTAAATCAA	AAGCTGACCA	AGATAAAATG	1000
	GGGGTTGCTT	TACAAAAACT	TGCTGAAGAA	GATCCATCAT	TCCGTGTGGA	1050
	AMCAAACGCT	GAAACAGGCG	AAACTGTTAT	CGCTGGTATG	GGAGAACTTC	1100
20	ACTTGGACGT	CTTAGTTGAC	CGTATGCGTC	GCGAATTTAA	AGTTGAAGCA	1150
	AACGTAGGTG	CGCCTCAAGT	TTCTTATCGT	GAAACATTCC	GTGCAGCAAC	1200
	ACAAGCGGAA	GGTAAATTTG	TACGTCAGTC	TGGTGGTAAA	GGTCAATACG	1250
	GTCACGTATG	GGTCGAATTT	ACACCAAACG	AAGAAGGTAA	AGGCTTCGAA	1300
	TTCGAAAACG	CGATTGTCGG	TGGTGTGGTT	CCTCGTGAAT	ACATCCCAGC	1350
25	AGTTGAAAAA	GGACTTGAAG	AATCAATGGC	GAACGGTGTC	TTAGCCGGTT	1400
	ACCCATTAGT	AGACATCAAA	GCAAACTTTT	ATGATGGTTC	ATACCATGAT	1450
	GTCGATTCAA	GTGAAACTGC	CTTCCGTGTT	GCAGCTTCTA	TGGCTTTACG	1500
	TGCTGCAGCG	AAGAAAGCAA	ACCCAGTAAT	TCTTGAACCA	ATGATGAAAG	1550
	TAGTTATCAC	TGTACCAGAA	GATTACTTAG	GTGATGTTAT	GGGTCACGTA	1600
30	ACTGCTCGTC	GTGGACGCGT	AGAAGGAATG	GAAGCACWCG	GTA ACTCACA	1650
	AATCGTGAAC	GCAATCGTGC	C			1671

35 2) INFORMATION FOR SEQ ID NO: 1579

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579

50	GAAGTACAAC	GTTC ACTACG	GGTTCTTGAC	GGWGCTGTAA	CAGTATTGGA	50
	CTCACAATCT	GGTGTAGAAC	CACAACTGA	AACAGTTTGG	CGTCAAGCGA	100
	CAGATTACCG	CGTACCACGT	ATCGTATTCT	GTAACAAAAT	GGATAAAATC	150

	GGTGCAGACT	TCTTATACTC	TGTATCTACT	TTACATGATC	GCTTGCAAGC	200
	AAATGCTCAT	CCAATCCAAT	TACCAATTGG	TGCGGAAGAT	GACTTTACTG	250
	GTATCATCGA	TCTAGTAAAA	ATGAAAGCTG	AGATCTATAC	AAACGATTTA	300
	GGAACAGAGA	TTCAAGAAAC	TGAAATTCCT	GAAGAGTACA	AAGAATTAGC	350
5	TGAAGAATGG	CGCGAAAAAT	TAGTTGAAGC	TGTTGCAGAT	ACTGACGAAG	400
	AGCTAATGAT	GAAATTCTTG	GAAGGTGAAG	AAATCACTGA	AGAAGAATTG	450
	AAAGCTGGTA	TCCGTCAAGC	GACATTGACT	GTTGAATTTT	TCCCAGTTCT	500
	TTGTGGTTCA	GCCTTCAAAA	ACAAAGGGGT	TCAATTGATG	TTGGATGCAG	550
	TCATCGACTA	CCTTCCTTCA	CCACTTGATG	TTCCTGCAAT	CAAAGGGATC	600
10	AATCCTAAAA	CTGACGAAGA	AACTGATCGT	CCTGCTGACG	ATGAAGCGCC	650
	TTTTGCTTCA	CTAGCATTTA	AAGTAATGAC	TGACCCATTC	GTAGGTCGTT	700
	TGACATTCTT	CCGTGTGTAT	TCAGGTGTCT	TGAACTCTGG	ATCATATGTC	750
	TTGAATGCTT	CAAAAGACAA	ACGCGAACGT	ATCGGTGCGT	TTCTGCAAAT	800
	GCACGCGAAC	ACTTGTGCAG	AAATCCAAAC	AGTTTATTCA	GGCGATATCG	850
15	CTGCAGCTGT	TGGTTTGAAA	GATTCCACAA	CAGGGGATAC	ATTGTGTGCG	900
	AAAAATCACC	CAGTAATCCT	TGAATCAATC	GAATTCCTCAG	AMCCAGTTAT	950
	CGAAGTAGCT	GTTGAACYTA	AATCAAAAGC	TGACCAAGAT	AAAATGGGTG	1000
	TGGCTTTACA	AAAACCTTGCT	GAAGAAGATC	CTTCATTCCG	TGTAGAAMCA	1050
	AACGCTGAAA	CTGGCGAAAC	TGTTATCGCA	GGGATGGGTG	AACTTCACTT	1100
20	GGACGTCCTT	GTTGACCGTA	TGCGTCGCGA	ATTTAAAGTT	GAAGCAAACG	1150
	TTGGTGCGCC	TCAAGTTTCT	TACCGCGAAA	CATTCCGTGC	TTCTACGCAA	1200
	GCCGAAGGTA	AATTTGTACG	TCAGTCTGGT	GGTAAAGGTC	AATACGGTCA	1250
	CGTATGGATC	GAATTTACAC	CAAACGAAGA	AGGTAAAGGC	TTCGAATTCG	1300
	AAAACGCAAT	TGTCGGTGGT	GTGGTTCCAC	GTGAATACAT	CCCAGCAGTT	1350
25	GAAAAAGGAC	TTGAAGACTC	AATGGCTAAC	GGTGTCTAG	CTGGTTATCC	1400
	ATTGGTTGAC	ATCAAAGCCA	AGCTTTACGA	TGGTTCATAC	CATGATGTCG	1450
	ATTCAAGTGA	AACAGCCTTC	CGTGTGGCAG	CTTCAATGGC	TTTACGTGCT	1500
	GCAGCGAAGA	AAGCTAATCC	AGTGATTCTT	GAACCAATGA	TGAAAGTTGT	1550
	TATCACTGTT	CCTGAAGATT	ACTTAGGTGA	TATTATGGGA	CACGTAAC TG	1600
30	CTCGTCGTGG	ACGTGTTGAA	GGTATGGAAG	CGCATGGTAA	CTCACAAATC	1650
	GTTAACGCGA	TT				1662

35 2) INFORMATION FOR SEQ ID NO: 1580

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1669 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580

50	CAATCGAAGT	ACAACGTTCT	CTTCGTGTAT	TGGATGGTGC	TGTTACCGTT	50
	CTTGACTCAC	AATCAGGTGT	TGAGCCTCAA	ACTGAAACAG	TTTGGCGTCA	100
	AGCAACTGAG	TATGGAGTTC	CACGTATCGT	ATTTGCCAAC	AAAATGGACA	150

	AAATCGGTGC	TGACTTCCTT	TACTCTGTAA	GCACACTTCA	CGATCGTCTT	200
	CAAGCAAATG	CACACCCAAT	CCAATTGCCA	ATCGGTTCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGACA	TCCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGATC	GAAGCAGTTG	CTGAAACTGA	400
	CGAAGAATTG	ATGATGAAAT	ACCTCGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGGTATCCGT	AAAGCGACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GCTCTGCCTT	CAAGAACAAA	GGTGTTC AAT	TGATGCTTGA	550
	TGCGGTTATT	GA CTACCTTC	CAAGCCC ACT	TGACATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGATGAA	650
	GAGCCATTTG	CAGCTCTTGC	CTTCAAGATC	ATGACAGACC	CATTCGTAAG	700
	TCGTTTGACA	TTCTTCCGTG	TTACTCARG	TGKTCTTCAA	TCAGGTT CAT	750
	ACGTATTGAA	CACTTCTAAA	GGKAAACGTG	AGCGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CCAACAGCCG	TCAAGAAATT	GACACTGGTT	ACTCAAGAGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TCCA ACTGGT	GACTCATTGC	900
	CAGATGAAAA	AGCTAAAATC	ATTCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGCCAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCTGGTAT	GGGTGAGCTT	1100
20	CACCTTGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTTGAAGC	1150
	AAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATT CGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	ACTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	TGCGGCTTCA	CTTGCTCTTA	1500
	AAGAAGCTGC	TAAATCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACAATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTCG	TGCTTACGT				1669

35 2) INFORMATION FOR SEQ ID NO: 1581

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581

AATTGGGGAC TACACCTATT ATGATG

26

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2) INFORMATION FOR SEQ ID NO: 1582

(i) SEQUENCE CHARACTERISTICS:

820

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582

10 GGCAAATCAG TCAGTTCAGG AGT

23

2) INFORMATION FOR SEQ ID NO: 1583

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583

25

CGATTGGCAA CAATACACTC CTG

23

30 2) INFORMATION FOR SEQ ID NO: 1584

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584

TCACCTATTT TTACGCCTGG TAGGAC

26

45

2) INFORMATION FOR SEQ ID NO: 1585

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Enterococcus faecium*
(C) ACCESSION NUMBER: AF139725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585

	ATGACTATAC	CTGACGCAAA	TGCAATCTAT	CCTAACTCAG	CCATCAAAGA	50
10	GGTTGTCTTT	ATCAAGAACG	TGATCAAAAG	TCCCAATATT	GAAATTGGGG	100
	ACTACACCTA	TTATGATGAC	CCAGTAAATC	CCACCGATTT	TGAGAAACAC	150
	GTTACCCATC	ACTATGAATT	TCTAGGCGAC	AAATTAATCA	TCGGTAAATT	200
	TTGTTCTATC	GCCAGTGGCA	TTGAATTTAT	CATGAACGGT	GCCAACCACG	250
	TAATGAAAGG	TATTTCTGACT	TATCCATTTA	ATATTTTAGG	TGGCGATTGG	300
15	CAACAATACA	CTCCTGAACT	GACTGATTTG	CCGTTGAAAG	GTGATACTGT	350
	AGTCGGAAAT	GACGTGTGGT	TTGGGCAAAA	TGTGACCGTC	CTACCAGGCG	400
	TAAAAATAGG	TGACGGTGCC	ATTATCGGAG	CAAATAGTGT	TGTAACAAAA	450
	GACGTCGCTC	CATATACAAT	TGTCGGTGGC	AATCCAATTC	AACTCATCGG	500
	ACCAAGATTT	GAACCGGAAG	TTATTCAAGC	ATTAGAAAAT	CTGGCATGGT	550
20	GGAATAAAGA	TATTGAATGG	ATAACTGCTA	ATGTTCTCTA	ACTAATGCAA	600
	ACAACACCCA	CACTTGAATT	GATAAACAGT	TTAATGGAAA	AATAA	645

25 2) INFORMATION FOR SEQ ID NO: 1586

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586

ATTCCCACAA TCTTTTTTTAT CAATAA 26

40

2) INFORMATION FOR SEQ ID NO: 1587

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587

CATTGTTTCAG ATTCGGTAAA GTTC 24

2) INFORMATION FOR SEQ ID NO: 1588

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588

GTTTTTGAAG TTAAATAGTG TTCTT

25

15

2) INFORMATION FOR SEQ ID NO: 1589

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589

CTTCCATTG TACTTTCCT A

21

30

2) INFORMATION FOR SEQ ID NO: 1590

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1920 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: Cloning vector pFW16
(C) ACCESSION NUMBER: U50983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1590

50 ATGAAAATTA TTAATATTGG AGTTTtagCT CATGTTGATG CAGGAAAAAC 50
TACCTTAACA GAAAGCTTAT TATATAACAG TGGAGCGATT ACAGAATTAG 100
GAAGCGTGGA CAAAGGTACA ACGAGGACGG ATAATACGCT TTTAGAACGT 150
CAGAGAGGAA TTACAATTCA GACAGGAATA ACCTCTTTTC AGTGGGAAAA 200
TACGAAGGTG AACATCATAG ACACGCCAGG ACATATGGAT TTCTTAGCAG 250

	AAGTATATCG	TTCATTATCA	GTTTTAGATG	GGGCAATTCT	ACTGATTTCT	300
	GCAAAAGATG	GCGTACAAGC	ACAAACTCGT	ATATTATTTT	ATGCACTTAG	350
	GAAAATGGGG	ATTCCCACAA	TCTTTTTTTT	CAATAAGATT	GACCAAAATG	400
	GAATTGATTT	ATCAACGGTT	TATCAGGATA	TTAAAGAGAA	ACTTTCTGCC	450
5	GAAATTGTAA	TCAAACAGAA	GGTAGAACTG	TATCCTAATG	TGTGTGTGAC	500
	GAACTTTACC	GAATCTGAAC	AATGGGATAC	GGTAATAGAG	GGAAACGATG	550
	ACCTTTTAGA	GAAATATATG	TCCGGTAAAT	CATTAGAAGC	ATTGGAACTC	600
	GAACAAGAGG	AAAGCATAAG	ATTTCAGAAT	TGTTCTCTGT	TCCCTCTTTA	650
	TCATGGAAGT	GCAAAAAGTA	ATATAGGGAT	TGATAACCTT	ATAGAAGTTA	700
10	TTACTAATAA	ATTTTATTCA	TCAACACATC	GAGGTCCGTC	TGAACTTTGC	750
	GGAAATGTTT	TCAAAATTGA	ATATACAAAA	AAAAGACAAC	GTCTTGCATA	800
	TATACGCCTT	TATAGTGGAG	TACTACATTT	ACGAGATTCG	GTTAGAGTAT	850
	CAGAAAAGGA	AAAAATAAAA	GTTACAGAAA	TGTATACTTC	AATAAATGGT	900
	GAATTATGTA	AGATTGATAG	AGCTTATTCT	GGAGAAATTG	TTATTTTGCA	950
15	AAATGAGTTT	TTGAAGTTAA	ATAGTGTTCT	TGGAGATACA	AAACTATTGC	1000
	CACAGAGAAA	AAAGATTGAA	AATCCGCACC	CTCTACTACA	AACAACGTGT	1050
	GAACCGAGTA	AACCTGAACA	GAGAGAAATG	TTGCTTGATG	CCCTTTTGGA	1100
	AATCTCAGAT	AGTGATCCGC	TTCTACGATA	TTACGTGGAT	TCTACGACAC	1150
	ATGAAATTAT	ACTTTCTTTC	TTAGGGAAAG	TACAAATGGA	AGTGATTAGT	1200
20	GCACTGTTGC	AAGAAAAGTA	TCATGTGGAG	ATAGAAATAA	CAGAGCCTAC	1250
	AGTCATTTAT	ATGGAGAGAC	CGTTAAAAAA	TGCAGAATAT	ACCATTACAC	1300
	TCGAAGTGCC	GCCAAATCCT	TTCTGGGCTT	CCATTGGTCT	ATCTGTATCA	1350
	CCGCTTCCGT	TGGGAAGTGG	AATGCAGTAT	GAGAGCTCGG	TTTCTCTTGG	1400
	ATACTTAAAT	CAATCATTTC	AAAATGCAGT	TATGGAAGGG	ATACGCTATG	1450
25	GTTGTGAACA	AGGATTGTAT	GGTTGGAATG	TGACGGACTG	TAAAATCTGT	1500
	TTTAAGTATG	GCTTATACTA	TAGCCCTGTT	AGTACCCCAG	CAGATTTTCG	1550
	GATGCTTGCT	CCTATTGTAT	TGGAACAAGT	CTTAAAAAAA	GCTGGAACAG	1600
	AATTGTTAGA	GCCATATCTT	AGTTTTAAAA	TTTATGCGCC	ACAGGAATAT	1650
	CTTTCACGAG	CATACAACGA	TGCTCCTAAA	TATTGTGCGA	ACATCGTAGA	1700
30	CACTCAATTG	AAAAATAATG	AGGTCATTCT	TAGTGAGAGAA	ATCCCTGCTC	1750
	GGTGTATTCA	AGAATATCGT	AGTGATTTAA	CTTTCTTTAC	AAATGGACGT	1800
	AGTGTTTGT	TAACAGAGTT	AAAAGGGTAC	CATGTACTTA	CCGGTGAACC	1850
	TGTTTGCCAG	CCCCGTCGTC	CAAATAGTCG	GATAGATAAA	GTACGATATA	1900
	TGTTCAATAA	AATAACTTAG				1920
35						

2) INFORMATION FOR SEQ ID NO: 1591

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591

50 ATGAGGTAAT AGAACGGATT

20

2) INFORMATION FOR SEQ ID NO: 1592

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592

CAGTATTTCA GTAAGCGTAA A

21

15

2) INFORMATION FOR SEQ ID NO: 1593

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593

CCGAGCGATT TACCGGATAC TTGGCTGCIC GCTCGG

36

30

2) INFORMATION FOR SEQ ID NO: 1594

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 1032 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: N97-330
45 (C) ACCESSION NUMBER: AF175293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594

ATGTTTAGAA	TTAAAGTTGC	AGTTCTGTTT	GGGGGCTGTT	CAGAGGAACA	50
50 TAATGTTTCG	ATAAAATCTG	CGATGGAGAT	TGCCGCAAAC	ATAGATACAA	100
AAAAGTATCA	GCCTTATTAT	ATTGGAATCA	CAAAATCCGG	CGTTTGGAAA	150
ATGTGTGAAA	AACCTTGTTT	GGAGTGGGAA	CAATATGCCG	GGGATCCGGT	200
TGTTTTTTCA	CCGGACAGAA	GTACGCATGG	TCTGCTGATA	CAAAAAGACA	250

	CTGGGTATGA	AATCCAGCCT	GTGGATGTGG	GATTACCGAT	GATTCATGGC	300
	AAGTTTGGCG	AGGATGGCTC	CATACAAGGC	TTGCTTGAAT	TGTCAGGCAT	350
	TCCGTATGTG	GGATGCGATA	TTCAAAGCTC	CGTGACCTGC	ATGGATAAGG	400
	CGCTTGCATA	TACCGTTGTG	AAAAATGCGG	GTATCGCTGT	GCCTGGGTTC	450
5	CGGATCCTTC	AGGAGGGGGA	TCGCCTGGAA	ACAGAGGATT	TCGTATATCC	500
	CGTTTTTTGTA	AAGCCTGCCC	GTTCCGGCTC	ATCCTTTGGC	GTAAACAAGG	550
	TATGCAAGGC	AGAAGAAGCTG	CAGGCAGCAA	TCGAAGATGC	AAGAAAATAT	600
	GACAGCAAGA	TTTTGATTGA	AGAGGCCGTT	ACCGGGAGTG	AGGTAGGCTG	650
	CGCCATACTG	GGAAACGGAA	ATGATCTCAT	GGCTGGCGAG	GTGGATCAGA	700
10	TTGAGCTGAG	ACACGGCTTT	TTTAAGATTC	ATCAGGAAGC	ACAGCCGGAG	750
	AAAGGATCTG	AAAATGCAGT	CATCCGAGTT	CCAGCCGCCT	TACCGGATGA	800
	GGTAATAGAA	CGGATTCAGA	AAACAGCAAT	GAAGATTTAC	CGGATACTTG	850
	GCTGCAGAGG	ATTGGCCCCG	ATTGACCTGT	TTTTGCGGGA	GGACGGCTGC	900
	ATTGTGTTGA	ATGAAGTGAA	TACCATGCCG	GGTTTTACTT	CCTACAGCCG	950
15	TTATCCCCGC	ATGATGACAG	CAGCCGGTTT	TACGCTTACT	GAAATACTGG	1000
	ATCGCTTGAT	TGAACCTTCA	CTTAGGAGGT	AA		1032

20 2) INFORMATION FOR SEQ ID NO: 1595

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595

AAATAATGCT CCATCAATTT GCTGA

25

35

2) INFORMATION FOR SEQ ID NO: 1596

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
 - 40 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596

ATAGTCGAAA AAGCCATCCA CAAG

24

50

2) INFORMATION FOR SEQ ID NO: 1597

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597
10 GATGAATTTG CGAAAATACA TGGA 24

15 2) INFORMATION FOR SEQ ID NO: 1598

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598

CAGCCAATTT CTACCCCTTT CAC 23

30 2) INFORMATION FOR SEQ ID NO: 1599

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
40

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: BM4405
 (C) ACCESSION NUMBER: AF136925
45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599

CAGGGAGTAT TTGAGTTATT AGATATTCCA TATGTAGGTT GTGGTATCGG 50
AGCTGCAGCA ATTTCCATGA ATAAAATAAT GCTCCATCAA TTTGCTGAAA 100
50 TAGTTGGTGT AAAAAGCACT CCTAGTATGA TTATAGAAAA GGGACAAGAC 150
CTACAAAAAG TCGATGAATT TGCGAAAATA CATGGATTTC CTTTATATAT 200
CAAACCGAAT GAGGCAGGCT CATCAAAAGG AATTAGCAAG GTAGAACAAA 250
AAAGTGATTT ATATAAAGCA ATAGACGAAG CTTCAAAATA TGATAGCCGT 300

ATTTTAATTC AAAAGGAAGT GAAAGGGGTA GAAATTGGCT GTGGGATTTT 350
 AGGGAATGAA CAATTGGTCG TTGGAGAATG TGATCAAATT AGTCTTGTGG 400
 ATGGCTTTTT CGACTATGAA GAGAAATACA ATTTAGTAAC AGCAGAAATT 450
 TTGTTACCAG CTAAACTATC AATAGACAAA AAAGAAGACA TCCAGATAAA 500
 5 AGCAAAAAAA CTATACAGAC TATTAGGGTG CAAAGGATTA GCGAGAATCG 550
 ACTTTTCTT AACGGATGAC GGAGAAATTT TATTAAATGA GATCAACACC 600
 CTCC 604

10

2) INFORMATION FOR SEQ ID NO: 1600

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
 (B) STRAIN: ATCC 49349

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600

ACCTCAAATT AATGAAGCAA TTGTTGTAAA TTTTGAAAGC GAAGGAAAAA 50
 AACATAAACT TGTTTTAGAA GTAGCAGCTC ATTTAGGAGA TAATAGAGTT 100
 AGAACTATTG CTATGGATAT GACAGATGGT TTGGTAAGGG GCTTAAAAGC 150
 30 TGAGGCTTTA GGTGCTCCTA TTAGTGTTCC TGTGTTGAG AAAGTTTTAG 200
 GAAGAATTTT CAATGTTACT GGAGATTGTA TCGATGAAGG TGAAGAAATT 250
 CCTTTTGATA AAAAATGGGC AATTCATAGA GATCCGCCAG CTTTTGAAGA 300
 TCAAAGCACA AAAAGTGAGA TTTTGAAGAC AGGGATTAAA GTTGTAGATT 350
 TACTTGCTCC TTATGCAAAA GGTGGTAAAG TAGGTCTTTT TGGTGGTGCA 400
 35 GGTGTTGGTA AAAGTGTAT TATTATGGAG CTTATTCACA ATGTTGCATT 450
 TAAGCATAGC GGCTATTCTG TATTGTCAGG TGTGGGTGAG AGAACTCGTG 500
 AAGGAAATGA CCTTTATAAT GAAATGAAAG AAAGTAATGT TTTAGACAAA 550
 GTTGCTCTAT GTTATGGACA AATGAATGAA CCACCAGGAG CAAGAAATCG 600
 TATTGCTTTA ACAGGTTTAA CAATGGCTGA GTATTTTAGA GATGAAATGG 650
 40 GTCTTGATGT GCTTATGTTT ATTGATAATA TCTTTAGATT TTCACAATCA 700
 GGTTCTGAAA TGTCAGCACT TTTAGGAAGA ATTCCATCAG CTGTGGGTGA 750
 TCAACCAACC CTAGCAAGTG AAATGGGTAA ATTCCAAGAA AGAATTACTT 800
 CAACT 805

45

2) INFORMATION FOR SEQ ID NO: 1601

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus sulfureus*
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601

10	CTCCTTACCA	GATATCAACA	ATGCGCTGGT	TGTATATAAA	AATGATGCCA	50
	ATAAAACAAA	AGTTGTTT	GAAGCAGCGT	TAGAATTAGG	TGACGGAATC	100
	ATTCGTGCGA	TTGCAATGGA	ATCGACTGAT	GGATTGCAAC	GTGGGATGGA	150
	AGTTGTTCGAT	ATGGGAGAAAT	CTATTTCTGT	ACCAGTTGGA	ACAGAAACTT	200
	TAGGACGTGT	GTTTAATGTA	TTAGGAGATA	CGATTGACTT	AGAAGCTCCT	250
15	TTTCCTAAAG	ATGCACCGCG	TAGTGGAATC	CATAAAAAAG	CCCCTAATTT	300
	TGATGAATTA	AGTACAAGCA	CAGAAATTCT	AGAAACAGGG	ATCAAAGTCA	350
	TCGATCTATT	AGCCCCCTTAT	TTAAAAGGTG	GTAAAGTTGG	ATTGTTTGGG	400
	GGAGCCGGTG	TAGGAAAAAC	GGTATTGATT	CAAGAGTTGA	TTCACAATAT	450
	CGCACAAGAA	CACGGTGCGA	TTTCGGTCTT	TACTGGTGTT	GGTGAGCGTA	500
20	CACGTGAAGG	AAACGATTTG	TATTATGAAA	TGAAAGATTC	AGGAGTCATT	550
	GAAAAAACAG	CGATGGTGTT	TGGACAAATG	AATGAGCCAC	CTGGTGCACG	600
	GATGCGTGTA	GCCTTGACTG	GATTAACGAT	TGCTGAATAT	TTCCGTGATG	650
	TTGAAGGACA	GGATGTACTG	TTGTTTATCG	ACAATATCTT	CCGTTTTACA	700
	CAAGCTGGTT	CTGAAGTGTC	TGCCTTGTTA	GGTCGTATGC	CATCAGCTGT	750
25	GGGATATCAA	CCAACATTAG	CTACCGAAAT	GGGGCAATTG	CAAGAGCGGA	800
	TCACGTCAAC	GAAAAAAGGA	TCGATC			826

30 2) INFORMATION FOR SEQ ID NO: 1602

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
(B) STRAIN: ATCC 49428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602

45	TGATACTTTA	CCAGATATTA	ATAATGCATT	AGTAGTATAT	AAAAAGGACG	50
	AGGACAAGAC	ACGCGTTGTC	TTAGAAGCCA	CCTTGGAAC	TGGAGATGGC	100
	ATGATTCGTG	CAATCTCTAT	GGGATCGACT	GATGGCTTGC	AACGGGGAAT	150
	GGAAGTTGTG	GACACACAAG	CACCTATTTC	TGTTCCAGTA	GGAAATGAAA	200
50	CCTTAGGACG	TGTTTTTAAT	GTCTTAGGAG	AAACGATTGA	TAAACAGGCA	250
	CCGTTTCCTG	AAGATGCCAA	AAAAAGTGGT	ATTCATAAAA	AAGCACCCGC	300
	TTTTGATGAA	TTAAGTACCA	GTTCTGAAAT	ATTGGAAACC	GGGATTAAAG	350
	TAATCGATTT	GCTAGCTCCT	TATTTACGAG	GTGGTAAAGT	TGGATTATTT	400

GGCGGTGCTG GCGTGGGTAA AACGGTATTA ATTCAAGAAT TAATTCATAA 450
CGTTGCCCAA GAACATGGGG GAATTTCTGT TTTTACGGGT GTCGGAGAGC 500
GTACTCGTGA AGGAAATGAC CTATATTATG AAATGCAGGA TTCAGGCGTT 550
ATTGAAAAAA CGGCTATGGT ATTTGGACAA ATGAACGAAC CCCCTGGTGC 600
5 ACGTATGCGT GTAGCGTTAA CTGGTTTGAC ACTTGCTGAG TACTTCCGTG 650
ATGTACAAGG TCAAGACGTA TTATTATTIA TAGATAATAT TTTCCGCTTT 700
ACTCAAGCAG GAACAGAAGT ATCTGCTTTA TTAGGACGGA TGCCGTCTGC 750
CGTTGGTTAC CAACCAACTC TAGCAACGGA AATGGGACAG TTGCAAGAAC 800
GAATCACATC GACAGATAAA GGATCAATTA CCT 833
10

2) INFORMATION FOR SEQ ID NO: 1603

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
20 (ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*
25 (B) STRAIN: ATCC 35980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603

ATCAGCCTAA AATTAACGAA GCAATAGAAG TTAATTATGA ATTAGATGGT 50
30 AAAAAAATAA GACTTATTCT TGAAGTAGCT GGACATCTTG GCGATAATAG 100
AGCAAGAACC ATTGCTATGG ATATGAGTGA TGGTTTACAA AGAGGATTAG 150
AAGTTACGGC TCTTGGTGCT CCTATAACAG TTCCTGTTGG AGATAAAGTT 200
TTAGGTAGAA TGTTTAATGT TGTAGGTGAC TTAATAGATG AAGGTGAAGT 250
AACAGATTTT GATAAAAGAT GGGCTATCCA TAGAGATCCT CCTTCGTTTG 300
35 AAGATCAAAG TACAAAAAGT GAAATTTTGT AAACAGGTAT AAAAGTAGTT 350
GATCTTCTTG CACCTTATGC AAAAGGTGGT AAAGTTGGCT TATTTGGTGG 400
TGCTGGCGTT GGAAAAACAG TTATCATAAT GGAGCTTATA CATAATGTTG 450
CATTTAAACA CAGCGGTTAT TCAATTTTGT CCGGTGTTGG AGAGAGAACA 500
AGAGAGGGAA ATGATCTTTA TAATGAGATG AAAGAGTCTG GTGTTTTGGA 550
40 TAAAGTTGCC TTATGTTATG GACAAATGAA TGAACCACCA GGAGCAAGAA 600
ACCGTATAGC ATTAACAGGT CTTACAATGG CTGAATATTT CCGTGATGAA 650
ATGGGGCTTG ATGTGTTGAT GTTTATAGAT AATATTTTGA GATTTTCTCA 700
ATCAGGTTCT GAAATGTCAG CGCTGCTTGG TAGAATTCCA TCTGCTGTTG 750
GTTATCAACC AACATTAGCA AGTGAGATGG GAAAACTTCA AGAAAGAATT 800
45 ACTTCC 806

2) INFORMATION FOR SEQ ID NO: 1604

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 738 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
- (B) STRAIN: ATCC 49372

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604

	GGTGTATCC	GCACAATCGC	TATGGAATCT	ACAGATGGAT	TGCAACGGGG	50
	GATGGAAGTT	GTGATACCG	GCAAACCAAT	CTCTGTTCCT	GTAGGTAAAG	100
	AAACATTAGG	TCGTGTGTTT	AACGTATTAG	GTGAAACGAT	CGACAAAGAA	150
15	GCACCTTTTC	CAGAAGATGT	AGAAAAGAGC	GGTATTCACA	AAAAGGCCCC	200
	CGCTTTTGAA	GACCTTAGCA	CCAGTAATGA	GATTTTAGAA	ACTGGGATCA	250
	AGGTTATCGA	CTTATTAGCC	CCTTACTTAA	AAGGTGGTAA	AGTTGGACTA	300
	TTCGGTGGTG	CCGGTGTTGG	TAAAACCGTC	TTAATTCAAG	AACTGATTCA	350
	TAATATCGCC	CAAGAACACG	GTGGGATTTC	TGTCTTTACC	GGGGTTGGGG	400
20	AACGGACTCG	TGAAGGGAAC	GACCTTTATT	ATGAAATGAA	AGAATCCGGC	450
	GTTATTGAAA	AAACAGCGAT	GGTCTTCGGA	CAAATGAATG	AGCCACCAGG	500
	TGCGCGGATG	CGCGTTGCCT	TGACTGGTTT	GACATTAGCT	GAATATTTC	550
	GTGATGAAGA	AGGTCAAGAT	GTGTTGCTAT	TTATCGATAA	CATTTTCCGC	600
	TTCACACAAG	CCGGATCAGA	AGTTTCGGCG	CTATTAGGTC	GGATGCCATC	650
25	TGCCGTTGGT	TATCAACCAA	CCTTGCAAC	AGAAATGGGT	CAATTACAAG	700
	AACGAATCAC	TTCAACGAAA	AAAGGCTCAA	TTACATCG		738

30 2) INFORMATION FOR SEQ ID NO: 1605

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- 35 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605

ATYATYGAAR TITAYGCICC

20

45

2) INFORMATION FOR SEQ ID NO: 1606

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 50 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606

5 CCRAACATIA YICCIAC TTT TTC

23

2) INFORMATION FOR SEQ ID NO: 1607

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607

25	CTGGATTATG CGATGTCGGT CATTGTTGGC CGTGCGCTGC CGGATGTCCG	50
	AGATGGCCTG AAACCGGTAC ACCGTCGCGT ACTTTACGCC ATGAACGTAT	100
	TGGGCAATGA CTGGAACAAA GCCTATAAAA AATCCGCCCG TGTCGTTGGT	150
	GACGTAATCG GTAAATACCA CCCTCATGGT GATACCGCCG TTTATGACAC	200
	CATTGTACGT ATGGCACAGC CATTCTCCTT GCGTTATATG CTGGTCGATG	250
30	GCCAGGGTAA CTTCGGTTCT GTCGATGGCG ACTCCGCCCG AGCGATGCGT	300
	TATACGGAAA TCCGTATGTC GAAAATCGCC CACGAG	336

35 2) INFORMATION FOR SEQ ID NO: 1608

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 bases

(B) TYPE: Nucleic acid

40

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608

50

CTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG CTGCCGGATG	50
TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTATA CGCCATGAAC	100
GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCTG CCCGTGTCGT	150

GGGTGACGTC	ATCGGTAAAT	ACCACCCTCA	TGGTGATACT	GCCGTATACG	200
ACACCATTTGT	ACGTATGGCG	CAGCCATTCT	CCCTGCGTTA	CATGCTGGTA	250
GATGGCCAGG	GTAACCTTGG	TTCGGTCGAC	GGCGACTCCG	CCGCAGCGAT	300
GCGTTATACG	GAAATCCGTA	TGTCGAAGAT	CGCCCATGAA	C	341

5

2) INFORMATION FOR SEQ ID NO: 1609

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609

20 GCCCTGATCC AAATAGCATA TA

22

2) INFORMATION FOR SEQ ID NO: 1610

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610

35

CCTGGCATAA CAGTAACATT CTG

23

40 2) INFORMATION FOR SEQ ID NO: 1611

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611

TGGGAAAAAG CAACTCCATC TC

22

2) INFORMATION FOR SEQ ID NO: 1612

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612

ACAACTGAAT TCGCAGCAAC AAT

23

15

2) INFORMATION FOR SEQ ID NO: 1613

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 639 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: U19459

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613

	ATGAAATATG	GCCCTGATCC	AAATAGCATA	TATCCACATG	AAGAAATAAA	50
	AAGTGTTTGT	TTTATTAAAA	ATACAATTAC	CAATCCAAAT	ATTATAGTTG	100
35	GAGATTATAC	TTACTATTCC	GATGTTAACG	GAGCTGAAAA	ATTTGAAGAA	150
	CATGTGACAC	ATCATTATGA	ATTTAGGGGT	GATAAACTTG	TAATTGGCAA	200
	GTTTTGTGCA	ATAGCTGAAG	GTATAGAATT	TATTATGAAT	GGAGCAAACC	250
	ATAGAATGAA	TTCAATAACA	ACTTATCCTT	TTAATATAAT	GGGAAATGGT	300
	TGGGAAAAAG	CAACTCCATC	TCTTGAAGAT	TTACCATTTA	AGGGAGATAC	350
40	TGTTGTTGGA	AATGATGTGT	GGATTGGTCA	GAATGTTACT	GTTATGCCAG	400
	GAATTCAAAT	AGGAGATGGA	GCAATTGTTG	CTGCGAATTC	AGTTGTTACA	450
	AAAGATGTAC	CACCATATCG	TATTATTGGT	GGAAATCCGA	GTAGAATTAT	500
	AAAGAAAAGG	TTTGAAGATG	AATTGATAGA	TTATTTATTG	CAAATAAAAT	550
	GGTGGGATTG	GTCAGCACAA	AAAATATTTT	CTAATCTTGA	AACACTTTGT	600
45	AGCTCTGATT	TAGAGAAAAT	AAAATCTATT	CGAGATTAG		639

2) INFORMATION FOR SEQ ID NO: 1614

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614

CCAATCCAGA AGAAATATAC CC

22

10

2) INFORMATION FOR SEQ ID NO: 1615

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615

ATTAGTTTAT CCCCAATCAA TTCA

24

25

2) INFORMATION FOR SEQ ID NO: 1616

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616

40

ATAATGAATG GGGCTAATCA TCGTAT

26

2) INFORMATION FOR SEQ ID NO: 1617

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617

GCCAACAACCT GAATAAGGAT CAAC

24

5

2) INFORMATION FOR SEQ ID NO: 1618

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 639 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
(C) ACCESSION NUMBER: AF015628

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618

	ATGAAATGGC	AAAATCAGCA	AGGCCCCAAT	CCAGAAGAAA	TATACCCTAT	50
	AGAAGGTAAT	AAACATGTTC	AATTTATTAA	ACCATCTATA	ACAAAGCCCA	100
25	ATATTTTAGT	TGGGGAATAT	TCATATTACG	ATAGTAAAGA	TGGTGAATCT	150
	TTTGAAAGCC	AAGTTCTTTA	TCACTATGAA	TTGATTGGGG	ATAAACTAAT	200
	ATTAGGGAAG	TTTTGTTCTA	TTGGACCCGG	AACGACATTT	ATAATGAATG	250
	GGGCTAATCA	TCGTATGGAT	GGTTCAACAT	TTCCATTCAA	TCTTTTCGGA	300
	AATGGTTGGG	AGAAGCATA	CCCTACATTG	GAAGACCTTC	CTTATAAGGG	350
30	TAACACGGAA	ATTGGGAACG	ATGTTTGGAT	TGGACGAGAT	GTGACAATTA	400
	TGCCCCGTGT	AAAAATAGGA	AACGGGGGCTA	TTATTGCAGC	AAAATCGGTT	450
	GTGACAAAGA	ACGTTGATCC	TTATTTCAGT	GTTGGCGGTA	ATCCTTCACG	500
	ATTAATTAAG	ATAAGGTTTT	CCAAGGAAAA	AATCGCAGCA	TTACTAAAAG	550
	TAAGGTGGTG	GGACCTAGAG	ATAGAGACGA	TAAATGAAAA	TATTGATTGC	600
35	ATCCTGAATG	GTGATATAAA	AAAGGTAAAA	AGAAGTTAG		639

2) INFORMATION FOR SEQ ID NO: 1619

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619

50

AAGGCAAAAT AAAAGGAGCA AAGC

24

2) INFORMATION FOR SEQ ID NO: 1620

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620

TGTACCCGAG ACATCTTCAC CAC

23

15

2) INFORMATION FOR SEQ ID NO: 1621

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621

AATTGAAGGA CGGGTATTGT GGAAAG

26

30

2) INFORMATION FOR SEQ ID NO: 1622

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622

45 CGATTTTGAC AGATGGCGAT AATGAA

26

2) INFORMATION FOR SEQ ID NO: 1623

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M90056

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623

	ATGAAAATAA	TGTTAGAGGG	ACTTAATATA	AAACATTATG	TTCAAGATCG	50
	TTTATTGTTG	AACATAAATC	GCCTAAAGAT	TTATCAGAAT	GATCGTATTG	100
	GTTTAATTGG	TAAAAATGGA	AGTGGAAAAA	CAACGTTACT	TCACATATTA	150
15	TATAAAAAAA	TTGTGCCTGA	AGAAGGTATT	GTAAACAAT	TTTCACATTG	200
	TGAACTTATT	CCTCAATTGA	AGCTCATAGA	ATCAACTAAA	AGTGGTGGTG	250
	AAGTAACACG	AAACTATATT	CGGCAAGCGC	TTGATAAAAA	TCCAGAACTG	300
	CTATTAGCAG	ATGAACCAAC	AACTAACTTA	GATAATAACT	ATATAGAAAA	350
	ATTAGAACAG	GATTTAAAAA	ATTGGCATGG	AGCATTATTT	ATAGTTTCAC	400
20	ATGATCGCGC	TTTTTTAGAT	AACTTGTGTA	CTACTATATG	GGAAATTGAC	450
	GAGGGAAGAA	TAACTGAATA	TAAGGGGAAT	TATAGTAACT	ATGTTGAACA	500
	AAAAGAATTA	GAAAGACATC	GAGAAGAATT	AGAATATGAA	AAATATGAAA	550
	AAGAAAAGAA	ACGATTGGAA	AAAGCTATAA	ATATAAAAGA	ACAGAAAGCT	600
	CAACGAGCAA	CTAAAAAACC	GAAAAACTTA	AGTTTATCTG	AAGGCAAAAT	650
25	AAAAGGAGCA	AAGCCATACT	TTGCAGGTAA	GCAAAAGAAG	TTACGAAAAA	700
	CTGTAAAATC	TCTAGAAACC	AGACTAGAAA	AACTTGAAAG	CGTCGAAAAG	750
	AGAAACGAAC	TTCCTCCACT	TAAAATGGAT	TTAGTGAACT	TAGAAAGTGT	800
	AAAAAATAGA	ACTATAATAC	GTGGTGAAGA	TGTCTCGGGT	ACAATTGAAG	850
	GACGGGTATT	GTGGAAAGCA	AAAAGTTTTA	GTATTCGCGG	AGGAGACAAG	900
30	ATGGCAATTA	TCGGATCTAA	TGGTACAGGA	AAGACAACGT	TTATTAAAAA	950
	AATTGTGCAT	GGGAATCCTG	GTATTTTCATT	ATCGCCATCT	GTCAAAATCG	1000
	GTTATTTTAG	CCAAAAAATA	GATACATTAG	AATTAGATAA	GAGCATTTTA	1050
	GAAAATGTTC	AATCTTCTTC	ACAACAAAAT	GAAACTCTTA	TTCGAACTAT	1100
	TCTAGCTAGA	ATGCATTTTT	TTAGAGATGA	TGTTTATAAA	CCAATAAGTG	1150
35	TCTTAAGTGG	TGGAGAGCGA	GTTAAAGTAG	CACTAACTAA	AGTATTCTTA	1200
	AGTGAAGTTA	ATACGTTGGT	ACTAGATGAA	CCAACAACT	TTCTTGATAT	1250
	GGAAGCTATA	GAGGCGTTTG	AATCTTTGTT	AAAGGAATAT	AATGGCAGTA	1300
	TAATCTTTGT	ATCTCACGAT	CGTAAATTTA	TCGAAAAAGT	AGCCACTCGA	1350
	ATAATGACAA	TTGATAATAA	AGAAATAAAA	ATATTTGATG	GCACATATGA	1400
40	ACAATTTAAA	CAAGCTGAAA	AGCCAACAAG	GAATATTAAA	GAAGATAAAA	1450
	AACTTTTACT	TGAGACAAAA	ATTACAGAAG	TACTCAGTCG	ATTGAGTATT	1500
	GAACCTTCGG	AAGAATTAGA	ACAAGAGTTT	CAAACTTAA	TAAATGAAAA	1550
	AAGAAATTTG	GATAAATAA				1569

45

2) INFORMATION FOR SEQ ID NO: 1624

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624

5

TTCTTTAATG CTCGTAGATG AACCTA

26

10 2) INFORMATION FOR SEQ ID NO: 1625

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1625

TTTTCGTATT CTTCTTGTTG CTTTC

25

25

2) INFORMATION FOR SEQ ID NO: 1626

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626

AGGAATGATT AAGCCCCCTT CAAAAA

26

40

2) INFORMATION FOR SEQ ID NO: 1627

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627

TTACATTGCG ACCATGAAAT TGCTCT

26

2) INFORMATION FOR SEQ ID NO: 1628

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (C) ACCESSION NUMBER: U82085

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628

20	ATGCTTAAAA	TCGACATGAA	GAATGTAAAA	AAATATTATG	CAGATAAATT	50
	AATTTTAAAT	ATAAAAGAAC	TAAAGATTTA	TAGTGGGGAT	AAAATAGGTA	100
	TTGTAGGTAA	GAATGGAGTT	GGCAAAACAA	CACTTTTAAA	AATAATAAAA	150
	GGACTAATAG	AGATTGACGA	AGGAAATATA	ATTATAAGTG	AAAAAACAAC	200
	TATTAAATAT	ATCTCTCAAT	TAGAAGAACC	ACATAGTAAG	ATAATTGATG	250
25	GAAAATATGC	TTCAATATTT	CAAGTTGAAA	ATAAGTGGAA	TGACAATATG	300
	AGTGGTGGTG	AAAAAACTAG	ATTTAAACTA	GCAGAGGGAT	TTCAAGATCA	350
	ATGTTCTTTA	ATGCTCGTAG	ATGAACCTAC	AAGTAATTTA	GATATCGAAG	400
	GAATAGAGTT	GATAACAAAT	ACTTTTAAAG	AGTACCGTGA	TACTTTTTTTG	450
	GTAGTATCTC	ATGATAGAAT	TTTTTTTAGAT	CAAGTTTGTA	CAAAAATTTT	500
30	TGAAATTGAA	AATGGATATA	TTAGAGAATT	CATCGGTAAT	TATACAAACT	550
	ATATAGAGCA	AAAAGAAATG	CTTCTACGAA	AGCAACAAGA	AGAATACGAA	600
	AAGTATAATT	CTAAAAGAAA	GCAATTGGAG	CAAGCTATAA	AGCTAAAAGA	650
	GAATAAGGCG	CAAGGAATGA	TTAAGCCCCC	TTCAAAAACA	ATGGGAACAT	700
	CTGAATCTAG	AATATGGAAA	ATGCAACATG	CTACTAAACA	AAAAAAGATG	750
35	CATAGAAATA	CGAAATCGTT	GGAAACACGA	ATAGATAAAT	TAAATCATGT	800
	AGAAAAAATA	AAAGAGCTTC	CTTCTATTAA	AATGGATTTA	CCTAATAGAG	850
	AGCAATTTCA	TGGTCGCAAT	GTAATTAGTT	TAAAAAACTT	ATCTATAAAA	900
	TTTAATAATC	AATTTCTTTG	GAGAGATGCT	TCATTTGTCA	TTAAAGGTGG	950
	AGAAAAGGTT	GCTATAATTG	GTAACAATGG	TGTAGGAAAA	ACAACATTGT	1000
40	TGAAGCTGAT	TCTAGAAAAA	GTAGAATCAG	TAATAATATC	ACCATCAGTT	1050
	AAAATTGGAT	ACGTCAGTCA	AAACTTAGAT	GTTCTACAAT	CTCATAAATC	1100
	TATCTTAGAA	AATGTTATGT	CTACCTCCAT	TCAAGATGAA	ACAATAGCAA	1150
	GAATTGTTCT	AGCAAGATTA	CATTTTTTATC	GCAATGATGT	TCATAAAGAA	1200
	ATAAATGTTT	TGAGTGGTGG	AGAACAAATA	AAGGTTGCTT	TTGCCAAGCT	1250
45	ATTTGTTAGC	GATTGTAATA	CATTAATTCT	TGATGAACCA	ACAAACTATT	1300
	TGGATATCGA	TGCTGTTGAG	GCATTAGAAG	AATTGTTAAT	TACCTATGAA	1350
	GGTGTGTGT	TATTTGCTTC	CCATGATAAA	AAATTTATAC	AAAACCTAGC	1400
	TGAACAATTG	TTAATAATAG	AAAATAATAA	AGTGAAAAAA	TTCGAAGGAA	1450
	CATATATAGA	ATATTTAAAA	ATTAAAGATA	AACCAAAATT	AAATACAAAT	1500
50	GAAAAAGAAC	TCAAAGAAAA	AAAGATGATA	CTAGAAATGC	AAATTTTCATC	1550
	ATTATTAAGT	AAAATCTCAA	TGGAAGAAAA	TGAAGAAAAA	AACAAAGAAT	1600
	TAGATGAAAA	GTACAAATTG	AAATTAAAG	AATTGAAAAG	CCTAAATAAA	1650
	AATATTTA					1658

2) INFORMATION FOR SEQ ID NO: 1629

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629

AAGGGGAAAG TTTGGATTAC ACAACA

26

15

2) INFORMATION FOR SEQ ID NO: 1630

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630

GAACCACAGG GCATTATCAG AACC

24

30

2) INFORMATION FOR SEQ ID NO: 1631

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631

45 CGACGATGCT TTATGGTTTG T

21

2) INFORMATION FOR SEQ ID NO: 1632

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632

GTAAATTTGC CTATCTTGTC ACACTC

26

10

2) INFORMATION FOR SEQ ID NO: 1633

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M36022

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633

	ATGGAATTTA	AATTACAAGA	ATTAAATCTT	ACTAACCAAG	ATACAGGACC	50
	ATATGGTATA	ACCGTTTCAG	ATAAGGGGAA	AGTTTGGATT	ACACAACATA	100
	AAGCAAATAT	GATAAGTTGC	ATCAATTTAG	ATGGAAAAAT	TACAGAGTAC	150
30	CCACTACCGA	CACCAGATGC	AAAAGTCATG	TGTTTAACTA	TATCCTCAGA	200
	TGGGGAAGTT	TGGTTTACTG	AGAATGCAGC	AAACAAAATA	GGGAGGATTA	250
	CAAAAAAAGG	GATTATTAAG	GAATATACAT	TGCCTAACCC	AGATTCAGCA	300
	CCCTACGGTA	TTACAGAAGG	ACCAAATGGA	GATATATGGT	TTACAGAAAT	350
	GAATGGCAAC	CGTATTGGAC	GTATTACGGA	CGACGGTAAA	ATTCGTGAAT	400
35	ACGAGCTGCC	TAATAAAGGA	TCTTACCCTT	CTTTTATCAC	TTTGGGTTCT	450
	GATAATGCCC	TGTGGTTCAC	AGAAAATCAA	AATAATGCTA	TTGGTAGAAT	500
	TACAGAAAGT	GGGGATATTA	CAGAGTTTAA	AATTCCTACA	CCTGCATCAG	550
	GACCAGTTGG	TATTACAAAG	GGGAACGACG	ATGCTTTATG	GTTTGTGGAA	600
	ATTATCGGTA	ATAAGATAGG	GCGAATAACT	CCTCTGGGGG	AAATTACCGA	650
40	ATTCAAAATT	CCAACGCCAA	ACGCTCGACC	TCATGCAATT	ACTGCTGGAG	700
	CAGGAATTGA	TTTATGGTTT	ACTGAATGGG	GGGCTAATAA	AATAGGAAGG	750
	CTGACAAGCA	ATAATATAAT	TGAGGAATAC	CCAATTCAAA	TCAAAAGTGG	800
	TGAACCACAT	GGCATTGTGT	TCGATGGTGA	AACAATTTGG	TTTGCAATGG	850
45	AGTGTGACAA	GATAGGCAAA	TTAACTCTCA	TTAAGGATAA	TATGGAGTGA	900

2) INFORMATION FOR SEQ ID NO: 1634

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634

TTAACTTGTC TATTCCCGAT TCAGG

25

10

2) INFORMATION FOR SEQ ID NO: 1635

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635

GCTGTGGCAA TGGATATTCT GTA

23

25

2) INFORMATION FOR SEQ ID NO: 1636

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636

TTCCTACCCC TGATGCTAAA GTGA

24

40

2) INFORMATION FOR SEQ ID NO: 1637

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637

CAAAGTGCGT TATCCGAACC TAA

23

5

2) INFORMATION FOR SEQ ID NO: 1638

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 527 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: WSA-172

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638

GGTGGGGAAG ACTGTCTTCA TCCAGGAATT GATTGTGAGT CGTTCCACAT 50
GCTCACCTAG TTTTCGCTCG ATCTTTTCAC TAACGCAAAC CATGTAGAAC 100
AACATTGCCA AGGCCACGG TGGTTACTCC GTCTTCACTG GTGTTGGTGA 150
25 GCGTACTCGT GAGGGTAACG ATCTGTACCA CGAAATGCAG GAGACTGGTG 200
TCATTCAGCT CGAGGGTGAA TCCAAGGTCG CACTGGTGTT CGGACAGATG 250
AACGAGCCCC CCGGTGCCCG TGCCCGTGTC GCCCTTACCG GTCTGACCAT 300
TGCCGAGTAC TTCCGTGACG AGGAGGGTCA GGACGTGCTG CTCTTCATTG 350
ACAACATTTT CCGTTTCACC CAGGCCGGTT CTGAGGTGTC TGCCCTTCTC 400
30 GGTCGTATCC CCTCTGCCGT CGGTTACCAG CCCACCCTGG CCGTCGACAT 450
GGGTGGTATG CAGGAGCGTA TCACCACCAC CAAGAAGGGT TCTATTACCT 500
CCGTCCARGC CGTCTACGTC CCCGCGA 527

35

2) INFORMATION FOR SEQ ID NO: 1639

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 452 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: ATCC 64746

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639

ACTGTCTTGA TTCAAGAACT TATTAACAAC ATTGCTAAAG CCCATGGTGG 50
TTACTCTATT TTCTGTGGTG TTGGTGAACG TACTCGTGAA GGTAACGATT 100

TATACCACGA AATGATGGAA ACTGGTGTCA TTAAACTTGA AGGTGACTCC 150
 AAGTGTGCTC TTGTATTCGG TCAAATGAAC GAACCTCCTG GTGCTCGTGC 200
 CCGTGTTGCT TTAAGTGGTT TAACCATTCG TGAATACTTC CGTGATGAAG 250
 AAGGTCAAGA TGTGTTACTT TTCATTGATA ACATTTTCCG TTCACTCAA 300
 5 GCTGGTTCTG AAGTATCTGC CCTTTTAGGT CGTATTCCAT CTGCTGTAGG 350
 TTACCAACCC ACTTTATCTA CTGATATGGG TGGTATGCAA GAACGTATTA 400
 CTACTACCAA GAATGGTTCC ATTACCTCTG TACARGCCGT CTACGTCCCC 450
 GC 452

10

2) INFORMATION FOR SEQ ID NO: 1640

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 783 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462
 25 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640

ACGCCCTTAC GGTAACACAA AGCAACGAAA ACGGAAGCAT GAACTTAACA 50
 30 TTTGAAGTTG CACTTCATTT AGGTGATGAT ACAGTTCGTA CAGTTGCGAT 100
 GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA GATACTGGTA 150
 AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG TGTATTCAAC 200
 GTATTAGGTG ATGCAATTGA CTTAGATGGT GAACTTCCTG CGGATGTACA 250
 CCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA TTATCTACTA 300
 35 AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT ACTTGCTCCT 350
 TACATTAAGG GTGGTAAGAT CGGCCTATTC GGTGGTGCCG GCGTAGGTAA 400
 AACAGTATTA ATTCAAGAAT TAATTAACAA CATCGCACAA GAGCACGGTG 450
 GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA GGGTAATGAC 500
 TTATACCATG AAATGAGCGA TTCTGGCGTA ATCAAGAAAA CTGCGATGGT 550
 40 ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT GTTGCATTAA 600
 CAGGTTTAAC AATGGCTGAG CATTTCCGTG ATGAGCAAGG ACAAGACGTA 650
 CTTCTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCGG GTTCTGAAGT 700
 ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC CAACCAACAC 750
 TTGCAACAGA AATGGGTCAA TTACAAGAGC GTA 783

45

2) INFORMATION FOR SEQ ID NO: 1641

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL NRS-319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641

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10 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAGCAAGCAT      50
   TAACTTAACA TTTGAAGTTG CACTTCATTT AGGTGATGAC ACAGTTCGTA      100
   CAGTTGCAAT GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA      150
   GATACTGGTA AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG      200
15 TGTATTCAAC GTATTAGGTG ATGCAATTGA CTTAGATGGT GATGTTTCCTG      250
   CGGATGTACG TCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA      300
   CTATCTACTA AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT      350
   ACTTGCTCCT TACATTAAGG GTGGTAAGAT CGGTCTATTC GGTGGTGCCG      400
   GTGTAGGTAA AACAGTATTA ATTCAGGAAT TAATTAACAA CATCGCACAA      450
20 GAACACGGTG GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA      500
   GGGTAACGAC TTATACCATG AAATGAGCGA TTCTGGCGTA ATTAAGAAAA      550
   CTGCGATGGT ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT      600
   GTTGCATTAA CAGGTTTAAC AATGGCTGAA CATTTCCGTG ATGAGCAAGG      650
   ACAAGACGTA CTATTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCAG      700
25 GTTCTGAAGT ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC      750
   CAACCAACAC TTGCAACAGA AATGGGTCAA TTACAAGAGC GTATTACATC      800
   TACAAATAAA GGATCTATCA CGT                                     823

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30

2) INFORMATION FOR SEQ ID NO: 1642

(i) SEQUENCE CHARACTERISTICS:

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35 (A) LENGTH: 829 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL BD-15

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642

```

   GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAAAG      50
   CAACGAAAAC GGAGCAAACA TTAAGTTAAC ATTTGAAGTT GCACTTCATT      100
   TAGGTGATGA TACAGTTCGT ACAGTTGCGA TGTCTTCCAC AGATGGACTT      150
50 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT      200
   TGGTGATGTA ACACTTGGTC GTGTATTCAA CGTATTAGGT GATGCAATTG      250
   ACTTAGATGG TGAAGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT      300
   CAAGCACCTG CATTCGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC      350

```

	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
	TTGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACAGTATT	AATTCAGGAA	450
	TTAATTAACA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCCGG	500
	TGTAGGTGAG	CGTACTCGTG	AAGGTAACGA	CTTATAACCAC	GAAATGAGCG	550
5	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCATTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGACGT	ACTACTGTTC	ATCGATAACA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	750
	ATGCCATCTG	CGGTAGGTTA	CCAGCCAACA	CTTGCAACAG	AAATGGGTCA	800
10	ATTACAAGAG	CGTATTACAT	CTACAAATA			829

2) INFORMATION FOR SEQ ID NO: 1643

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Bacillus pseudomycoides*
 (B) STRAIN: NRRL BD-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643

30	AATCTACAAT	GCCCTTACGG	TAAAACAAAG	CAACGAAAAC	GGAGCAAGCA	50
	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	TAGGTGATGA	CACAGTTCGT	100
	ACAGTTGCGA	TGTCTTCCAC	AGATGGACTT	GTTCGTGGCA	CAGAAGTAGA	150
	AGATACTGGT	AAACCAATCT	CTGTACCGGT	TGGTGATGCA	AACTTTGGTC	200
	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	ACTTAGATGG	TGAAGTTCCT	250
35	GCGGATGTAC	GCCGTGATCC	AATTCACCGT	CAAGCACCTG	CGTTCGAAGA	300
	GTTATCTACG	AAAGTAGAAA	TTCTTGAAAC	TGGTATTAAA	GTAGTAGACT	350
	TACTTGCTCC	TTACATTAAA	GGTGGTAAAA	TCGGTCTATT	CGGTGGTGCC	400
	GGTGTAGGTA	AAACAGTATT	AATCCAGGAA	TTAATTAACA	ACATCGCACA	450
	AGAGCACGGT	GGTATTTCTG	TATTCGCTGG	TGTAGGTGAG	CGTACTCGTG	500
40	AAGGTAATGA	CTTATAACCAC	GAAATGAGCG	ATTCTGGCGT	AATCAAGAAA	550
	ACAGCGATGG	TATTCGGACA	AATGAACGAG	CCACCTGGTG	CACGTCAACG	600
	TGTTGCATTA	ACAGGATTAA	CAATGGCTGA	ACATTTCCGT	GATGAGCAAG	650
	GACAAGACGT	ACTATTGTTC	ATCGATAACA	TCTTCCGTTT	CACGCAAGCG	700
	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	ATGCCATCTG	CGGTAGGTTA	750
45	CCAACCAACT	CTTGCAACAG	AAATGGGTCA	ATTACAAGAG	CGTATTACAT	800
	CTACAAATAA	AGGATCTATC	ACG			823

50 2) INFORMATION FOR SEQ ID NO: 1644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL B-617

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644

	GGAAAGCTAC	CTGAAATCTA	CAATGCCCTT	AGAATTAAAC	AAGACGCAGT	50
	TAAGTTAACT	TTAGAAGTTG	CACTTCACTT	AGGTGATGAT	ACAGTTCGTA	100
15	CAGTTGCGAT	GTCTTCCACA	GACGGACTTG	TTCGTGGTAC	TGCAGTAGAA	150
	GATACTGGCA	AAGCGATTTC	TGTTCCAGTT	GGTGATGCAA	CACTTGGTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGT	GAGGTTCCAG	250
	CAGATGTACG	CCGTGATCCA	ATTCACCGTC	AAGCACCTGC	ATTCGAAGAG	300
	TTATCTACAA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
20	ACTTGCTCCT	TACATTAAAG	GTGGTAAAT	CGGTCTATTC	GGTGGTGCCG	400
	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTAAGCTGTA	500
	AGGTAACGAC	TTATACCATG	AAATGAGCGA	TTCTGGCGTA	ATCAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGTGC	ACGTCAACGT	600
25	GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
	ACAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
	GTTCTGAA					708

30

2) INFORMATION FOR SEQ ID NO: 1645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- 35 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
- (B) STRAIN: ATCC 35567

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645

	GTACGATGCG	CTTGAAGTTC	AAAACGATGT	CAAAC TAGTG	CTGGAAGTTC	50
	AACAGCAGCT	CGGTGGTGGT	GTCGTTGCTT	GTATCGCTAT	GGGTACCTCA	100
	GATGGCCTAA	GCCGCGGTCT	GAAAGTACTT	GATTTAGAAC	ACCCTATCGA	150
50	AGTTCCTGTC	GGTGTGGCAA	CTCTGGGCCG	TATTATGAAC	GTGCTTGGTG	200
	AGCCTATCGA	TATGAAGGGT	GACATTGGTG	AAGAAGAGCG	TTGGGCTATC	250
	CATCGCGCTG	CACCAAGCTA	CGAAGATTTA	TCCAGTGCTA	ACGAAGTCTG	300
	GGAAACGGGC	ATCAAGGTTA	TCGACCTGAT	TTGTCCGTTT	GCCAAAGGCG	350

GTAAAGTTGG TCTGTTTGGT GGTGCCGGCG TAGGTAAAAC GGTAACATG 400
 ATGGAGCTGA TTCGTAATAT TGCGACTGAG CACTCAGGTT ACTCTGTATT 450
 TGCCGGCGTT GGTGAGCGTA CTCGTGAGGG TAATGACTTC TACCACGAAA 500
 TGACAGAATC TAACGTATTA GACAAAGTAT CTCTGGTTTA TGGCCAAATG 550
 5 AATGAGCCAC CGGGAAACCG TCTGCGCGTT GCGTTAACCG GCCTGACCAT 600
 GGCGGAAAAA TTCCGTGATG AAGGCCGTGA CGTTCTGCTG TTTATCGATA 650
 ACATTTATCG TTATACCTTA GCCGGTACAG AAGTATCAGC ACTGTTAGGT 700
 CGTATGCCAT CAGCGGTAGG TTACCAACCA ACGCTGGCGG AAGAGATGGG 750
 TACTGCAA GAACGTATCA CYTCAACC 778
 10

2) INFORMATION FOR SEQ ID NO: 1646

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*
 25 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646

GATGCCGTAC CAAAAGTGTA CGACGCTCTT GAGGTTACAA ATGGTAAAGA 50
 30 CCGTCTGGTG CTGGAAGTTC AGCAACAGTT AGGTGGTGGC GTAGTGCGTA 100
 CTATCGCCAT GGGTACTTCT GATGGTTTGC GTCGTGGTCT GGAAGTTTCT 150
 AACCTCGATC ACCCAATTGA AGTGCCAGTA GGTAAGCAA CTCTGGGCCG 200
 TATCATGAAC GTCCTGGGCG AGCCTATCGA CATGAAAGGC GATATCGGCG 250
 AAGAAGAGCG TTGGGCGATT CACCGTGCTG CTCCTAGCTA CGAAGAACTG 300
 35 TCTAGCTCCC AGGATCTGCT GGAAACCGGC ATCAAAGTAA TGGACCTGAT 350
 TTGCCCCTTC GCTAAGGGTG GTAAAGTCGG TCTGTTCCGT GGTGCGGGTG 400
 TGGGTAAAAC TGTAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCAGTGTT TGCAGGCGTG GGGGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCATGAAA TGACCGATTC CAACGTTCTG GACAAAGTAT 550
 40 CACTGGTTTA TGGCCAGATG AACGAGCCAC CAGGTAACCG TCTGCGCGTT 600
 GCGTTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
 CGTTCTGCTG TTCGTTGATA ACATTTACCG TTATACCCTG GCCGGTACAG 700
 AAGTATCTGC GCTGCTGGGT CGTATGCCAT CTGCGGTAGG TTACCAGCCA 750
 ACTCTGGCAG AAGAGATGGG TGTTTTGCAG GAGCGTATTA CCTCCACCAA 800
 45 AACTGG 806

2) INFORMATION FOR SEQ ID NO: 1647

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*
(B) STRAIN: ATCC 36586

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647

	GAAACCGTTG	TTGACACTGG	TTCCCCAATC	ACCGTCCCAG	TTGGTCGTGA	50
	AACCTTGGGT	CGTATCATTA	ACGTTATCGG	TGAACCAATC	GATGAACGTG	100
	GTCCAATCAA	CACCAAGCAA	AGAAACCCAA	TCCATGCTGA	TCCTCCTTCA	150
15	TTTGCTGAAC	AATCCACTTC	TGCTGAAGTT	TTAGAAACCG	GTATTAAAGT	200
	TGTCGATTTA	TTGGCTCCTT	ATGCCAGAGG	TGGTAAAATT	GGTTTATTCG	250
	GTGGTGCCGG	TGTCGGTAAA	ACCGTCTTTA	TCCAAGAATT	GATTAACAAC	300
	ATTGCTAAAG	CTCATGGTGG	TTTCTCAGTC	TTCACCGGTG	TCGGTGAAAG	350
	AACCAGAGAA	GGTAACGATT	TATACCGTGA	AATGAAAGAA	ACCGGTGTCA	400
20	TTAACTTGGA	AGGTGACTCT	AAAGTCGCTT	TAGTCTTCGG	TCAAATGAAC	450
	GAACCTCCAG	GTGCTAGAGC	CCGTGTTGCC	TTAACCGGTC	TAACCATTGC	500
	TGAATACTTC	AGAGATGAAG	AAGGTCAAGA	TGTCTTGTTA	TTCGTTGATA	550
	ACATTTTCAG	ATTCACCCAA	GCTGGTTCAG	AAGTCTCTGC	CTTATTAGGT	600
	CGTATTCCAT	CTGCTGTCGG	TTATCAACCA	ACCTTGGCCA	CTGATATGGG	650
25	TTTGTTGCAA	GAACGTATCA	CCACCACCAG	AAAAGGTTCC	GTCACTTCTG	700
	TCCAAGCTGT	TTATGTCCCA	GCTGATGATT	TGACTGATCC	TGCCCCAGCC	750
	ACCACTTTCG	CGCATTTGGA	TGCTACTACT	GTCTTGCTCTC	GTGGTATCTC	800
	AGAATTGGGT	ATCTACCCAG	CTGTCGATCC	ATTGGATTCC	AAATCAAGAT	850
	TATTAGATGC	CGCTGTTGTT	GGTCAAGAAC	ATTACGATGT	TGCTACTCAA	900
30	GTTCAACAAA	CTTTACAAGC	CTACAAATCT	TTACAAGATA	TTATCGCTAT	950
	TTTAGGTATG	GATGAATTAT	CAGAACAAGA	TAAATTGACC	GTTGAAAGAG	1000
	CTAGAAAGAT	CCAACGTTTC	TTATCTCAAC	CATTTGCTGT	CGCTGAAGTT	1050
	TTCACTGGTA	TTCCAGGTAG	ATTAGTTAGA	TTGAAAGAAA	CCGTTGCTTC	1100
	ATTCAGAGAC	GTTTTAGCTG	GT			1122

35

2) INFORMATION FOR SEQ ID NO: 1648

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: ATCC 700677

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648

	TACGTCTCTT	ACCCTGACGA	TGATTTGCAA	GTCGCATCTA	CGGTCGTAGA	50
	TGTTTCAAAT	GGTAAAGTCA	TCGCCCAACT	TGGAGCTCGT	CACCAAGCAA	100
	GTAACGTTTC	ATTTGGTACC	AACCAAGCTG	TGGAAACCAA	TCGTGACTGG	150
	GGATCAACTA	TGAAACCAAT	CACAGACTAT	GCTCCTGCCT	TGGAGTACGG	200
5	TGTCTACGAT	TCAACTGCTA	CTATCGTTCA	CGATGAGCCC	TATAACTACC	250
	CTGGGACAGA	TATCCCTCTC	TATAACTGGG	ATCGAGCATA	TTTCGGTAAT	300
	ATTACTCTGC	AATATGCCCT	TCAACAATCT	CGTAACGTAC	CTGCCGTTGA	350
	AACACTAAAC	AAGGTCGGTC	TAGATAAGGC	TAAAACCTTC	CTTAATGGTC	400
	TTGGTATCGA	CTATCCAAGC	ATGCATTATG	CAAACGCCAT	TTCAAGTAAT	450
10	ACAACCTGAAT	CCAACAAAAA	ATATGGTGCA	AGTAGTGAAA	AAATAGCTAC	500
	CGCCTATGCC	GCATTGCGAA	ATGGTGGTAT	TTACCACAAA	CCAATGTACA	550
	TCAATAAAGT	TGTCTTTAGC	GATGGTAGCG	AAAAAGAATT	TTCTGACCCT	600
	GGCACAAGAG	CCATGAAAGA	AACGACTGCT	TACATGATGA	CAGAAATGAT	650
	GAAAACAGTC	TGGACGTACG	GAAGTGGTCG	TGGTGCCTAC	CTGCCTTGGC	700
15	TTCCTCAAGC	TGGTAAAACA	GGTACCTCTA	ACTATACTGA	CGAAGAAATT	750
	GAAAAGTATA	TCAAGAACAC	TGGTTACGTA	GCTCCAGATG	AAATGTTTGT	800
	GGGTTATACC	CGT				813

20

2) INFORMATION FOR SEQ ID NO: 1649

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*
 (B) STRAIN: ATCC 43675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649

	ATTAATGAAG	CTATTGTTGT	TAATTATGAA	TTAGAAGGAA	AAGAATGCAA	50
	GCTAGTTCTT	GAAGTAGCTG	CACATTTAGG	CGATAATAAA	GTAAGAACCA	100
	TCGCTATGGA	TATGACAGAT	GGTCTTGTTA	GAGGTTTAAAC	AGCCGTCGCA	150
40	ACTGGAAATC	CAATTAGTGT	TCCAGTAGGC	GAAAAAGTTC	TTGGAAGAAT	200
	TTTTAATGTA	ACGGGTGATT	TGATTGATGA	GGGCGAAGAA	ATCAATTTTG	250
	ATAAGCACTG	GTCAATTCAT	AGAGATCCAC	CTCCATTTGA	AGAACAAAGT	300
	ACAAAAAGCG	AAATCTTTGA	AACAGGTATA	AAGGTTGTTG	ATTTGCTAGC	350
	TCCTTATGCT	AAAGGTGGAA	AAGTTGGTCT	TTTTGGTGGT	GCAGGTGTTG	400
45	GTAAAACCGT	TATTATTATG	GAATTAATTC	ACAATGTTGC	ATTTAAACAT	450
	AGCGGATATT	CTGTTTTTGC	AGGTGTTGGC	GAAAGAACTC	GTGAGGGTAA	500
	TGACCTTTAC	AATGAAATGA	AAGAAAGTAA	TGTATTAGAT	AAAGTTGCAT	550
	TGTGTTATGG	TCAAATGAAT	GAACCACCAG	GGGCAAGAAA	TCGTATAGCT	600
	TTAACAGGTC	TTACTATGGC	TGAGTATTTT	AGAGATGAAA	TGGGACTTGA	650
50	TGTTTTAATG	ATTATTGATA	ATATTTTCAG	ATTTTCTCAA	TCAGGCTCAG	700
	AAATGTCAGC	ACTTTTAGGA	AGAATTCCTT	CAGCTGTTGG	TTATCAACCA	750
	ACCTTAGCTA	GTGAAATGGG	TAAGTTCCAA	GAAAGAATTA	CTTCAACCAA	800
	GAAAGGATCT	ATT				813

2) INFORMATION FOR SEQ ID NO: 1650

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 bases
 5 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
 10
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650

	GGTGGGGAAG	ACTGTGTTCA	TTCAGGAATT	GATTGTAAGT	TCTGTTATCA	50
	ACTAAAGCCG	ACAGCGGTTG	CTGATATGCT	CTAGAACAAC	ATTGCTAAGG	100
	CTCACGGTGG	TTACTCCGTG	TTCAGTGGTG	TCGGTGAGCG	TACCCGTGAG	150
20	GGTAACGATT	TGTACCATGA	AATGCAAGAG	ACCCGTGTCA	TTCAACTCGA	200
	CGGAGAGTCC	AAGGTCGCTC	TTGTCTTCGG	TCAAATGAAC	GAGCCCCCTG	250
	GTGCCCCGTG	CCGTGTTGCC	CTTACCGGTT	TGACCATTCG	TGAATACTTC	300
	CGTGACGAGG	AAGGCCAAGA	CGGTAGGCTT	CATGCTTCTA	TCGCTAGGGG	350
	CGTGTGATAC	AGGAGGCTAA	TCGCTTTTCT	AGTGCTTCTC	TTTATTGACA	400
25	ACATTTTCCG	TTTCACTCAA	GCTGGTTCTG	AAGTGTCTGC	CTTGCTCGGT	450
	CGTATTCCTT	CCGCTGTCGG	TTACCAACCT	ACTCTCGCCG	TCGACATGGG	500
	TGTTATGCAG	GAACGTATCA	CCACCACCAC	CAAGGGATCC	ATTACTTCAG	550
	TGCARGCCGT	CTACGTCCCC				570

30

2) INFORMATION FOR SEQ ID NO: 1651

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 560 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651

	TGTCTTCATC	CAGGAGTTAA	TTGTACGTTT	TTTGTCTGCC	TACTATAATA	50
	GACGAAGAAA	TATTTTGATT	TATTTTCTA	ATAATTCAA	TAGAACAACA	100
50	TTGCCAAAGC	CCACGGTGGT	TACTCTGTCT	TCACTGGTGT	TGGCGAGCGG	150
	ACCCGTGAAG	GAAACGATCT	GTACCACGAA	ATGCAGGAGA	CCCGTGTCAT	200
	CCAGCTCGAT	GGCGAGTCCA	AGGTCGCCCT	CGTCTTCGGT	CAAATGAACG	250
	AACCCCCCGG	AGCCCGTGCC	CGTGTTGCC	TCACTGGTCT	GACCGTTGCT	300

	GAATACTTCC	GTGACGAGGA	AGGTCAAGAT	GGTGCGTATA	TATATATTCG	350
	CCAGTAATTT	GACTCGAAGC	TCCACTCACA	CATATATTAG	TGCTCCTCTT	400
	CATCGACAAC	ATTTTCCGCT	TCACCCAGGC	AGGTTCCGAA	GTGTCCGCCC	450
	TGCTCGGCCG	TATCCCCTCC	GCCGTCGGTT	ACCAGCCCAC	CCTCGCTGTC	500
5	GACATGGGTA	TGATGCAGGA	ACGTATCACC	ACCACCACCA	AGGGCTCCAT	550
	CACCTCCGTG					560

10 2) INFORMATION FOR SEQ ID NO: 1652

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652

25	CCACAAGTGT	ACAGCGCCCT	TGAGGTAAA	AATGGTGATG	CTCGTCTGGT	50
	GCTGGAAGTT	CAGCAGCAGC	TGGGCGGTGG	CGTGGTTCGT	ACCATCGCCA	100
	TGGGTTCTTC	AGACGGCCTT	AAGCGTGGTC	TGGAAGCCGT	TGACCTTCAG	150
	CACCCAATTG	AAGTACCGGT	AGGTACTGCC	ACACTTGGCC	GTATCATGAA	200
30	CGTGCTGGGT	GAGCCGATCG	ATATGAAAGG	CGACATTGGC	GAAGAAGAGC	250
	GCTGGGCGAT	TCACCGCTCT	GCACCTTCTT	ACGAAGATCA	GTCGAACTCT	300
	CAGGATCTGC	TGGAAACCGG	CATCAAGGTG	ATTGACCTGA	TGTGTCCGTT	350
	CGCCAAGGGC	GGTAAAGTCG	GCTTGTTTCGG	TGGTGCGGGC	GTAGGTAAAA	400
	CCGTCAACAT	GATGGAGCTT	ATTCGTAACA	TTGCGGCTGA	GCACTCAGGT	450
35	TTCTCGGTAT	TTGCCGGTGT	GGGTGAGCGT	ACCCGTGAAG	GTAACGACTT	500
	CTACCACGAA	ATGACCGACT	CCAACGTTAT	CGACAAAGTT	TCGCTGGTCT	550
	ATGGTCAGAT	GAACGAGCCA	CCGGGTAAAC	GTCTGCGCGT	TGCGCTGACC	600
	GGTCTGACCA	TGGCGGAGAA	GTTCCGTGAC	GAAGGTCGTG	ACGTACTGCT	650
	GTTTATCGAT	AACATCTATC	GTTACACCCT	GGCCGGTACT	GAAGTCTCCG	700
40	CTCTGCTGGG	TCGTATGCCT	TCTGCGGTAG	GTTACCAGCC	AACGCTGGCG	750
	GAAGAGATGG	GCGTTCTGCA	GGAACGTATC			780

45 2) INFORMATION FOR SEQ ID NO: 1653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653

	TGTGTTTCATT	CAGGAGCTGA	TTGTGAGTAC	CCCGGAGATT	TTCCTGCGAT	50
	TGCGCATGAA	GCAAGCGCTG	ACGTCCATCT	AGAACAACAT	CGCCAAGGCT	100
10	CACGGTGGTT	ACTCCGTGTT	CTGCGGTGTC	GGCGAGCGTA	CTCGTGAGGG	150
	TAACGATTTG	TACCACGAAA	TGCAGGAGAC	CGGTGTCATC	AACCTCGAGG	200
	GCGAGTCCAA	GGTCGCCCTT	GTCTTCGGTC	AGATGAACGA	GCCCCCGGGA	250
	GCCCGTGCCC	GTGTCGCCCT	TACTGGTCTT	ACCGTCGCTG	AGTAAGTTTT	300
	GACAACCAGA	AGCGAGTATT	GCCACAATTA	CTGACTAAAA	ATCAAGATAT	350
15	TTCCGTGACG	AGGAGGGCCA	GGATGTGCTT	CTCTTCATTG	ACAACATTTT	400
	CCGTTTCACC	CAGGCCGGTT	CTGAGGTGTC	CGCTCTTCTC	GGCCGTATTC	450
	CCTCTGCCGT	CGGTTACCAG	CCCCTCTCTG	CCGTCGACAT	GGGTATGATG	500
	CAGGAGCGTA	TCACCACCAC	CCAGAAGGGT	TCCATCACTT	CCGTC	545

20

2) INFORMATION FOR SEQ ID NO: 1654

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 564 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium moniliforme*

(B) STRAIN: WSA-213

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654

	TGTGTTTATT	CAGGAGCTCA	TCAACAACAT	CGCCAAGGCC	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CCCGTGAGGG	TAACGATCTG	100
40	TACCACGAAA	TGCAGGAGAC	TTCCGTTATT	CAGCTTGATG	GCGAGTCCAA	150
	GGTTGCCCTG	GTTTTCGGTC	AGATGAACGA	GCCCCCTGGA	GCTCGTGCCC	200
	GTGTCGCTCT	TACCGGGTAA	GTTGATAGAT	AGTGCCTTCC	CTTCCTGTTT	250
	CAACACCTCA	ACACCACCAC	TCCCCAAGAC	ATTGCTACTC	ATACTGCACC	300
	ATGATATTAT	ATTTACGCCT	CTTGACGCT	AGCTAATGTT	GTATCGACAG	350
45	TTTGACTGTT	GCTGAGTACT	TCAGAGACGA	GGAGGGTCAG	GACGTGCTGC	400
	TTTTCATTGA	CAACATTTTC	CGATTCACTC	AGGCCGGTTC	CGAGGTGTCT	450
	GCCCTTCTCG	GTCGTATCCC	CTCTGCCGTC	GGTTACCAGC	CCACTCTGGC	500
	CGTCGACATG	GGTGGTATGC	AGGAGCGTAT	TACCACCACC	ACCAAGGGTT	550
	CCATTACCTC	AGTC				564

50

2) INFORMATION FOR SEQ ID NO: 1655

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 776 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655

15 CGTACCGCGC GTGTACGAGG CTCTTGAGGT ACAAATGGT AGTGAGAATC 50
 TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATTGT TCGTACCATC 100
 GCCATGGGTT CTTCCGACGG TCTGCGTCGC GGTCTGGAAG TCAAAGACCT 150
 CGAGCATCCG ATCGAAGTCC CGGTAGGTAA AGCAACGCTG GGTCGTATCA 200
 20 TGAACGTACT GGGCCAACCG GTAGACATGA AAGGCGACAT CGGCGAAGAA 250
 GAGCGTTGGG CGATTCACCG CGCAGCGCCT TCCTACGAAG AGTTGTCAAA 300
 CTCTCAGGAA CTGCTGGAAA CCGGCATCAA AGTTATCGAC CTGATGTGTC 350
 CGTTTGCGAA GGGCGGTAAA GTTGGTCTGT TCGGTGGTGC GGGTGTAGGT 400
 AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA TCGAGCACTC 450
 25 CGGTTACTCC GTGTTTGCGG GCGTAGGTGA ACGTACTCGT GAGGGTAACG 500
 ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGATAA AGTATCCCTG 550
 GTGTATGGCC AGATGAACGA GCCGCCGGGA AACCGTCTGC GCGTTGCGCT 600
 GACCGGCCTG ACCATGGCTG AGAAGTTCCG TGACGAAGGT CGTGACGTTC 650
 TGCTGTTCGT CGATAACATC TATCGTTACA CCCTGGCCGG TACTGAAGTA 700
 30 TCCGCACTGC TGGGTCGTAT GCCTTCAGCG GTAGGTACC AGCCGACTCT 750
 GCGGAAGAG ATGGGCGTTC TGCAGG 776

35 2) INFORMATION FOR SEQ ID NO: 1656

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Microsporum audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656

50 GTGTTTCATCC AGGAGTTGAT TGTAAGTGAT TATATTCCTC TAGAAAGAAA 50
 TGTTTTGAAC AAAAGTCTCG AATTAGAAAA TTCTTTTCAG ATACTAATTT 100
 ACTATAGAAC AACATTGCCA AGGCTCACGG TGGTTACTCC GTCTTCACCG 150

5 GTGTCGGAGA GCGAACCCGT GAAGGAAACG ATCTGTACCA TGAAATGCAG 200
 GAAACTCGTG TCATCCAAC T GATGGCGAG TCCAAGGTCG CCCTGGTCTT 250
 CGGTCAGATG AACGAGCCCC CAGGTGCCCCG TGCCCGTGTT GCTCTTACTG 300
 GTTTGACCAT TGCTGAGTAC TTCCGTGATG AGGAAGGTCA AGACGGTATG 350
 5 TTCTTTAAAT TAGATATCTT CTGGAGAAAC AGCGTCTAAC AAATTCTTCC 400
 AGTGCTTCTC TTCATCGACA ACATCTTCCG TTTCACTCAG GCTGGTTCCG 450
 AAGTGTCTGC CCTGCTTGGT CGTATTCCAT CTGCCGTCGG TTACCAACCC 500
 ACTCTTGCCG TCGACATGGG TGGTATGCAG GAACGTATTA CCACCACCAA 550
 10 GAAGGGATCC ATTACCTCCG TC 572

2) INFORMATION FOR SEQ ID NO: 1657

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Obesumbacterium proteus*
 25 (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657

30 GCCTAAAGTG TATAACGCAC TTGAGGTGAA AGGCGGTGCC ACTAAACTGG 50
 TACTGGAAGT TCAGCAGCAG CTAGGCGGCG GCGTTGTACG CTGTATCGCT 100
 ATGGGTACTT CTGACGGTCT GCGTCGCGGA CTGGACGTTG TTGACCTGGA 150
 GCACCCGATT GAAGTCCCAG TAGGTAAAGC GACCTTAGGC CGCATTATGA 200
 ACGTACTGGG TGAGCCAATT GATATGAAGG GTGATATCGG CGAAGAAGAT 250
 CGCTGGGCTA TTCACCGTGA AGCTCCAAGC TACGAAGAAC TGTCTAACTC 300
 35 GCAAGAACTG CTGGAAACCG GTATCAAGGT AATGGACTTG ATTTGTCCGT 350
 TCGCTAAGGG CGGTAAAGTC GGTCTGTTCG GTGGTGCGGG TGTTGGTAAA 400
 ACAGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG AGCACTCAGG 450
 TTA CTCTGTA TTTGCCGGCG TGGGTGAACG TACTCGTGAG GGTAACGACT 500
 TCTACCACGA AATGACCGAC TCCAACGTAT TGGACAAAGT ATCACTGGTT 550
 40 TATGGCCAGA TGAACGAGCC ACCAGGAAAC CGTCTGCGCG TTGCGCTGAC 600
 CGGTCTGACT ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT GACGTACTGC 650
 TGTTCATCGA TAACATCTAC CGTTATACCT TGGCCGGTAC CGAAGTATCT 700
 GCACTGCTGG GTCGTATGCC TTCTGCGGTA GGTATCAGC CAACGCTGGC 750
 45 GGAAGAGATG GGTGTTCTGC AAGAACGTAT CACCTCTACC 790

2) INFORMATION FOR SEQ ID NO: 1658

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

(B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658

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10 TGTCTTCATT CAGGAGCTTA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
   ACTCCGTCTT CACTGGTGTG GGAGAGCGCA CTCGTGAGGG AAACGACTTG      100
   TATCACGAGA TGCAAGAGAC TTCCGTTATC CAGCTCGAAG GCGAATCCAA      150
   GGTTGCCCTC GTCTTCGGTC AAATGAACGA GCCTCCGGGT GCTCGTGCTC      200
15 GTGTTGCTCT CACCGGTCGT AAGTGCTCCT TCCCAGATTT CTCTTCCCCA      250
   GTTCTGGAC  CCACTTTTTC CTTCCACCAC CATTCTACTG GGTAGGACCA      300
   AGATAGCACT GCCTATTCTG GTGCCTTCCT ACCGCCTACT CTACTGCCTA      350
   TTCCACCACC TTTTCTACCG CCTCTTCTAC TTGCTATTGT ATACTAACTT      400
   ACTCAAACAG TTACTATTGC TGAGTACTTC CGTGACGCTG AGGGCCAGGA      450
20 TGTGCTTCTC TTCATCGACA ACATTTTCCG TTTCACCCAG GCCGGTTCCG      500
   AGGTGTCCGC TCTTCTCGGT CGTATCCCCT CCGCCGTCGG TTACCAGCCC      550
   ACCCTTGCCG TCGACATGGG TGGTATGCAG GAGCGTATCA CCACCACCAA      600
   GAAGGGATCC ATTACCTCCG TC                                     622

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25

2) INFORMATION FOR SEQ ID NO: 1659

(i) SEQUENCE CHARACTERISTICS:

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30 (A) LENGTH: 794 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659

```

   GACGCTGTAC CTCAGGTGTA CGATGCACTG ACAGTTGAGG GTGCTGAGCT      50
   GGTACTGGAA GTGCAGCAGC AGCTGGGTGG TGGTGTGTGTT CGCTGTATCG      100
45 CGATGGGTGC CTCTGATGGC CTCAAGCGCG GTCTGAAAGC GCACAATACT      150
   GGTGCTCCTA TCACTGTACC GGTGGGTGTG GAAACACTGG GCCGGATCAT      200
   GGATGTGTTG GGTAACCCGA TTGACCAGAA AGGTCCAATC GGTGAACAAG      250
   ATCGCTGGGT GATCCACCGT GAAGCACCAA GCTACGAAGA TCAGGCTAAC      300
   AGCACTGAAC TGCTGGAAAC CGGTATCAAG GTTATCGACC TGGTATGCCC      350
50 GTTTGCGAAA GGCGGTAAAG TCGGTCTGTT CGGTGGTGCC GGTGTAGGTA      400
   AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC      450
   GGTTATTCCG TGTTTGCGGG CGTGGGTGAG CGTACCCGTG AAGGTAACGA      500
   CTTCTACCAC GAAATGACAG ACTCCAACGT ACTGGACAAA GTATCCCTGG      550

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	TGTACGGTCA	GATGAACGAG	CCGCCAGGTA	ACCGTCTGCG	CGTAGCACTG	600
	ACCGGCCTGA	CCATTGCGGA	GAAATTCCGT	GATGAAGGTC	GTGACGTACT	650
	GCTGTTTCATC	GATAACATCT	ACCGTTATAC	CCTGGCGGGG	ACCGAAGTAT	700
	CGGCACTGCT	GGGCCGTATG	CCTTCTGCGG	TAGGTTATCA	GCCAACGCTG	750
5	GCGGAAGAGA	TGGGTGTACT	GCAAGAGCGT	ATTACCTCTA	CCCG	794

2) INFORMATION FOR SEQ ID NO: 1660

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660

25	AGGTATATGA	CGCTSTGAAG	ATCACAGGTG	AAGGCGCCTG	TAATGGTTTG	50
	GTGCTGGAAG	TTCAGCAACA	GCTAGGCGGT	GGTGTAGTTC	GTACTATCGC	100
	TATGGGTTCT	TCTGATGGTC	TGCGTCGTGG	TCTTGAGGTT	GTTAACTCAG	150
	GTTACCTAT	TTCTGTTCCT	GTTGGTACCG	CCACGCTTGG	CCGTATCATG	200
	AACGTATTAG	GTGAGCCTAT	TGATGAAGCG	GGTCCAATCG	GTGAAGAAGA	250
30	GCGTTATGTT	ATTCACCGTG	CAGCACCTTC	ATATGAAGAT	CAATCGAACA	300
	CTACTGAAC	GTTAGAGACA	GGTATCAAGG	TTATTGACCT	TGTTTGTCCA	350
	TTCGCTAAGG	GTGGTAAAGT	AGGTCTGTTC	GGTGGTGCGG	GTGTTGGTAA	400
	AACAGTTAAC	ATGATGGAAC	TGATTAACAA	CATCGCTAAA	GCTCACTCGG	450
	GTCTTTCGGT	GTTCCGCCGT	GTGGGTGAAC	GTAATCGTGA	AGGTAACGAC	500
35	TTCTACTACG	AGATGAAAGA	TTCTGGCGTT	CTCGACAAAG	TGGCCATGGT	550
	TTATGGTCAG	ATGAACGAGC	CACCAGGAAA	CCGTTTACGC	GTAGCACTGT	600
	CAGGTCTGAC	AATGGCTGAG	AAGTTCCGTG	ACGAAGGTCG	TGACGTATTG	650
	TTGTTTCGTTG	ACAACATCTA	CCGTTATACC	TTAGCCGGTA	CTGAAGTATC	700
	TGCACTGTTA	GGCCGTATGC	CTTCTGCGGT	AGGTTATCAA	CCAACATTGG	750
40	CTGAAGAAAT	GGGCGTTCTG	CAAGAGCGTA	TACTTCAAC	TAAGACGGG	799

2) INFORMATION FOR SEQ ID NO: 1661

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661

TGGGAAGCGA AAATCCTG

18

5.

2) INFORMATION FOR SEQ ID NO: 1662

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 774 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662

	CTATGCCTCA	AACTAGAGAG	CATATCTTGC	TATCTCGCCA	AGTAGGCGTT	50
	CCATATATCG	TTGTATTTAT	GAACAAAGCC	GATATGGTCG	ATGACGCTGA	100
25	GCTTCTTGAG	CTAGTCGAGA	TGGAAATTCG	CGAGCTTCTT	AACGAGTACA	150
	ACTTCCCTGG	CGATGATACT	CCTATCATAT	CAGGTTCTGC	TCTTAAAGCC	200
	CTCGAAGAGG	CTAAAGCAGG	CGTTGATGGC	GAGTGGTCAG	CAAAAGTTCT	250
	TGAGCTTATG	GATAAAGTCG	ATGAGTATAT	CCCAACTCCA	GTTCGTGCTA	300
	CCGATAAAGA	CTTCCTGATG	CCTATCGAAG	ACGTTTTCTC	TATCTCAGGT	350
30	CGTGGAACGG	TCGTTACTGG	TAGGATCGAA	AAAGGTGTCG	TAAAAGTTGG	400
	CGATACTATC	GAGATCGTTG	GTATCAAACC	TACTCAAAC	ACGACAGTTA	450
	CTGGCGTTGA	GATGTTTAGG	AAAGAGATGG	AACAAGGCGA	GGCCGGTGAT	500
	AACGTAGGTG	TTCTTTTAAG	AGGTACTAAA	AAAGAAGACG	TCGAGCGCGG	550
	CATGGTTCTT	TGTAAGCCAA	AATCAATCAC	TCCTCATACA	AAATTTGAGG	600
35	GTGAGGTTTA	TATCCTAACA	AAAGAGGAAG	GCGGACGCCA	CACTCCATTC	650
	TTTAACAAC	ATAGACCACA	ATTTTATGTA	AGAACAACAG	ACGTTACAGG	700
	TTCTATCACA	CTTCCAGAAG	GAAGTGAAG	GGTTATGCCT	GGAGATAATG	750
	TCAGAATTTT	CGTTGAACTC	ATCG			774

10

2) INFORMATION FOR SEQ ID NO: 1663

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*

(B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663

5	TTCTGCGGCT	GACGGCCCAA	TGCCACAAAC	TAGAGAGCAC	ATCTTGCTAT	50
	CTCGCCAAGT	AGGCGTTCCG	TATATCGTTG	TTTTTATGAA	CAAAGCCGAT	100
	ATGGTCGATG	ATGCCGAGCT	TCTTGAGCTG	GTTGAGATGG	AGATTCGCGA	150
	GCTTCTAAAC	GAGTATGATT	TCCCTGGTGA	CGATACTCCA	ATCGTAGCAG	200
	GCTCTGCTCT	TCAAGCTCTT	AATGAAGCCA	AAGCCGGAAC	AGAAGGCGAG	250
10	TGGTCTGCAA	AAATTCTTGA	GCTTATGGCT	AAAGTTGACG	AGTATATCCC	300
	GACTCCGGTT	CGTGCAACGG	ATAAAGACTT	CTTGATGCCT	ATTGAGGACG	350
	TTTTCTCTAT	CTCCGGTCGC	GGCACCGTCG	TTACCGGCAG	AATCGAAAAA	400
	GGTATCGTAA	AAGTCGGTGA	TACTATCGAG	ATCGTAGGTA	TCCGCGATAC	450
	TCAAACAAC	ACCGTTACCG	GCGTTGAGAT	G TTCAGAAAA	GAGATGGATC	500
15	AAGGCGAAGC	GGGCGATAAC	G TAGGCGTTC	TTCTAAGAGG	CACTAAAAAA	550
	GAAGACGTTG	AGCGCGGTAT	GGTTCCTTGC	AAACCTAAAT	CAATCACTCC	600
	TCACACTAAA	TTTGAGGGAG	AGGTTTATAT	CTTAACTAAA	GAGGAAGGCG	650
	GACGCCATAC	TCCATTCTTT	AATAACTATA	GACCGCAGTT	TTATGTAAGA	700
	ACTACCGACG	TTACCGGTTC	TATCACTCTT	CCGGAAGGAA	CAGAGATGGT	750
20	TATGCCTGGC	GATAACTTAA	AGATAAGCGT	TGAGCTTATC	G	791

2) INFORMATION FOR SEQ ID NO: 1664

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Fonsecaea pedrosoi*
- (B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664

40	CGACGGACAG	ATGCCCCAGA	CCAGGGAGCA	CTTGCTCCTC	GCCCGCCAGG	50
	TCGGTGTCAA	GCGCATTGTC	GTCTTCGTCA	ACAAGGTCGA	TGCCATTGAG	100
	GACAAGGAGA	TGTTGGAGCT	CGTCGAGATG	GAGATGCGTG	AGCTTCTCTC	150
	CAGCTACGGC	TTCGAGGGTG	ACGACACTCC	CATCGTCATG	GGTTCCGCCC	200
	TTTGCGCCAT	TGAGGGCCGC	GAGCCCGACA	TTGGTGTCTG	GAAGATTGAC	250
45	GAGCTCCTCG	AGCACGTCGA	CACCTGGATC	CCCACCCCCG	AGCGTGACAT	300
	CGCCAAGCCT	TTCCTCATGT	CCGTTGAGGA	CGTCTTCTCC	ATTCCC GGCC	350
	GTGGTACCGT	CGCTTCTGGC	CGTGTCGAGC	GTGGTGTCTT	GAAGAAGGAT	400
	TCCGAAGTCG	AGCTTGTCGG	CAAGAACAAG	AACCCCATCA	AGACCAAGGT	450
	TACCGACATC	GAGACCTTCA	AGAAGTCTTG	CGACGAGTCC	CGCGCTGGTG	500
50	ACA ACTCCGG	TCTCCTTCTC	CGTGGTGTCA	AGCGTGACGA	TGTCCTCCGT	550
	GGCATGGTCG	TTGTCCAGCC	CGGCACCACC	AAGGCCCACA	AGAAGTTCCT	600
	TGCCTCCATG	TACGTCCTCA	CCAAGGAGGA	GGGTGGCCGC	CACACTGGTT	650
	TCGCCAACAA	CTACAAGCCC	CAGATGTTCA	TCCGTACCGC	CGATGAGGCC	700

GCCACTCTTA	CCTGGCCCCGA	GGGTACCGAG	GAGGACAAGA	TGGTCATGCC	750
CGGTGACAAT	GTCGAGATGA	TCTGCGAGAT	CCACAAGCCC	ATTGCCGTCG	800
AGCAAGGCCA					810

5

2) INFORMATION FOR SEQ ID NO: 1665

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665

CAGTACAGGT AGACTTCTG

19

20

2) INFORMATION FOR SEQ ID NO: 1666

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporum audouinii*
 35 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666

ATGATTGCGA	AACCTACTTG	CTGTGGAAGA	ATTTGGATAT	TCTAACATTT	50
40 CTCTAGGCCT	CAAACCAGAG	AGCATCTGCT	CCTTGCCCGC	CAGGTCGGTG	100
TTCAGAAGCT	CGTCGTTTTC	GTTAACAAGG	TCGACGCTGT	TGAGGACCCA	150
GAGATGTTGG	AACTTGTCGA	GCTAGAGATG	CGTGAGCTGC	TCAGCCACTA	200
TGGTTTCGAG	GGTGAGGAGA	CCCCAATCAT	TTTTGGCTCT	GCTCTCTGCG	250
CCCTTGAATC	TCGACGACCA	GAATTGGGTG	TTGAGAAGAT	CGATGAGCTA	300
45 TTGAACGCTG	TGGATACCTG	GATTCCCACC	CCAGAGCGTG	CCACTGATAA	350
GCCTTTCCTT	ATGTCCATTG	AGGAAGTTTT	CTCCATCTCT	GGTCGTGGTA	400
CCGTCGTTTC	CGGTCGTGTC	GAGCGTGGTA	TCCTCAAGAA	GGACTCTGAT	450
GTCGAAATTG	TGGGTGGATC	TGATACACCC	ATCAAGACGA	AGGTCACCGA	500
CATTGAAACC	TTCAAGAAGT	CTTGTGACGA	ATCCCGAGCT	GGTGACAACCT	550
50 CCGGTCTACT	TCTCCGAGGT	GTCAAGCGTG	AGGACTTGAG	ACGTGGAATG	600
GTTGTTGCTG	CTCCCGGATC	GACCAAGGCT	CATACCGACT	TCATGGTCTC	650
CCTTTATGTT	CTGACCGAGG	CTGAGGGTGG	CCGTTCCAAT	GGATTCACCC	700
ACAAGTACCG	CCCACAGATG	TTCATCCGTA	CTGCCGGTAT	GTAAACCCTT	750

TTTCTACCAT TCACTTTGTT TCACCACTGA CTTGTATACT TTACCGCAGA 800
CGAAGCCGCA TCTTTCAGCT GGCCTGGAGA GGATCAAGAC AAGAAGGCCA 850
TGCCTGGTGA CAATGTCGAG ATGATTTGCA AGACCCTC 888

5

2) INFORMATION FOR SEQ ID NO: 1667

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 793 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
(B) STRAIN: ATCC 24292

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667

ATGCCGCAGA CCCGCGAGCA CTTGCTGCTC GCCCGTCAGG TCGGTGTCCA 50
GAAGATCGTT GTTTTCGTCA ACAAGGTTGA TGCTATCGAC GACCCGGAGA 100
25 TGCTGGAGCT TGTCGAGATG GAGATGCGTG AACTTCTCAG CACATACGGT 150
TTCGAGGGTG ACGAGACCCC TGTTATTATG GGCTCCGCGC TCATGGCTCT 200
CAACAACCAG CGCCCCGAGA TTGGTCAACA GAAGATTGAT GAACTCATGG 250
CCGCTGTCGA CGAGTGGATC CCTACTCCCC AGCGTGACCT CGACAAGCCT 300
TTCCTGATGT CTGTTGAGGA TGTCTTCTCC ATTGCTGGCC GTGGTACCGT 350
30 TGTGTCCGGC CGTGTGGAGC GCGGTACCCT CAAGCGTGAT GAGGAAGTCG 400
AGCTTGTCGG CAAGGGTGTC GACCCCATCA AGACCAAGGT CACCGATATC 450
GAGACTTTCA AGAAGTCCTG CGAGGAGGCT CAGGCTGGTG ACAACTCTGG 500
TCTTCTGATC CGTGGTGTCC GCCGCGAGGA TGTTCTGTCG GGTATGGTTG 550
TCTCCAAGCC CGGCACCGTC AAGTCTCACA CTCAGTTCCT GGCCTCGCTT 600
35 TACGTTCTCA CCAAGGAGGA GGGTGGTCGC CACACTGGTT TCGGCGAGCA 650
CTACCGTCCC CAGCTCTACC TCCGTACCTC AGACGAGTCT GTCGATCTGA 700
CCTTCCCCGA GGGAAGTGAG GATCACCCT CCAAGATCGT CATGCCTGGT 750
GACAACATCG AGATGGTCGT CACGATGACT CACGCCAACG CTA 793

40

2) INFORMATION FOR SEQ ID NO: 1668

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 891 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 KL1699
(C) ACCESSION NUMBER: J01717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668

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5  AACATGATCA CCGGTGCTGC GCAGATGGAC GCGCGCATCC TGGTAGTTGC      50
   TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC      100
   GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG      150
   GTTGATGACG AAGAGCTGCT GGAACTGGTT GAAATGGAAG TTCGTGAACT      200
10  TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC GTTCGTGGTT      250
   CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG      300
   GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT      350
   TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC      400
   GTGGTACCGT TGTTACCGGT CGTGTAAGAC GCGGTATCAT CAAAGTTGGT      450
15  GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT CTACCTGTAC      500
   TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT GCTGGTGAGA      550
   ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT      600
   CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC      650
   TGAAGTGTAC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT      700
20  TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA CGTGACTGGT      750
   ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG GCGACAACAT      800
   CAAAATGGTT GTTACCCTGA TCCACCCGAT CCGCATGGAC GACGGTCTGC      850
   GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C              891

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2) INFORMATION FOR SEQ ID NO: 1669

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30  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 805 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

35  (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Saksenaea vasiformis
          (B) STRAIN: ATCC 60625

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40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669

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45  TCCTCGTGGT CGCCGCCACC GACGGCCCGA TGCCGCAGAC CAAGGAGCAC      50
   GTGCTCCTGG CCCGCCAGGT CGGCGTTCCG TACATCGTCG TCGCCCTCAA      100
   CAAGGCCGAC ATGGTGGACG ACGAGGAGAT CCTGGAGCTC GTCGAGCTCG      150
   AGGTCCGTGA GTCCTCTCC GAGTACGAGT TCCCGGGCGA CGACGTTCCC      200
   GTCGTCAAGG TCTCCGCTCT GAAGGCCCTC GAGGGCGACA AGGAGTGGGG      250
   CAACTCGGTT CTCGAGCTCA TGAACGCCGT CGACACGGCG ATCCCCGAGC      300
   CCGAGCGTGA CGTCGACAAG CCGTTCCTCA TGCCGATCGA GGACGTCTTC      350
50  ACGATCACCG GTCGCGGTAC GGTGCTCACC GGCCGTATCG AGCGTGGTGT      400
   CCTGAAGGTC AACGAGACCG TCGACATCAT CGGCATCAAG ACCGAGAAGA      450
   CCACCACCAC GGTCACCGGC ATCGAGATGT TCCGGAAGCT CCTCGACGAG      500
   GGCCAGGCCG GTGAGAACGT CGGTCTGCTC CTCCGTGGCA TCAAGCGCGA      550

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	GGACGTCGAG	CGCGGCCAGG	TCATCATCAA	GCCGGGCTCG	GTCACGCCGC	600
	ACACGGAGTT	CGAGGCGCAG	GCCTACATCC	TGTCCAAGGA	CGAGGGTGGC	650
	CGCCACACGC	CGTTCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGTAC	700
	GACGGACGTG	ACCGGCGTGG	TGACCCTCCC	CGAGGGCACC	GAGATGGTCA	750
5	TGCCGGGTGA	CAACACCGAG	ATGAAGGTGG	AGCTCATCCA	GCCCGTCGCC	800
	ATGGA					805

10 2) INFORMATION FOR SEQ ID NO: 1670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 935 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670

25	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACA	GATGAAAGGA	50
	TTTGACGTTT	CTAACATCAG	TCTAGGCCTC	AGACCAGAGA	ACATTTGCTC	100
	CTTGCCCGCC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	TTAACAAGGT	150
	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	CTTGAAATGC	200
30	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	CCCCATCATT	250
	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	AGCTTGGTGT	300
	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	ATCCCCACCC	350
	CAGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	GGAAGTGTTT	400
	TCTATCTCTG	GTCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	AGCGTGGTAT	450
35	CCTCAAGAAG	GATTCGGACG	TCGAAATTGT	TGGTGGCTCT	ACCACCCCTA	500
	TCAAGACCAA	GGTCACCGAT	ATCGAAACCT	TCAAGAAGTC	CTGCGATGAA	550
	TCTCGAGCTG	GTGACAACTC	TGGTCTCCTT	CTCCGAGGTA	TCAAGCGTGA	600
	GGACTTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	ACCAAGGCTC	650
	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	TGAGGGTGGT	700
40	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	TCATCCGTAC	750
	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	ATCATTGCTA	800
	ACTTGTATTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	TGGCCTGGAG	850
	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCTG	GATGATTTCG	900
45	AAGACCCTCC	ACCCCATTCG	TGCCGAGGCT	GGCCA		935

2) INFORMATION FOR SEQ ID NO: 1671

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter aerogenes*

(B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671

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10  ACGATGCCCT TGAGGTACAG AATGGTAATG AGAGCCTGGT GCTGGAAGTT      50
    CAGCAGCAGC TCGGCGGTGG CGTAGTCCGT GCTATCGCCA TGGGTTCCTC      100
    CGACGGTCTG CGTCGTGGTC TGGAAAGTTAA AGACCTTGAG CACCCGATCG      150
    AAGTCCCGGT AGGTAAAGCG ACTCTGGGCC GTATCATGAA CGTCCTGGGT      200
15  CAGCCGATCG ACATGAAAGG CGACATCGGC GAAGAAGAAC GTTGGGCTAT      250
    CCACCGCGCG GCGCCTTCCT ATGAAGAGCT GTCCAGCTCT CAGGAACTGC      300
    TGGAAACCGG CATCAAAGTT ATCGACTTGA TGTGTCCGTT CGCTAAGGGC      350
    GGTAAGATTG GTCTGTTCGG TGGTGCGGGT GTAGGTAAAA CCGTAAACAT      400
    GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT TACTCCGTGT      450
20  TTGCGGGCGT TGGTGAGCGT ACTCGTGAGG GTAACGACTT CTATCACGAA      500
    ATGACCGACT CCAACGTTCT GGATAAAGTA TCCCTGGTTT ACGGCCAGAT      550
    GAACGAGCCG CCGGGAACC GTCTGCGCGT TGCCTGACC GGCCTGACCA      600
    TGGCTGAGAA ATTCCGTGAC GAAGGTCGTG ACGTTCTGCT GTTCGTCGAT      650
    AACATCTATC GTTACACCCT GGCCGGTACT GAAGTATCTG CACTGCTGGG      700
25  CCGTATGCCT TCAGCGGTAG GTTATCAGCC GACTCTGGCG GAAGAGATGG      750
    GCGTTCTGCA GGAACGTATC AC                                     772

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30 2) INFORMATION FOR SEQ ID NO: 1672

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1401 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bordetella pertussis*

(B) STRAIN: Tohama 1

(C) ACCESSION NUMBER: Genome project

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1672

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    ATGAGCAACG GAACCATCGT TCAGTGCATC GGCGCCGTGG TGGATATTCA      50
    GTTCCCCCGC GATAACATGC CCAAGATCTA CGAAGCGCTC ACCCTGGTCG      100
    ACGAGGGTTC CTCGTTTCGCC GAGAAGGGCT TGACGCTGGA AGTGCAACAA      150
50  CAGCTGGGCG ACGGCGTGGT GCGTACCATC GCGCTGGGTT CCAGCGACGG      200
    GCTGCGCCGC GGCATGCAAG TGGCCGGCAC CGGCGCACCG ATCTCGGTGC      250
    CCGTGGGCCA CGGCACCCTG GGCCGCATCA TGGACGTGCT GGGCCGTCCC      300
    ATCGACGAAG CCGGTCCCAT CGCCTCCGAC GAGAAGCGCG CCATCCACCA      350

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	GCCCGCGCCC	CGTTTCGACG	AGCTGTCGCC	GTCGGTCGAG	CTGCTGGAAA	400
	CCGGCATCAA	GGTTATCGAC	CTGGTGTGCC	CGTTCGCCAA	GGGCGGCAAG	450
	GTCGGCCTGT	TCGGCGGCGC	CGGCGTGGGC	AAGACCGTCA	ACATGATGGA	500
	ACTGATCAAC	AACATCGCCA	AGCAGCACAG	CGGCTTGTCG	GTGTTGCGCCG	550
5	GCGTGGGCGA	GCGTACCCGC	GAAGGCAACG	ACTTCTACCA	CGAAATGGAA	600
	GAGTCGAACG	TTCTGGACAA	GGTGGCCATG	GTGTTGCGCC	AGATGAACGA	650
	GCCCCCGGGC	AACCGCCTGC	GCGTGGCGCT	GACCGGCCTG	ACCATGGCCG	700
	AGAAGTTCCG	CGACGAAGGC	CGTGACATCC	TGTTCTTCGT	CGACAACATC	750
	TACCGCTACA	CCCTGGCCGG	TACCGAAGTG	TCGGCGCTGC	TGGGCCGTAT	800
10	GCCGTCGGCG	GTGGGCTACC	AGCCTACGCT	GGCCGAGGAA	ATGGGCGTGC	850
	TGCAAGAGCG	CATCACCTCG	ACCAAGACCG	GTTGATCAC	CTCGATCCAG	900
	GCCGTGTACG	TGCCTGCCGA	CGACTTGACC	GACCCGTCGC	CCGCCACGAC	950
	CTTCCAGCAC	TTGGACTCGA	CCGTGCTGCT	GTCGCGTGAC	ATCGCTGCGC	1000
	TGGGCATCTA	TCCCGCCGTG	GACCCGCTGG	ATTCCTCCAG	CCGCCAGCTC	1050
15	GACCCGCAAG	TCGTGGGCGA	AGAGCACTAC	CAGGTGGCCC	GTGGCGTGCA	1100
	GCAGACGCTG	CAGCGCTACA	AGGAACTGCG	CGACATCATC	GCGATTCTGG	1150
	GCATGGACGA	ACTGTCGCCG	GAAGACAAGC	AGGCCGTGGC	CCGCGCGCGC	1200
	AAGATCCAGC	GCTTCCTGTC	GCAGCCCTTC	TACGTGGCCG	AAGTGTTTAC	1250
	CGGCTCGCCG	GGCAAGTACG	TGTCGCTGGC	CGAAACGATC	CGTGGCTTCA	1300
20	AGATGATCGT	CGACGGCGAG	TGCGACGCGC	TGCCCAGACA	GGCGTTCTAC	1350
	ATGGTCGGCA	CGATCGACGA	GGCCTTCGAG	AAGGCCAAGA	AACTCCAATA	1400
	A					1401

25

2) INFORMATION FOR SEQ ID NO: 1673

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*
 (B) STRAIN: ATCC 9345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673

	CAGCTACCGA	CGGTCCAATG	GCTCAGACCC	GCGAGCACGT	TCTTCTTGCT	50
	CGCCAGGTTG	GCGTTCCACA	GATCATCGTT	GCTCTCAACA	AGGCTGACAT	100
	GGTTGACGAC	GAGGAAATCC	TCGAACTCGT	CGAAATGGAA	GTTGCTGAGC	150
45	TTCTCTCTTC	CCAGGAGTAC	CCAGGTGACG	ACCTCCCAGT	CGTCAAGATC	200
	TCGGCACTCA	AGGCTCTCGA	AGGCGATGCC	GAATGGAGCA	AGGCAATCGA	250
	AGATCTCATG	GAAGCTGTCG	ATACCTACTT	CGACGATCCA	GTGCGTGACC	300
	TCGATAAGCC	ATTCCTCATG	CCAATCGAAG	ACGTCTTCAC	CATCACCAGT	350
	CGTGGCACCG	TTGTTACCGG	CCGTGCAGAG	CGCGGTATGC	TCAACTTGAA	400
50	CGAAGAAGTT	GAAATCCTCG	GTATCCGTGC	ACCACAGAAG	ACAACCGTTA	450
	CCGGTATCGA	AATGTTCCAC	AAGTCGATGG	ATCACGCAGA	TGCAGGCGAA	500
	AACTGTGGTC	TTCTCCTCCG	TGGCACCAAG	CGCGAAGATG	TTGAACGTGG	550
	TCAGGTTGTT	GCCAAGCCAG	GCACCATCAC	CCCACACACC	AACTTCGAAG	600

CTCAGGTCTA	CGTGCTCGGT	AAGGAAGAAG	GTGGCCGTCA	CAACCCATTC	650
TTCTCCAAC	ACCGTCCACA	GTTCTACTTC	CGTACCACGG	ATGTTACCGG	700
CGTGATCACC	CTTCCAGAGG	GCACCGAAAT	GGTTATGCCA	GGCGACAACA	750
CCGACATGAC	AGTTGAGCTC	ATCCAGCCAA	TCGCTATGGA	AGAGGGC	797

5

2) INFORMATION FOR SEQ ID NO: 1674

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Butyrivibrio fibrisolvens*
- (B) STRAIN: ATCC 19171

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674

CTGATGGTCC	TATGCCACAG	ACCCGTGAGC	ACATCCTATT	AGCACGTCAG	50
GTAGGCGTAC	CATACATCAT	CGTATTCCTA	AACAAGTGCG	ATATGGTTGA	100
CGACGAGGAA	TTATTAGAGT	TAGTTGAGAT	GGACGTACGT	GATCTATTAA	150
ATCAGTACCA	GTTCCCAGGC	GACGACACTC	CAATCATCCG	TGGTTCAGCA	200
CTAGGTGCAT	TAAACGGCGA	AGAGAAGTGG	AAAGAGGCAA	TCTATCAGTT	250
AGCAGACACT	CTAGATTCAT	ACATTCCAGA	GCCAAAGCGT	GATATCGATG	300
ATCCATTCCT	ATTACCAATC	GAAGATATCT	TCTCAATCTC	AGGTCGTGGT	350
ACTGTAGTAA	CCGGCCGTGT	AGAGCGTGGT	ATTGTACACG	TAGGTGACGA	400
AGTTGAAATC	GTTGGTATTC	GTCCAACCAC	CAAGACCACT	GTAAGTGGCG	450
TTGAAATGTT	CCGTAAGTTA	CTAGACGAAG	GTCGTGCAGG	TGATAACGTT	500
GGTGTTCTAC	TACGTGGTAC	CAAGCGTGAT	GAGGTTGAGC	GTGGTCAGGT	550
TCTAGCTGCT	CCAGGCACAA	TCACTCCACA	CACCAAGTTC	ACTGGTCAGG	600
TTTACGTACT	AAGCAAGGAT	GAAGGTGGTC	GTCACACTCC	ATTCTTCAAG	650
GGCTACCGTC	CACAGTTCTT	CTTCCGTACA	ACCGATATTA	CCGGTTCCTAT	700
CGATCTGAAA	GAGGGCGTAG	AGATGGTAAT	GCCAGGTGAT	AACACCGACA	750
TGACCGTAAC	CCTAATCCAC	CCAGTAGCTA	TGGCT		785

40

2) INFORMATION FOR SEQ ID NO: 1675

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
 (B) STRAIN: ATCC 49349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675

5
 TGGGGCGATC TTGGTTGTTT CTGCTGCAGA TGGTCCTATG CCACAAACTA 50
 GAGAGCACAT TCTTCTTTCT CGTCAAGTAG GCGTTCCATA TATTGTTGTT 100
 TTTATGAATA AAGCAGATAT GGTGATGAT GCTGAGCTTT TAGAGTTAGT 150
 TGAAATGGAA ATTAGAGAAT TATTAAGCTC TTATGATTTC CCAGGCGATG 200
 10 ATACACCTAT TATTTCTGGT TCTGCTTTAA AAGCTCTTGA AGAAGCTAAA 250
 GCTGGACAAG ATGGTGAATG GTCAGCAAAA ATTATGGATC TTATGGCTGC 300
 AGTTGATAGT TATATTCCAA CTCCAACCTCG TGATACTGAA AAAGACTTCT 350
 TGATGCCAAT TGAAGACGTT TTCTCAATTT CAGGTCGTGG TACTGTTGTT 400
 ACAGGTAGAA TTGAAAAAGG TGTGTGAAAA GTAGGTGATA CTATCGAAAT 450
 15 CGTTGGTATT AAAGACACTC AAACAACAAC TGTAACAGGT GTTGAAATGT 500
 TCAGAAAAGA AATGGATCAA GGCGAGGCAG GAGATAACGT AGGTGTTCTT 550
 CTTCGTGGTA CTAAAAAAGA AGAAGTTATT CGCGGTATGG TTCTTGCTAA 600
 ACCAAAATCA ATTACTCCAC ACACTGACTT CGAAGCTGAA GTTTATATCT 650
 TAAATAAAGA TGAAGGTGGT AGACATACTC CATTCCTTAA CAACTATAGA 700
 20 CCACAGTTTT ATGTAAGAAC AACTGATGTT ACAGGTTCTGA TTAAATTAGC 750
 TGATGGTGTT GAAATGGTTA TGCCAGGTGA AAATGTGAGA ATTACTGTAA 800
 GCTTGATCGC TCCAGTAGCA CTTGAAGAAG GAACT 835

25

2) INFORMATION FOR SEQ ID NO: 1676

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*
 (B) STRAIN: ATCC 43675

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676

TTCTGCAGCA GACGGCCCTA TGCCACAAAC TAGAGAGCAT ATCTTACTTT 50
 CTCGTCAAGT AGGTGTACCA TATATTGTTG TTTTCATGAA CAAAGCTGAT 100
 ATGGTTGATG ATGCAGAATT ATTAGAATTA GTTGAAATGG AAATTAGAGA 150
 45 ATTACTAAGC TCTTATGATT TCCCAGGAGA TGATACTCCA ATTATTTTCAG 200
 GTTCAGCATT ACAAGCTCTT GAAGAAGCAA AAGCTGGTCA AGATGGTGAA 250
 TGGTCTAAAA AAATCTTAGA TCTTATGGCT GCAGTTGATG ATTATATTCC 300
 AACTCCGGCT CGTGATACAG ATAAAGATTT CTTGATGCCA ATCGAAGATG 350
 TTTTCTCAAT CTCAGGTCGT GGAAGTGTG TTACCGGTAG AATTGAAAAA 400
 50 GGTGTTGTAA AAGTTGGTGA TACTATAGAA ATCGTTGGTA TTAGAGACAC 450
 TCAAACAACC ACAGTTACTG GTGTTGAAAT GTTTAGAAAA GAAATGGATC 500
 AAGGTGAAGC TGGTGATAAT GTTGGTGTAT TACTTCGTGG AACTAAAAAA 550
 GAAGATGTTG AACGTGGTAT GGTTCCTTGCT AAACCAAAT CAATCACTCC 600

	ACATACTGAT	TTTGAAGCAG	AAGTTTATAT	CTTAAATAAA	GATGAAGGTG	650
	GTCGTCATAC	TCCATTCTTT	AATAATTATA	GACCGCAATT	TTATGTAAGA	700
	ACAACTGATG	TTACAGGTGC	TATTAAACTT	GCAGAAGGCG	TTGAGATGGT	750
	TATGCCAGGC	GATAATGATA	GAATTACTGT	AAGTCTTATT	GCTCCAGTTG	800
5	CACTTGAGGA	AG				812

2) INFORMATION FOR SEQ ID NO: 1677

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*
 (B) STRAIN: ATCC 35980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677

25	GCTATTCTTG	TATGTTTCAGC	TGCAGATGGT	CCAATGCCAC	AGACTAGAGA	50
	GCATATTCTA	CTATCAAGAC	AAGTTGGTGT	TCCATACATA	GTTGTTTTCT	100
	TAAATAAAGA	AGATATGGTT	GATGATGCTG	AGCTTATAGA	GTTGGTTGAA	150
	GTTGAGGTTA	GAGATTTATT	AAATGAATAT	GATTTCCCTG	GAGATGATAC	200
	TCCAATCGTA	ATAGGTTCTG	CTCTTAAAGC	TTTAGAAGAA	GCAAAAGCTG	250
30	GAACAGAGGG	TGAATGGTCT	GCTAAAATTA	TGAAACTTAT	GGATGCTGTT	300
	GATAGCTATA	TCCCAACTCC	AACAAGAGAT	ACAGATAAAG	ATTCCTTAT	350
	GCCAATCGAA	GATATCTTCT	CAATTTCTGG	TCGTGGTACA	GTTGTAACAG	400
	GTAGAATTGA	AAAAGGTGTA	GTAAAAGTTG	GCGAGACTAT	TGAGATAGTT	450
	GGTATTAGAC	CTACTCAAAC	AACAACAGTT	ACTGGTGTTG	AAATGTTTAG	500
35	AAAAGAGCTA	GATCAAGGTG	AAGCTGGAGA	TAATGTTGGT	ATCTTGTTAA	550
	GAGGTACAAA	AAAAGAAGAT	GTTGAAAGAG	GTATGGTTTT	ATGTAAACCA	600
	AAATCAATCA	CTCCTCACAA	GAAATTTGAA	GGCGAAGTTT	ATATTCTTAC	650
	AAAAGATGAA	GGTGGTAGAC	ATACTCCTTT	CTTTAGTAAC	TATAGACCAC	700
	AATTTTATGT	TAGAACAACA	GATGTAACAG	GTTCTATATC	TCTTCCTGAG	750
40	GGAACAGAGA	TGGATATGCC	TGGTGATAAT	GTAAAACCTTA	CAGTTGAACT	800
	TATAAACCCA	ATTGCTCTTG	AGCAAGGA			828

45 2) INFORMATION FOR SEQ ID NO: 1678

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter upsaliensis*

(B) STRAIN: ATCC 49815

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678

	CGATTTTGGT	TGTTTCTGCT	GCTGATGGTC	CTATGCCACA	AACTAGAGAG	50
	CACATTTTGC	TTTCTCGTCA	AGTGGGTGTT	CCTTATATCG	TAGTTTTTAT	100
10	GAATAAGGCT	GATATGGTTG	ATGATGCAGA	GCTTTTAGAA	TTGGTTGAAA	150
	TGGAAATTAG	AGAACTTTTA	AGCTCTTATG	ATTTCCCGGG	CGATGACACT	200
	CCTATCATTT	CAGGCTCTGC	TCTTCAAGCC	TTAGAAGAGG	CTAAGGCGGG	250
	ACAAGATGGC	GAGTGGTCAG	CTAAGATTTT	AGAGCTTATG	AAGGCAGTTG	300
	ATGAGTATAT	CCCAACTCCT	GTTCGCGATA	CTGAAAAAGA	TTTCTTGATG	350
15	CCTATTGAAG	ATGTTTTTTC	AATTTCTGGT	CGTGGAAGTG	TTGTAACAGG	400
	TAGAATTGAA	AAAGGTGTGG	TTAAAGTCGG	CGATACTATT	GAGATAGTAG	450
	GTATCAAAGA	TACTCAAAC	ACAACAGTTA	CAGGCGTTGA	GATGTTTAGA	500
	AAAGAAATGG	ATCAAGGTGA	GGCTGGCGAT	AATGTCGGTG	TGCTTTTAAG	550
	AGGAACAAAA	AAAGAAGATG	TTCTTCGTGG	TATGGTTCTT	GCAAAGCCTA	600
20	AATCTATCAC	TCCTCATACT	GATTTTGAAG	CAGAAGTTTA	TATTCTAAAT	650
	AAAGATGAGG	GCGGTCGCCA	TACTCCTTTC	TTTAACAATT	ATCGTCCGCA	700
	GTTTTATGTA	AGAACGACTG	ATGTAAGTGG	TTCTATTAAA	TTAGCTGATG	750
	GTGTTGAGAT	GGTTATGCCG	GGTGAAAATG	TAAGAATTAC	AGTTAGCCTT	800
	ATCGCTCCAG	TTGCACTTGA				820

25

2) INFORMATION FOR SEQ ID NO: 1679

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Globicatella sanguis*

40

(B) STRAIN: ATCC 51173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679

	CTGCAGCTGA	TGGTCCAATG	CCTCAAACAC	GTGAACATAT	CTTATTATCA	50
45	CGTCAAGTAG	GTGTTCCCTTA	CATGGTTGTC	TTCTTAAACA	AAGTTGACAT	100
	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	TGAAATGGAA	GTTCGTGATT	150
	TATTATCTGA	ATACGAATTC	CCTGGAGACG	ACGTTCCAGT	AATCGCTGGT	200
	TCAGCTTTAA	AAGCTTTAGA	AGGCGAAGAA	CAATATGAAG	CAAAAGTATT	250
	AGAATTAATG	GAAGCTGTAG	ATACATACAT	TCCAGAACCA	GTTCGTGATA	300
50	CTGAAAAACC	ATTCATGATG	CCAGTTGAAG	ATGTGTTCTC	AATCACAGGT	350
	CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	CGTGGACAAG	TTAAAGTTGG	400
	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	AGAAATTAGC	AAAACAACCTG	450
	TAACTGGTGT	TGAAATGTTC	CGTAAATTAT	TAGATTACGC	TGAAGCTGGA	500

	GATAACATTG	GTGCGTTATT	ACGTGGTGT	ACACGTGAAC	AAATCCAACG	550
	TGGTCAAGTA	TTAGCAAAAC	CAGGAACAAT	TACACCTCAT	ACTAAATTCG	600
	AGGCGGAAGT	TTACGTATTA	TCAAAAGAAG	AAGGTGGACG	TCATACTCCA	650
	TTCTTCGCTA	ACTACCGTCC	TCAATTCTAC	TTCCGTACAA	CTGACGTTAC	700
5	AGGTGTTGTA	GAATTACCAG	AAGGTACAGA	AATGGTAATG	CCTGGAGATA	750
	ACGTATCAAT	GACAGTTGAA	TTAATTCACC	CAA		783

10 2) INFORMATION FOR SEQ ID NO: 1680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus acidophilus*
 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680

25	GCTATCTTAG	TTGTTGCTGC	AACTGATGGT	CCTATGCCAC	AAACTCGTGA	50
	ACACATTTTG	CTTGCTCGTC	AAGTTGGTGT	TAACATACATC	GTAGTATTCT	100
	TGAACAAGTG	CGATTTAGTT	GACGACCCAG	AATTGATCGA	CTTGGTTGAA	150
	ATGGAAGTTC	GTGACTTGTT	GACTGAATAC	GATTACCCTG	GTGATGATAT	200
30	TCCAGTTGTT	CGTGGTTCAG	CATTAAAGGC	TTTACAAGGT	GACAAGGAAG	250
	CTCAAGACCA	AATCATGAAG	TTGATGGACA	TTGTTGATGA	ATACATCCCA	300
	ACTCCAGAAC	GTCAAACCTGA	CAAGCCATTC	TTGATGCCAG	TTGAAGACGT	350
	ATTCACATATC	ACTGGTCGTG	GTACTGTTGC	TTCAGGTCGT	ATCGACCGTG	400
	GTACTGTTAA	GGTCGGTGAC	GAAGTTGAAA	TCGTTGGTTT	GGTAGATAAA	450
35	GTTCTTAAGT	CAGTTGTTAC	TGGTTTGGA	ATGTTCCACA	AGACTTTGGA	500
	CTTAGGTGAA	GCCGGCGATA	ACGTTGGTGT	ATTGCTTCGT	GGTGTGACC	550
	GTGATCAAGT	TGTTTCGTGGT	CAAGTATTGG	CTGCACCCGG	CTCAATCCAA	600
	ACTCATAAGA	AGTTTAAGGC	ACAAGTTTAT	GTTTTGAAGA	AGGACGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCTCAGACTA	CCGTCCACAA	TTCTACTTCC	700
40	ACACCACTGA	TATTACTGGT	GAAATTGAAT	TGCCAGAAGG	TACTGAAATG	750
	GTTATGCCTG	GTGATAACAC	TGAATTCACT	GTTACTTTGA	TCAAGCCAGC	800
	TGCCATCGAA	AAGGGTACTA	AGT			823

45

2) INFORMATION FOR SEQ ID NO: 1681

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leuconostoc mesenteroides* subsp.
dextranicum
 (B) STRAIN: ATCC 19255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681

10	GCTGCAACTG	ATGGTCCTAT	GCCACAAACA	CGTGAACACA	TCTTGTTGGC	50
	ACGTCAAGTT	GGTGTTGACT	ACTTGGTTGT	CTTCTTGAAC	AAGACTGATT	100
	TGGTTGATGA	TGAAGAATTA	GTTGAATTGG	TTGAAATGGA	AGTTCGTGAA	150
	TTGTTGTCAG	AATATGACTT	CCCAGGTGAC	GATATTCCTG	TACTTAAGGG	200
	TTCAGCTTTG	AAGGCTTTGG	AAGGTGATCC	TGAACAAGTT	AAGGTTATCG	250
15	AAGAATTGAT	GGATACTGTT	GATTCATACA	TTCCAGAACC	AGCACGTGAA	300
	ACAGACAAGC	CATTCTTGAT	GCCTGTCGAA	GACGTCTTCA	CAATCACTGG	350
	TCGTGGTACA	GTTGCTTCTG	GTCGTGTTGA	CCGTGGTGTA	TTGACTACAG	400
	GAACTGAAAT	TGAAATCGTT	GGTTTGAAGG	ACGAAGTTCA	AAAGACTACT	450
	GTTACAGGTA	TCGAAATGTT	CCGTAAGACT	TTGGAAGAAG	CTCAAGCGGG	500
20	TGATAACATT	GGTGCATTGT	TGCGTGGTGT	TGATCGTAGC	AACATTGAAC	550
	GTGGTCAAGT	TTTGGCAAAG	CCAGGTTCAA	TTAAGACACA	CAAGAAGTTC	600
	AAGGCTGAAG	TTTATGTCTT	GACAAAGGAA	GAAGGTGGTC	GTCATACACC	650
	ATTCTTCACT	AACTACCGTC	CACAATTCTA	CTTCCACACA	ACTGATGTTA	700
	CAGGTGTTGT	TGAATTGCCA	GCCGGTGTTG	AAATGGTTAT	GCCTGGTGAC	750
25	CAAGTGACAT	TCGAAATCGA	ATTGATCTCA	CCAGTTGCCA	TCG	793

2) INFORMATION FOR SEQ ID NO: 1682

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Prevotella buccalis*
 (B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682

45	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTT	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAAGTTCTTG	AGCAATACGA	ATTGGAAGAG	GATACTCCAA	200
	TCGTTTCGTG	TTCTGCACTG	GGTGCAATTG	ATGGTGTTGA	CAAGTGGGTT	250
50	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAACAG	GACGTATTGA	GAAGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450

	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCACTTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
5	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GCGGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	GTAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

10

2) INFORMATION FOR SEQ ID NO: 1683

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 800 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ruminococcus bromii*
(B) STRAIN: ATCC 27255

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683

	GGTTGCTGCT	ACTGACGGCC	CGATGCCTCA	GACTCGTGAG	CACGTTCTGC	50
	TCGCTCGTCA	GGTGGGTGTG	CCCGCCATCG	TCGTCGCCCT	CAACAAGTGC	100
	GACATGGTTG	ACGATGAGGA	GCTCATTGAG	CTTGTCGAGA	TGGAGGTCCG	150
30	CGAGCTGCTG	ACCTCGCAGG	AGTTCGACGG	CGACAACCTGC	CCTGTCGTTC	200
	GCATCTCCGC	CTTCCAGGCC	CTCCAGGGTG	ACGAGAAGTG	GACCCAGTCG	250
	ATCCTCGACC	TCATGGACGC	CGTGGACGAG	TACATCCCGC	AGCCTGAGCG	300
	CGATCTCGAC	AAGCCCTTCC	TTATGCCGAT	CGAGGACGTC	TTCACCATCA	350
	CCGGCCGTGG	CACCGTTGTC	ACCGGTCGTG	TCGAGCGTGG	TGTCGTCAAG	400
35	ACTGGCGAAG	AGGTCGAGAT	CGTCGGTATC	CACGAGAAGA	CCCAGAAGAC	450
	CACCGTTACC	GGTGTCGAGA	TGTTCCGTAA	GATCCTCGAC	GAGGGCCGCG	500
	CTGGTGAGAA	CGTCGGCGTT	CTGCTCCGTG	GCACCAAGAA	GGAGGACGTC	550
	GTTCGCGGCA	TGGTCCTCTC	CAAGCCTGGT	TCCACCACCC	CCCACACCGA	600
	CTTCGAGGGC	CAGGTCTACG	TCCTCAAGAA	GGATGAGGGT	GGCCGCCACA	650
40	AGCCGTTCTT	CTCCCATTAC	AGCCCCCAGT	TCTACTTCCG	TACCACGGAC	700
	GTGACTGGCA	CTGTTGAGCT	CCCCGAGGGC	ACCGAGATGG	TCATGCCTGG	750
	CGACAACACC	GACATGACTG	TGCACCTGAT	TCACCCGGTT	GCCATGGAGG	800

45

2) INFORMATION FOR SEQ ID NO: 1684

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 545 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 5 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684

	TGTCTTTATT	CAGGAACTGA	TTGTATGTTT	CTTCTCGTTT	ATATATAACA	50
10	TACCTTCTAT	ATTTCATGTG	TTTCTAACGA	ACTCATAGAA	CAACATTGCC	100
	AAGGCTCACG	GTGGTACTC	CGTGTTACC	GGTGTGCGTG	AGCGTACCCG	150
	TGAAGGAAAC	GATCTGTACC	ACGAAATGCA	GGAAACCCGC	GTCATCCAGC	200
	TGGACGGCGA	GTCCAAAGTC	GCCCTCGTCT	TCGGCCAGAT	GAACGAGCCC	250
	CCCGGAGCCC	GTGCCCCTGT	TGCCCTGACC	GGTCTGACCA	TCGCTGAATA	300
15	CTTCCGTGAC	GAAGAAGGCC	AAGATGGTAC	GTTCCCCCAT	TCCATATATG	350
	TTTCTTGTGC	GCTTTGCCAA	CTAAACACCA	CCTAGTGCTC	CTCTTCATCG	400
	ACAATATCTT	CCGCTTCACC	CAAGCCGGTT	CCGAAGTGTC	CGCCCTGCTA	450
	GGCCGCATCC	CCTCCGCCGT	CGGCTATCAA	CCCACCCTCG	CCGTCGACAT	500
	GGGTGGTATG	CAGGAGCGCA	TCACAACCTAC	AACAAAAGGC	TCCAT	545
20						

2) INFORMATION FOR SEQ ID NO: 1685

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*
 35 (B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685

	GATATCGCTT	TATGGAAATT	CGAAACTCCA	AAATTCCACG	TTACYGTTAT	50
40	CGATGCTCCA	GGTCACAGAG	ATTTCATCAA	GAATATGATT	ACYGGTACCT	100
	CCCAAGCTGA	TTGTGCTATT	TTAATCATTG	CTGGTGGTGT	TGGTGAATTC	150
	GAAGCTGGTA	TCTCCAAAGA	TGGTCAAACC	AGAGAACACG	CTTTGTTAGC	200
	TTTCACCTTA	GGTGTYAAAC	AATTGATTGT	TGCCGTTAAC	AAAATGGACT	250
	CTGTCAAATG	GGATCAATCC	CGTTTCGAAG	AAATCGTCAA	GGAAGCTTCC	300
45	GGTTTCATCA	AGAAAGTTGG	TTACAACCCA	AAGACTGTTC	CATTCGTTCC	350
	AATCTCTGGT	TGGAATGGTG	ACAACATGAT	TGAAGTYTCW	GCTAACGCYC	400
	CATGGTACAA	AGGTTGGGAA	AAGGAAACCA	AAGCYGGTGT	CGTTAAAGGT	450
	AAAACCTTAT	TAGAAGCCAT	TGATGCTATT	GAACCACCTT	CAAGACCAAC	500
	TGAAAACCA	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATTGGTGGTA	550
50	TCGGAACCGT	ACCAGTCGGT	ARAGTTGAAA	CCGGTGTGTCAT	TAAACCAGGT	600
	ATGATTGTTA	CTTTCGCCCC	AGCCGGTGTT	ACTACTGAAG	TCAAATCTGT	650
	TGAAATGCAT	CACGAACAAT	TAGAAGCTGG	TTACCCAGGT	GACAATGTTG	700
	GTTTCAACGT	CAAGAATGTT	TCAGTTAAAG	AAATCAGAAG	AGGTAAHGTT	750

	GCTGGTGA	CTCCAAGA	ACGATCC	ACCAAA	GGTGCTGA	ATCTTTCA	ACGC	800
	TCAAGTTA	TGTCTTGA	ACCATCC	AGGTCA	AATCTYT	GCTGGTTA	CTYTC	850
	CAGTTTTG	GATGTCAC	ACTGCC	CACATTG	CTTGTA	AAATCG	ATC	900
	TTGGAAA	AGATTGAC	AGATCC	CGGTAAG	AAATTG	GGAAG	AAAATC	950
5	ATTCATCA	AAATCTG	GTGACG	CTGCTA	WTGT	CAAATT	TGTT	1000
	CATTRTGT	GTGTAAG	CTTTC					1020

10 2) INFORMATION FOR SEQ ID NO: 1686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 929 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686

25	TGCTGCTTCC	GATGGTCAAA	TGTACGATTG	ATATTCCTTC	CAGCCAGTCA	50
	GGATAACAGC	TGATACCAGT	TGCAAATAGG	CCCCAGACTC	GTGAGCACTT	100
	GTTGCTTGCC	CGTCAGGTTG	GTGTCCAGAA	GATCGTTGTC	TTCGTCAACA	150
	AGGTTGACGC	TGTCGATGAC	CCTGAGATGT	TGGAGCTTGT	TGAGCTCGAG	200
30	ATGCGTGAGC	TCCTCAACAC	TTACGGTTTC	GAGGGAGAGG	AGACCCCTAT	250
	CATCTTCGGT	TCCGCCCTGT	GCGCTCTCGA	AGGCCGCCGC	GAGGACATTG	300
	GTACTCAGCG	TATTGACTCC	CTCCTCGAGG	CCGTTGACAC	TTGGATCCCT	350
	ACCCCCCAGC	GTGACTTGGA	CAAGCCCTTC	CTGATGTCCA	TTGAGGAAGT	400
	TTTCTCCATT	GGTGGTCGTG	GTACCGTCGC	CTCTGGTCGT	GTCGAGCGTG	450
35	GTCTCCTCAA	GAAGGATACC	GAAGTTGAAA	TTCACGGTGC	TGATGGTATT	500
	CTGAAGACCA	AGGTCACCGA	CATTGAGACC	TTCAAGAAGA	GCTGCGATGA	550
	GTCTCGTGCT	GGTGACAACT	CCGGTCTTCT	CCTCCGTGGT	ATCCGTCGTG	600
	AGGATGTTTCG	TCGTGGTATG	GTCATCGCTG	CCCCTGGCTC	CATCAAGGCC	650
	TCCAAGAAGT	TCATGGTCTC	CATGTACGTC	TTGACTGAGG	CTGAAGGTGG	700
40	CCGCAAGAAC	GGCTTCGGTG	CCAACTACCG	CCCCCAGGCT	TTCATCCGCA	750
	CTGCTGGTAA	GTTTCGAACT	ATTTGATTCA	TTGATCACGT	CCCTAACTGT	800
	TACTTTAGAC	GAGGCTTGCG	ACCTTCATTT	CCCTGATGAG	GCCGACAAGG	850
	ACCGCCACGT	CATGCCCGGT	GACAACGTCG	AAATGGTCCT	CAACCTCAAC	900
	AACCCCGTTG	CTGCTGAGGC	TGGACAGCG			929

45

2) INFORMATION FOR SEQ ID NO: 1687

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus terreus*

(B) STRAIN: WSA-174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687

10 TGCCGCTTCC GATGGTCAGA TGTACGCTCA AGCCCCAGTT TCCATATAAA 50
 CATAAACGAT CTATCATCAG CACAACGCTG ACTTCTTCGC TTCCAGGCCC 100
 CAGACCCGTG AGCACTTGCT GTTGGCCCGT CAGGTCGGTG TCCAGAAGAT 150
 CGTGGTCTTC GTCAACAAGG TCGATGCCGT TGATGACCCG GAGATGTTGG 200
 15 AGCTCGTTGA GCTGGAAATG CGCGAGCTCC TGACCAGCTA CGGATTCGAG 250
 GGTGAAGAGA CCCCCATCAT CTTCGGTTCT GCTCTCTGCG CTCTTGAGGG 300
 CCGCCGTCCT GAGATTGGTA CTGAGAAGAT TGACGAGCTG ATGCACGCCG 350
 TCGACACCTG GATCCCCACC CCCCAGCGTG ACCTCGACAA GCCCTTCCTG 400
 ATGTCCGTCG AGGAAGTCTT CTCCATTGCT GGTCTGTGTA CCGTCGCTTC 450
 20 CGGCCGTGTC GAGCGTGGTA TTCTGAAGAA GGATAGCGAA GTCGAGATCA 500
 TCGGTGGTGC TTTCGACGCC ACGAAGACCA AGGTCACTGA CATCGAGACC 550
 TTCAAGAAGT CTTGCGACGA GTCTCGCGCT GGTGACAACCT CTGGTCTCCT 600
 CCTCCGTGGT ATCCGTCGTG AGGATGTTCTG GCGTGGTATG GTCATTGCTG 650
 CTCCTGGCAG CACCAAGGCC CACGACAAGT TCCTTGTCTC TATGTACGTC 700
 25 CTCACTGAGG CTGAGGGTGG CCGTCGTACC GGATTCGGTA CCAACTACCG 750
 CCCCCAGGTC TTCATCCGTA CTGCCGGTAA GTGTTCTCTG AAGAGGCTTT 800
 GAGCCTATAT AGGATCTCGG ATAATTTACT AATCCACCAT ATAGATGAGG 850
 CCGCTGACCT CAGCTTCCCC GACAACGATG ACTCCCGCCG TGTCATGCCC 900
 GGTGACAACG TTGAGATGGT CCTGAAGACC CACCGCCCCG TGGCTGCTGA 950
 30 G 951

2) INFORMATION FOR SEQ ID NO: 1688

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Candida norvegica*

(B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688

50 CGTTGCCGCT ACCGATGGTC AAATGCCTCA AACTAGAGAA CATTTGCTAT 50
 TGGCTAGACA GGTTGGTGTT CAACACATTG TCGTGTTTGT TAACAAGGTT 100
 GACACTATTG ATGATCCAGA AATGTTGGAA TTGGTTGAAA TGGAAATGAG 150
 AGAGTTGATT GCCACTTATG GTTTCGATGG TGATAACACC CCAGTTATCA 200

	TGGGTTCTGC	TCTATGTGCT	TTGGAAGGTC	GTGAACCTGA	AATCGGTGCT	250
	CAATCAATCG	ACAGATTGTT	GGAAGCCGTT	GATGAATACA	TTCCAACCTCC	300
	AACTAGAGAT	TTGGAAAAAC	CATTCTTGAT	GGGTGTTGAA	GATGTCTTCT	350
	CCATTTCTGG	TAGAGGTACC	GTCTGTACCG	GTCGTGTTGA	AAGAGGTAAC	400
5	TTGAAGAAAG	GTGATGAAAT	CGAAATTGTC	GGCTACAACA	AGACTCCAAT	450
	CAAAACCACC	GTCACCGGTA	TTGAGATGTT	CAAAAAGGAA	TTAGACCAAG	500
	CTATGGCTGG	TGATAACTGT	GGTATCTTAT	TACGTGGTGT	TAAGAGAGAT	550
	GATATCAAGA	GAGGTATGGT	TATCTCTAAA	GTCAACACCG	TTTCCGCACA	600
	CACCAAATTC	TTGGCCTCTT	TATACGTCTT	GAATAAGAA	GAAGGTGGTC	650
10	GTCATTCAGG	TTTGTCTGAA	AACTACAGAC	CTCAATTGTT	CATCAGAACC	700
	GGTGATGTCA	CTGTACTTTT	AACCTTCCCA	GAAGATGCTG	ATCACTCTCA	750
	GCAAGTCTTA	CCAGGTGACA	ACGTTGAAAT	GGAATGTACC	TTGGTTCATC	800
	CAACTGCTCT	TGAAACCGGT	CAA			823

15

2) INFORMATION FOR SEQ ID NO: 1689

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 803 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*

(B) STRAIN: ATCC 201076

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689

	GCTGCTACTG	ACGGTCAAAT	GCCTCAAAC	AGGGAACATA	TGTTGTTGGC	50
	GAGACAAGTT	GGTATCCAAA	ACTTGTTTGT	TTTTGTAAAC	AAAGTTGATA	100
35	CCATTGATGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGGGAA	150
	TTATTGAGCT	CTTATGGGTT	TGATGGTGAA	AACACTCCAG	TTATCATGGG	200
	ATCAGCCTTG	TGTGCTTTAG	AAGGTAAACA	ACCAGAAATC	GGTGTTCAAG	250
	CCATTCAAAA	ATTATTGGAT	GCTGTTGATG	AATATATTCC	AACTCCAGAA	300
	AGAGATGCTG	ACCAACCATT	TTTGATGCCA	GTGGAAGATG	TGTTTTCTAT	350
40	TTCAGGTAGA	GGAACCGTTG	TCACCGGAAG	AGTTGAAAGA	GGTATGTTGA	400
	AGAAAGGTGA	AGAAGTAKAA	GTCATTGGTG	AAAACCTCATT	TAAGGCTACT	450
	TCCACGGGTA	TTGAGATGTT	CAAAAAGGAA	TTGGATGCCG	CTATGGCCGG	500
	TGACAACTGT	GGTATTTTGT	TGAGAGGTGT	CAAGAGAGAC	GAAGTCAAGA	550
	GGGGTATGGT	TTTGGCCAAA	CCAGGTACCA	CCACCCACA	CCAAAAGTTT	600
45	TTGGCTTCCA	TTTATATCTT	GACTGCTGAA	GAAGGTGGAC	GTAGTACCCC	650
	TTTCAGTGAA	GGATACAAAC	CACAATGTTT	CTTTAGAACT	AGTGATGTTA	700
	CCACGACATT	TACTTTCCCA	GAAGGTGAAG	GTGTTGACCA	CTCACAAATG	750
	GTTATGCCAG	GAGRCAATGT	TGAAATGGTG	GGAACCTTAA	TCAAGAAAGC	800
	TCC					803

50

2) INFORMATION FOR SEQ ID NO: 1690

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690

CAGGTCCTGT TGCGACTGAA GAA

23

15

2) INFORMATION FOR SEQ ID NO: 1691

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691

CACAGATAAA CCTGAGTGTG CTTTC

25

30

2) INFORMATION FOR SEQ ID NO: 1692

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692

GGTGAGAACT GTGGTATCTT ACTT

24

45

2) INFORMATION FOR SEQ ID NO: 1693

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693

CATTCAACG CCTTCTTTCA ACTG

24

10

2) INFORMATION FOR SEQ ID NO: 1694

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694

AAGGCAAGGA TGACAACGGC

20

25

2) INFORMATION FOR SEQ ID NO: 1695

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695

ACGATTCCA CTTCTTCCTG G

21

40

2) INFORMATION FOR SEQ ID NO: 1696

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696

ATG TTCCTGT AGTTGCTGGA

20

5

2) INFORMATION FOR SEQ ID NO: 1697

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697

TTTCTTCAGC AATACCAACA AC

22

20

2) INFORMATION FOR SEQ ID NO: 1698

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698

35 GGAATCAACA GATGGTTTAC AAA

23

2) INFORMATION FOR SEQ ID NO: 1699

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699

50

GCATCTTCTG GGAAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1700

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700

AAGATGCGGA AAGAAGCGAA

20

2) INFORMATION FOR SEQ ID NO: 1701

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701

30 ATTATGGATC AGTTCTTGGA TCA

23

2) INFORMATION FOR SEQ ID NO: 1702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: Challis V288
 (C) ACCESSION NUMBER: L20574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702

50 TTCATAGACG CTGAGCACGC TTTGGATCCA TCTTACGCGG CTGCTCTAGG 50
 TGTAATATT GATGAGCTGT TGCTATCTCA ACCAGATTCT GGTGAGCAAG 100
 GTTTAGAAAT TGCAGGAAAA TTGATTGACT CTGGGGCAGT TGATTTAGTT 150

GTCATCGACT	CTGTTGCAGC	TCTTGTACCA	CGTGCGGAAA	TCGATGGAGA	200
TATCGGTGAT	AGC				213

5

2) INFORMATION FOR SEQ ID NO: 1703

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: strain GS-5
 (C) ACCESSION NUMBER: M61897

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703

GGGCCGGAAT	CTTCTGGTAA	GACAACTGTC	GCTCTTCATG	CTGCTGCTCA	50
GGCGCAAAAA	GATGGCGGTA	TTGCCGCTTT	CATTGATGCA	GAACATGCCC	100
25 TTGATCCAGC	CTATGCTGCT	GCTCTTGGCG	TTAATATTGA	TGAGCTTTTG	150
CTTTCACAAC	CAGATTCAGG	AGAACAGGGT	CTTGAAATTG	CAGGGAAATT	200
GATTGATTCT	GGCGCTGTTG	ATTTAGTTGT	TGTTGACTCA	GTGGCAGCTT	250
TAGTACCACG	TGCGGAGATT	GACGGAGATA	TTGGTAATAG	TCATGTTGGC	300
TTACAAGCAC	GCATGATGAG	TCAAGCGATG	CGTAAATTAT	CAGCTTCAAT	350
30 CAATAAAACA	AAAACCATTG	CTATTTTAT	TAATCAATTG	CGGGAAAAG	400
TTGGTATTAT	GTTTGGTAAT	CCAGAAACAA	CCCCTGGCGG	GCGTGCCTTG	450
AAGTTTTATT	CTTCTGTGCG	TCTTGATGTC	CGCGGCAATA	CTCAAATTAA	500
AGGAACCGGG	GAACAAAAG	ACAGCAATAT	TGGTAAAGAG	ACCAAATTA	550
AAGTTGTTAA	AAATAAAGTT	GCTCCACCAT	TTAAGGAAGC	TTTTGTAGAA	600
35 ATTATATATG	GTGAAGGCAT	TTCTCGTACA	GGTGAATTAG	TTAAGATTGC	650
CAGTGATTTG	GGAATTATCC	AAAAGCTGG	AGCTTGGTAC	TC	692

40 2) INFORMATION FOR SEQ ID NO: 1704

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (C) ACCESSION NUMBER: Z17307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704

	ATGGCGAAAA	AACCAAAAAA	ATTAGAAGAA	ATTTCAAAAA	AATTTGGGGC	50
	AGAACGTGAA	AAGGCCTTGA	ATGACGCTCT	TAAATTGATT	GAGAAAGACT	100
5	TTGGTAAAGG	ATCAATCATG	CGTTTGGGTG	AACGTGCGGA	GCAAAAGGTG	150
	CAAGTGATGA	GCTCAGGTTC	TTTAGCTCTT	GACATTGCCC	TTGGCTCAGG	200
	TGGTTATCCT	AAGGGACGTA	TCATCGAAAT	CTATGGCCCA	GAGTCATCTG	250
	GTAAGACAAC	GGTTGCCCTT	CATGCAGTTG	CACAAGCGCA	AAAAGAAGGT	300
	GGGATTGCTG	CCTTTATCGA	TGCGGAACAT	GCCCTTGATC	CAGCTTATGC	350
10	TGCGGCCCTT	GGTGTCATA	TTGACGAATT	GCTCTTGTCT	CAACCAGACT	400
	CAGGAGAGCA	AGGTCTTGAG	ATTGCGGGAA	AATTGATTGA	CTCAGGTGCA	450
	GTTGATCTTG	TCGTAGTCGA	CTCAGTTGCT	GCCCTTGTTT	CTCGTGCGGA	500
	AATTGATGGA	GATATCGGAG	ATAGCCATGT	TGGTTTGCAG	GCTCGTATGA	550
	TGAGCCAGGC	CATGCGTAAA	CTTGGCGCCT	CTATCAATAA	AACCAAAACA	600
15	ATTGCCATTT	TTATCAACCA	ATTGCGTGAA	AAAGTTGGAG	TGATGTTTGG	650
	AAATCCAGAA	ACAACACCGG	GCGGACGTGC	TTTGAAATTC	TATGCTTCAG	700
	TCCGCTTGGA	TGTTTCGTGGT	AATACACAAA	TTAAGGGAAC	TGGTGATCAA	750
	AAAGAAACCA	ATGTCGGTAA	AGAAACTAAG	ATTAAGGTTG	TAAAAAATAA	800
	GGTAGCTCCA	CCGTTTAAGG	AAGCCGTAGT	TGAAATTATG	TACGGAGAAG	850
20	GAATTTCTAA	GACTGGTGAG	CTTTTGAAGA	TTGCAAGCGA	TTTGGATATT	900
	ATCAAAAAAG	CAGGGGCTTG	GTATTCTTAC	AAAGATGAAA	AAATTGGGCA	950
	AGGTTCCTGAG	AATGCTAAGA	AATACTTGGC	AGAGCACCCA	GAAATCTTTG	1000
	ATGAAATTGA	TAAGCAAGTC	CGTTCTAAAT	TTGGCTTGAT	TGATGGAGAA	1050
	GAAGTTTCAG	AACAAGATAC	TGAAAACAAA	AAAGATGAGC	CAAAGAAAGA	1100
25	AGAAGCAGTG	AATGAAGAAG	TTCCGCTTGA	CTTAGGCGAT	GAAGTTGAAA	1150
	TCGAAATTGA	AGAATAAGCT	GTTAAAGCAG	TGGAGAAATC	CGCTACTTTT	1200
	TCGA					1204

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2) INFORMATION FOR SEQ ID NO: 1705

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 981 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: NZ131
- (C) ACCESSION NUMBER: U21934

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705

	ATGCGTTCAG	GAAGTCTAGC	TCTTGATATT	GCTTGGATAG	CTGGTGGTTA	50
	TCCTAAAGGA	CGTATCATCG	AAATCTATGG	TCCAGAGTCT	TCCGGTAAAA	100
50	CGACTGTGGC	TTTACATGCT	GTAGCACAAG	CTCAAAAAGA	AGGTGGAATC	150
	GCAGCCTTTA	TCGATGCCGA	GCATGCGCTT	GATCCAGCTT	ATGCTGCTGC	200
	GCTTGGGGTT	AATATTGATG	AACTTCTCTT	GTCTCAACCA	GATTCTGGAG	250
	AACAAGGACT	TGAAATTGCA	GGTAAATTGA	TTGATTCTGG	TGCGGTTGAC	300

	CTGGTTGTTG	TCGATTCAGT	AGCAGCTTTA	GTGCCACGTG	CTGAAATTGA	350
	TGGTGATATT	GGCGATAGCC	ATGTCGGATT	GCAAGCACGT	ATGATGAGTC	400
	AGGCCATGCG	TAAATTATCA	GCTTCTATTA	ATAAAACAAA	AACTATCGCA	450
	ATCTTTATCA	ACCAATTGCG	TGAAAAAGTT	GGTGTGATGT	TTGGAAATCC	500
5	TGAAACAACA	CCAGGTGGTC	GAGCTTTGAA	ATTCTATGCT	TCTGTTCTGGC	550
	TGGATGTGCG	TGGAAACAAC	CAAATTAAAG	GAAGTGGTGA	CCAAAAGATA	600
	GCCAGCATTG	GTAAGGAGAC	CAAAATCAAG	GTTGTTAAAA	ACAAGGTCGC	650
	TCCGCCATTT	AAGGTAGCAG	AAGTTGAAAT	CATGTATGGG	GAAGGTATTT	700
	CTCGTACAGG	GGAGCTTGTG	AAAATTGCTT	CTGATTTGGA	CATTATCCAA	750
10	AAAGCAGGTG	CTTGGTTCTC	TTATAATGGT	GAGAAGATTG	GCCAAGGTTC	800
	TGAAAATGCT	AAGCGTTATT	TGGCCGATCA	TCCACAATTG	TTTGATGAAA	850
	TCGACCGTAA	AGTACGTGTT	AAATTTGGTT	TGCTTGAAGA	AAGCGAAGAA	900
	GAATCTGCTA	TGGCAGTAGC	ATCAGAAGAA	ACCGATGATC	TTGCTTTAGA	950
	TTTAGATAAT	GGTATTGAAA	TTGAAGATTA	A		981
15						

2) INFORMATION FOR SEQ ID NO: 1706

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius* subsp. *thermophilus*
 (C) ACCESSION NUMBER: M94062

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706

35	GCGTATGCAC	GAGCTCTAGG	TGTTAATATC	GATGAGCTTC	TTTTGTCGCA	50
	GCCTGATTCT	GGTGAGCAAG	GTCTCGAAAT	TGCAGGTAAG	CTGATTGACT	100
	CTGGTGCAGT	GGATTTAGTT	GTTGTTGACT	CAGTTGCGGC	CTTCGTACCA	150
	CGTGCAGAAA	TTGATGGAGA	TAGTGGTGAC	AGTCATGTAG	GACTTCAAGC	200
	GCGTATGATG	AGTCAAGCCA	TGCGTAAACT	TTCTGCATCT	ATTAATAAAA	250
40	CAAAAACGAT	TGCTATCTTT	ATTAACCAGT	TGCGTGAAAA	AGTTGGTATC	300
	ATGTTTGGTA	AC				312

45 2) INFORMATION FOR SEQ ID NO: 1707

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: J02967

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707

	ATGAAAAACA	CAATACATAT	CAACTTCGCT	ATTTTTTTTAA	TAATTGCAAA	50
	TATTATCTAC	AGCAGCGCCA	GTGCATCAAC	AGATATCTCT	ACTGTTGCAT	100
10	CTCCATTATT	TGAAGGAAC	GAAGGTTGTT	TTTTACTTTA	CGATGCATCC	150
	ACAAACGCTG	AAATTGCTCA	ATTCAATAAA	GCAAAGTGTG	CAACGCAAAT	200
	GGCACCAGAT	TCAACTTTCA	AGATCGCATT	ATCACTTATG	GCATTTGATG	250
	CGGAAATAAT	AGATCAGAAA	ACCATATTCA	AATGGGATAA	AACCCCCAAA	300
	GGAATGGAGA	TCTGGAACAG	CAATCATACA	CCAAAGACGT	GGATGCAATT	350
15	TTCTGTTGTT	TGGGTTTCGC	AAGAAATAAC	CCAAAAAATT	AGATTAAATA	400
	AAATCAAGAA	TTATCTCAAA	GATTTTGATT	ATGGAAATCA	AGACTTCTCT	450
	GGAGATAAAG	AAAGAAACAA	CGGATTAACA	GAAGCATGGC	TCGAAAGTAG	500
	CTTAAAAATT	TCACCAGAAG	AACAAATTCA	ATTCCTGCGT	AAAATTATTA	550
	ATCACAATCT	CCCAGTTAAA	AACTCAGCCA	TAGAAAACAC	CATAGAGAAC	600
20	ATGTATCTAC	AAGATCTGGA	TAATAGTACA	AACTGTATG	GGAAAACCTG	650
	TGCAGGATTC	ACAGCAAATA	GAACCTTACA	AAACGGATGG	TTTGAAGGGT	700
	TTATTATAAG	CAAATCAGGA	CATAAATATG	TTTTTGTGTC	CGCACTTACA	750
	GGAAACTTGG	GGTCGAATTT	AACATCAAGC	ATAAAAGCCA	AGAAAAATGC	800
	GATCACCATT	CTAAACACAC	TAAATTTATA	A		831
25						

2) INFORMATION FOR SEQ ID NO: 1708

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

40 (B) STRAIN: HH22

(C) ACCESSION NUMBER: M60253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708

45	TTGAAAAAGT	TAATATTTTT	AATTGTAATT	GCTTTAGTTT	TAAGTGCATG	50
	TAATTCAAAC	AGTTCACATG	CCAAAGAGTT	AAATGATTTA	GAAAAAAAAT	100
	ATAATGCTCA	TATTGGTGTT	TATGCTTTAG	ATACTAAAAG	TGGTAAGGAA	150
	GTAAAATTTA	ATTCAGATAA	GAGATTTGCC	TATGCTTCAA	CTTCAAAGC	200
	GATAAATAGT	GCTATTTTGT	TAGAACAAGT	ACCTTATAAT	AAGTTAAATA	250
50	AAAAAGTACA	TATTAACAAA	GATGATATAG	TTGCTTATTC	TCCTATTTTA	300
	GAAAAATATG	TAGGAAAAGA	TATCACTTTA	AAAGCACTTA	TTGAGGCTTC	350
	AATGACATAT	AGTGATAATA	CAGCAAACAA	TAAAATTATA	AAAGAAATCG	400
	GTGGAATCAA	AAAAGTTAAA	CAACGTCTAA	AAGAACTAGG	AGATAAAGTA	450

	ACAAATCCAG	TTAGATATGA	GATAGAATTA	AATTACTATT	CACCAAAGAG	500
	CAAAAAAGAT	ACTTCAACAC	CTGCTGCTTT	CGGTAAGACT	TTAAATAAAC	550
	TTATCGCAAA	TGGAAAATTA	AGCAAAGAAA	ACAAAAAATT	CTTACTTGAT	600
	TTAATGTTAA	ATAATAAAAG	CGGAGATACT	TTAATTAAAG	ACGGTGTTCC	650
5	AAAAGACTAT	AAGGTTGCTG	ATAAAAGTGG	TCAAGCAATA	ACATATGCTT	700
	CTAGAAATGA	TGTTGCTTTT	GTTTATCCTA	AGGGCCAATC	TGAACCTATT	750
	GTTTTAGTCA	TTTTTACGAA	TAAAGACAAT	AAAAGTGATA	AGCCAAATGA	800
	TAAGTTGATA	AGTGAAACCG	CCAAGAGTGT	AATGAAGGAA	TTTTAA	846

10

2) INFORMATION FOR SEQ ID NO: 1709

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 555 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: M29695

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709

	ATGTCCGCGA	GCACCCCCCC	CATAACTCTT	CGCCTCATGA	CCGAGCGCGA	50
	CCTGCCGATG	CTCCATGACT	GGCTCAACCG	GCCGCACATC	GTTGAGTGGT	100
30	GGGGTGGCGA	CGAAGAGCGA	CCGACTCTTG	ATGAAGTGCT	GGAACACTAC	150
	CTGCCCAGAG	CGATGGCGGA	AGAGTCCGTA	ACACCGTACA	TCGCAATGCT	200
	GGGCGAGGAA	CCGATCGGCT	ATGCTCAGTC	GTACGTCGCG	CTCGGAAGCG	250
	GTGATGGCTG	GTGGGAAGAT	GAAACTGATC	CAGGAGTGCG	AGGAATAGAC	300
	CAGTCTCTGG	CTGACCCGAC	ACAGTTGAAC	AAAGGCCTAG	GAACAAGGCT	350
35	TGTCCGCGCT	CTCGTTGAAC	TACTGTTCTC	GGACCCCACC	GTGACGAAGA	400
	TTCAGACCGA	CCCGACTCCG	AACAACCATC	GAGCCATACG	CTGCTATGAG	450
	AAGGCAGGAT	TCGTGCGGGA	GAAGATCATC	ACCACGCCTG	ACGGGCCGGC	500
	GGTTTACATG	GTTCAAACAC	GACAAGCCTT	CGAGAGAAAG	CGCGGTGTTG	550
	CCTAA					555

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2) INFORMATION FOR SEQ ID NO: 1710

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: K02987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710

5
 ATGAACCAGA AAAACCCTAA AGACACGCAA AATTTTATTA CTTCTAAAAA 50
 GCATGTAAAA GAAATATTGA ATCACACGAA TATCAGTAAA CAAGACAACG 100
 TAATAGAAAT CGGATCAGGA AAAGGACATT TTACCAAAGA GCTAGTCAAA 150
 ATGAGTCGAT CAGTTACTGC TATAGAAATT GATGGAGGCT TATGTCAAGT 200
 10 GACTAAAGAA GCGGTAAACC CCTCTGAGAA TATAAAAGTG ATTCAAACGG 250
 ATATTCTAAA ATTTTCCTTC CCAAAACATA TAAACTATAA GATATATGGT 300
 AATATTCCTT ATAACATCAG TACGGATATT GTCAAAGAGT TTACCTTTGA 350
 AAGTCAGGCT AAATATAGCT ATCTTATCGT TGAGAAGGGA TTTGCGAAAA 400
 GATTGCAAAA TCTGCAACGA GCTTTGGGTT TACTATTAAT GGTGGAGATG 450
 15 GATATAAAAA TGCTCAAAAA AGTACCACCA CTATATTTTC ATCCTAAGCC 500
 AAGTGTAGAC TCTGTATTGA TTGTTCTTGA ACGACATCAA CCATTGATTT 550
 CAAAGAAGGA CTACAAAAAG TATCGATCTT TTGTTTATAA GTGGGTAAAC 600
 CGTGAATATC GTGTTCTTTT CACTAAAAAC CAATTCCGAC AGGCTTTGAA 650
 GCATGCAAAAT GTCACTAATA TTAATAAACT ATCGAAGGAA CAATTTCTTT 700
 20 CTATTTTCAA TAGTTACAAA TTGTTTCACT AA 732

2) INFORMATION FOR SEQ ID NO: 1711

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Escherichia coli*

(B) STRAIN: BM2570

(C) ACCESSION NUMBER: M19270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711

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ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTAAACGA GTGAAAAAGT 50
 ACTCAACCAA ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT 100
 ACGAAATTGG AACAGGTAAA GGGCATTTAA CGACGAAACT GGCTAAAATA 150
 AGTAAACAGG TAACGTCTAT TGAATTAGAC AGTCATCTAT TCAACTTATC 200
 45 GTCAGAAAAA TTAATAATCGA ATACTCGTGT CACTTTAATT CACCAAGATA 250
 TTCTACAGTT TCAATTCCCT AACAAACAGA GGTATAAAAT TGTTGGGAAT 300
 ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGTAAAG 350
 CCATGCGTCT GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA 400
 CCTTGGATAT TCACCGAACA CTAGGGTTGC TCTTGCACAC TCAAGTCTCG 450
 50 ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA TGCTTTCATC CTAAACCAAG 500
 AGTAAACAGT GTCTTAATAA AACTTACCCG CCATACCACA GATGTTCCAG 550
 ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAATG GGTCAATCGA 600
 GAATATCGTC AACTGTTTAC TAAAATCAG TTTCATCAAG CAATGAAACA 650

CGCCAAAGTA	AACAATTTAA	GTACCGTTAC	TTATGAGCAA	GTATTGTCTA	700
TTTTTAATAG	TTATCTATTA	TTTAACGGGA	GGAAATAA		738

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2) INFORMATION FOR SEQ ID NO: 1712

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: RN451
 (C) ACCESSION NUMBER: M17990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712

ATGAACGAGA	AAAATATAAA	ACACAGTCAA	AACTTTATTA	CTTCAAAACA	50
TAATATAGAT	AAAATAATGA	CAAATATAAG	ATTAAATGAA	CATGATAATA	100
25 TCTTTGAAAT	CGGCTCAGGA	AAAGGGCATT	TTACCCCTGA	ATTAGTACAG	150
AGGTGTAATT	TCGTAACTGC	CATTGAAATA	GACCATAAAT	TATGCAAAAC	200
TACAGAAAAT	AAACTTGTTG	ATCACGATAA	TTTCCAAGTT	TTAAACAAGG	250
ATATATTGCA	GTTTAAATTT	CCTAAAAACC	AATCCTATAA	AATATTTGGT	300
AATATACCTT	ATAACATAAG	TACGGATATA	ATACGCAAAA	TTGTTTTTGA	350
30 TAGTATAGCT	GATGAGATTT	ATTTAATCGT	GGAATACGGG	TTTGCTAAAA	400
GATTATTAAA	TACAAAACGC	TCATTGGCAT	TATTTTTAAT	GGCAGAAGTT	450
GATATTTCTA	TATTAAGTAT	GGTTCCAAGA	GAATATTTTC	ATCCTAAACC	500
TAGAGTGAAT	AGCTCACTTA	TCAGATTAAA	TAGAAAAAAA	TCAAGAATAT	550
CACACAAAGA	TAAACAGAAG	TATAATTATT	TCGTTATGAA	ATGGGTTAAC	600
35 AAAGAATACA	AGAAAATATT	TACAAAAAAT	CAATTTAACA	ATTCCTTAAA	650
ACATGCAGGA	ATTGACGATT	TAAACAATAT	TAGCTTTGAA	CAATTCTTAT	700
CTCTTTTCAA	TAGCTATAAA	TTATTTAATA	AGTAA		735

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2) INFORMATION FOR SEQ ID NO: 1713

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

50

(C) ACCESSION NUMBER: U00456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713

5	ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
	TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
	AAAAATTCGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
	CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
	ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
10	AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
	TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
	CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGTCATG	GACAAATCAC	400
	TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
	ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
15	CTTTGTGAAG	CCGGCACGGT	CAGGTTCGTC	CTTTGGCGTA	ACCAAAGTAA	550
	ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
	GGAAAAATCT	TAATTGAGCA	AGCGATTTCG	GGCTGTGAGG	TCGGCTGCGC	650
	GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
	GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
20	GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
	ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
	GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
	GTTCTAAACG	AGGTCAATAC	CCTGCCCGGT	TTTACATCGT	ACAGCCGCTA	950
	TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
25	GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 1714

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714

45	GCACAGGTTT	AGTTGGGCTT	GATCTTGCTT	TAGGTATAGG	CGGTGTTCCA	50
	AAAGGAAGAA	TTATAGAAAT	TTATGGRCCT	GAAAGTTCAG	GTAAAACCAC	100
	TCTAACTCTA	CACATTATCG	CAGAATGCCA	AAAAGCAGGT	GGRGTTTGTG	150
	CTTTTATCGA	TGCAGAACAT	GCRCTTGATG	TRAAATATGC	TAAAAATTTG	200
	GGTGTAATA	CAGATGATTT	GTATGTTTCT	CAGCCTGATT	TTGGAGARCA	250
50	AGCCTTAGAA	ATTGTAGAAA	CTATAGCAAG	AAGTGGCGCA	GTAGATCTTA	300
	TCGTAGTAGA	TAGCGTTGCA	GCGCTTACCC	CAAAGCAGA	AATTGAAGGC	350
	GATATGGGTG	ATCAACATGT	AGGACTTCAA	GCAAGACTTA	TGTCTCAAGC	400
	TCTAAGAAAA	CTTACAGGTA	TAGTTCATAA	AATGAATACC	ACAGTAATTT	450

	TYATCAACCA	AATTCGTATG	AAAATCGGTG	CTATGGGTTA	TGGTACTCCT	500
	GAAACCACAA	CAGGTGGAAA	TGCATTAAAA	TTTTATGCTT	CTGTGCGTTT	550
	AGATGTTAGA	AAAGTAGCAA	CCTTAAAACA	AAACGAAGAA	CCTATAGGAA	600
	ACCGCGTTAA	AGTAAAAGTA	GTTAAAAATA	AAGTTGCTCC	TCCATTCAGA	650
5	CAAGCTGAAT	TTGATGTGAT	GTTTGGAGAG	GGTTTAAGCC	GTGAAGGTGA	700
	ATTGATCGAT	TATGGTGTAA	AACTTGATAT	CGTAGATAAA	AGTGGTGCGT	750
	GGTTTTCTTA	TAAAGATAAA	AAACTTGGAC	AAGGTAGAGA	AAATTCAAAA	800
	GCTTTCTTAA	AAGAAAAC				818

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2) INFORMATION FOR SEQ ID NO: 1715

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175
 25 (C) ACCESSION NUMBER: AF124224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715

	TGGTGCTATC	TTAGTAGTAT	CTGCAGCTGA	TGGTCCAATG	CCTCAAACAC	50
30	GTGAACACAT	CTTATTATCA	CGTCAAGTAG	GTGTTTCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
	ACACTCCAGT	TGTTGCAGGT	TCTGCTTTAC	GCGCTTTAGA	AGGCGACGCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ACGAATACAT	300
35	TCCAACCTCA	GAACGYGACG	TTGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATCACAGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGTGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTTTCAGA	450
	AGAAACTTCA	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGG	GATAACATTG	GTACATTATT	ACGTGGTGTT	550
40	ACACGTGACA	ACATCGAACG	TGGACAAGTT	CTTGCTAAAC	CAGGAACAAT	600
	CACTCCACAT	ACTAAATTCA	AAGCTGAAGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CAGACATCAC	TGGTGTTTGT	GTGTTACCAG	AAGGCGTTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATTCACC	800
45	CAGTAGCGA					809

2) INFORMATION FOR SEQ ID NO: 1716

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia defectiva*
(B) STRAIN: ATCC 49176
(C) ACCESSION NUMBER: AF124225

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716

	CGGCGCGATC	CTCGTTGTAT	CTGCTGCTGA	CGGCCCAATG	CCACAAACTC	50
	GTGAACACAT	CCTCTTGTCT	CGTCAAGTTG	GTGTTCTTA	CATCGTAGTA	100
15	TTCTTGAACA	AAGTTGACAT	GGTTGACGAC	GAAGAATTGC	TCGAATTAGT	150
	TGAAATGGAA	GTTCTGTACC	TCTTGTCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	AACTACGAAG	CTAAAGTTTT	AGAATTGATG	GAACAAGTTG	ATGCTTACAT	300
	TCCAGAACCA	GAACGTGACA	CTGACAAGCC	ATTCATGATG	CCAGTCGAAG	350
20	ACGTATTCTC	TATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGTCAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCGAAGA	450
	AGAAACTTCT	AAGACTACCG	TTACCGGTGT	TGAAATGTTC	CGTAAGTTAT	500
	TGGATTACGC	TGAAGCTGGG	GACAACGTTG	GTACCTTGTT	ACGTGGTGTA	550
	ACTCGTGACC	AAATCCAACG	TGGTCAAGTA	TTATCTAAAC	CAGGTTCAAT	600
25	CACTCCGYAC	ACTAAGTTCG	AAGCTGAAGT	GTACGTATTG	TCTAAAGAAG	650
	AAGGTGGTCG	TCACACTCCA	TTCTTCTCTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCAGGCGACA	ACGTACAAAT	GGTTGTTGAA	TTGATCCACC	800
30	CAATCGCGAT	CGAAGAA				817

2) INFORMATION FOR SEQ ID NO: 1717

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*
(B) STRAIN: ATCC 49725

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717

	CGGCGCTATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
50	GCGAGCACGT	TCTGCTTGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTCGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAAATCA	TCGAGCTCGT	150
	GGAGATGGAG	ATCTCCGAGC	TGCTCGCAGA	GCAGGACTAC	GATGAGGAAG	200
	CTCCTATCGT	TCACATCTCC	GCTCTGAAGG	CACTCGAGGG	TGACGAGAAG	250

	TGGGTACAGT	CCATCGTTGA	CCTGATGGAT	GCCTGCGACA	ACTCCATCCC	300
	TGATCCGGAG	CGCGCTACCG	ATCAGCCGTT	CTTGATGCCT	ATCGAGGACA	350
	TCTTCACCAT	TACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGTCGTCTGA	ACGTCAACGA	GGACGTTGAG	ATCATCGGTA	TCCAGGAGAA	450
5	GTCCCAGAAC	ACCACCGTTA	CCGGTATCGA	GATGTTCCGC	AAGATGATGG	500
	ACTACACCGA	GGCTGGCGAC	AACTGTGGTC	TGCTTCTGCG	TGGTACCAAG	550
	CGTGAGGACG	TTGAGCGTGG	CCAGGTGTGT	ATCAAGCCGG	GCGCTTACAC	600
	CCCTCACACC	AAGTTCGAGG	GTTCCGTCTA	CGTCCTGAAG	AAGGAAGAGG	650
	GCGGCCGCCA	CACCCCGYTC	ATGAACAAC	ACCGTCCTCA	GTTCTACTTC	700
10	CGCACCACCG	ACGTTACCGG	TGTTGTGAAC	CTGCCTGAGG	GCACCGAGAT	750
	GGTTATGCCT	GGCGACAACG	TTGAGATGTC	TGTTGAGCTC	ATCCAGCCTG	800
	TTGCTATGGA	CGAG				814

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2) INFORMATION FOR SEQ ID NO: 1718

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*
 (B) STRAIN: ATCC 33031

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718

	CGGCGCCATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GTGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTAGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAGCTGC	TGGAGCTCGT	150
35	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CACCTGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
	TGGGCTAAGC	AGATCCTGGA	GCTCATGGAG	GCTTGCGACA	ACTCCATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGRGGACA	350
	TCTTCACCAT	TACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
40	GGCGTCCTGA	ACCTGAACGA	CGAGGTCGAG	ATCCTGGGCA	TCCGCGAGAA	450
	GTCCACCAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
	ACACCGCAGA	GGCTGGCGAC	AACGCCGCAC	TGCTGCTGCG	TGGCCTGAAG	550
	CGCGAAGATG	TTGAGCGTGG	TCAGATCGTT	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
45	GTGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTATTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCGGAGG	GCACCGAGAT	750
	GGTTATGCCG	GGCGACAACG	TTGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

50

2) INFORMATION FOR SEQ ID NO: 1719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Corynebacterium jeikeium*
 (B) STRAIN: ATCC 43216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719

15	CGGCGCCATC	CTGGTTGTTG	CCGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GCGAGCACGT	TCTGCTGGCY	CGCCAGGTTG	GCGTTCGTA	CATCCTGGTT	100
	GCACTGAACA	AGTGTGACAT	GGTTGACGAT	GAGGAGCTGC	TGGAGCTCGT	150
	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CTCCGGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
20	TGGGCTAACC	AGATTCTCGA	GCTGATGCAG	GCTTGCGACG	AGTCTATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGWGGACA	350
	TCTTCACCAT	TACCGGTCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGCATCCTGA	ACCTGAACGA	CGAGGTTGAG	ATCCTGGGTA	TCCGCGAGAA	450
	GTCCCAGAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
25	ACACCGCAGA	GGCTGGCRAC	AACGCTGCAC	TGCTGCTGCG	TGGTCTGAAG	550
	CGCGAGGACG	TTGAGCGTGG	CCAGATCATC	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCTGAGG	GCACCGAGAT	750
30	GGTTATGCCG	GGCGACAACG	TYGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

35 2) INFORMATION FOR SEQ ID NO: 1720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720

50	CGGCGCTATC	TTGGTTGTTG	CAGCTACCGA	CGGCCCAATG	CCACAGACTC	50
	GCGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTGGTT	100
	GCACTAAACA	AGTGCGACAT	GGTTGACGAC	GAGGAAATCC	TCGAGCTCGT	150

	CGAGATGGAG	ATCCGCGAAT	TGCTGGCTGA	CCAGGAATTC	GACGAAGAAG	200
	CTCCAATCGT	TCACATCTCC	GCAGTCGGCG	CCTTGGAAGG	CGAAGAGAGG	250
	TGGGTAAACG	CCATCGTTGA	ACTGATGGAT	GCTTGTGACG	AGTCGATCCC	300
	TGATCCAGAC	CGTGCTACCG	ACAAGCCATT	CCTGATGCCT	ATCGAGGACA	350
5	TCTTCACCAT	TACCGGTCGT	GGCACC GTTG	TTACGGGTCTG	TGTTGAGCGT	400
	GGTTCCCTGA	AGGTCAACGA	AGAAGTCGAG	ATCATCGGCA	TCAAGGAAAA	450
	GTCCCAGAAG	ACCACCATCA	CCGGTATCGA	AATGTTCCGC	AAGATGCTGG	500
	ACTACACCGA	GGCCGGCGAC	AACGCTGGTC	TGCTGCTTCG	CGGTACCAAG	550
	CGTGAAGACG	TTGAGCGTGG	ACAGGTTATC	GTTGCTCCAG	GTGCTTACAG	600
10	CACCCACAAG	AAGTTCGAAG	GTTCCGTCTA	CGTTCCTTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCTCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTTACC	CTGCCTGAGG	GCACCGAG	748

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2) INFORMATION FOR SEQ ID NO: 1721

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium striatum*
 (B) STRAIN: ATCC 6940

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721

	GGCGCTATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCGRTGC	CGCAGACCCG	50
	CGAGCACGTT	CTTCTGGCTC	GCCAGGTTGG	CGTTCCTTAC	ATCCTCGTTG	100
	CACTGAACAA	GTGCGACATG	GTTGACGACG	AGGAAATTAT	CGAGCTCGTC	150
35	GAGATGGAGA	TCCGCGAACT	GCTCGCAGAG	CAGGACTACG	ATGAGGAAGC	200
	TCCGATCGTT	CACATCTCTG	CTCTGAAGGC	TCTTGAGGGC	GRCGAGAAGT	250
	GGGTACAGGC	TATCGTTGAC	CTGATGCAGG	CTTGCGATGA	CTCCATCCCG	300
	GATCCGGAGC	GCGAGCTGGA	CAAGCCGTTC	CTGATGCCAA	TCGAGGACAT	350
	CTTCACCATC	ACCGGCCGCG	GTACCGTTGT	TACTGGCCGT	GTTGAGCGTG	400
40	GCTCCCTGAA	CGTCAACGAG	GACGTTGAGA	TCATCGGTAT	CCAGGACARG	450
	TCCATCTCCA	CCACCGTTAC	CGGTATCGAG	ATGYTCCGCA	AGATGATGGA	500
	CTACACCGAG	GCTGGCGACA	ACTGTGGTCT	GCTTCTGCGT	GGTACCAAGC	550
	GTGAAGAGGT	TGAGCGCGGC	CAGGTTGTTA	TTAAGCCGGG	CGCTTACACC	600
	CCTCACACCC	AGTTCGAGGG	TTCCGTCTAC	GTCCTGAAGA	AGGAAGAGGG	650
45	CGGCCGCCAC	ACCCCGTTCA	TGGACAAC	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTTACCGGC	GTCATCAAGC	TGCCTGAGGG	CACCGAGATG	750
	GTTATGCCTG	GCGACAACGT	CGAGATGTCY	GTCGAGCTGA	TCCAGCCGGT	800
	CGCTATGGAC	GAG				813

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2) INFORMATION FOR SEQ ID NO: 1722

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025
 (C) ACCESSION NUMBER: AF124220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722

15 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC 50
 GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCTTA CATCGTTGTA 100
 TTCTTAAACA AAATGGATAT GGTTGACGAT GAAGAATTAC TTGAATTAGT 150
 TGAAATGGAA GTTCGTGACT TATTAAGTGA ATACGACTTC CCAGGCGACG 200
 20 ACACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA AGGCGACGCT 250
 TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT 300
 CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG 350
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA 400
 CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA 450
 25 CGAAACTGCT AAAACAAGT TTACAGGTGT TGAAATGTTC CGTAAATTGT 500
 TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT ACGTGGTGTT 550
 GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT 600
 CACTCCACAT ACAAATTTCT CTGCAGAAGT TTATGTTCTA ACTAAAGAAG 650
 AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
 30 TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA 750
 AATGGTWATG CCTGGGGATA ACGTAACTAT GGAAGTTGAA TTGATYCACC 800
 CAATYGCGGT AGAAGAC 817

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2) INFORMATION FOR SEQ ID NO: 1723

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
 (B) STRAIN: ATCC 14018

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723

TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC 50
 GTGAACACGT CTTGCTTGCT AAGCAGGTCG GCGTTCCAAA AATTCTTGTT 100

	GCTTTGAACA	AGTGCGATAT	GGTTGACGAC	GAAGAGCTTA	TCGATCTCGT	150
	TGAAGAAGAG	GTCCGTGACC	TCCTCGAAGA	AAACGGCTTC	GATCGCGATT	200
	GCCCAGTCYT	CCGTACTTCC	GCTTACGGCG	CTTTGCATGA	TGACGCTCCA	250
	GACCACGACA	AGTGGGTAGA	GACCGTCAAG	GAATCATGA	AGGCTGTTGA	300
5	CGAGTACATC	CCAACCCCAA	CTCACGATCT	TGACAAGCCA	TTCTTGATGC	350
	CAATCGAAGA	TGTGTTCCACC	ATCTCCGGTC	GTGGTYCCGT	TGTCACCGGT	400
	CGTGTTGAGC	GTGGTAAGCT	CCCAATCAAC	ACCCAGTTG	AGATCGTTGG	450
	TTTGCGCGAT	ACCCAGACCA	CCACCGTCAC	CTCTATCGAG	ACCTTCCACA	500
	AGCAGATGGA	TGAGGCAGAG	GCTGGCGATA	ACACTGGTCT	TCTTCTCCGC	550
10	GGTATCAACC	GTACCGACGT	TGAGCGTGGT	CAGGTTGTGG	CTGCTCCAGG	600
	TTCTGTGACT	CCACACACCA	AGTTCGAAGG	CGAAGTTTAC	GTCTTGACCA	650
	AGGACGAAGG	TGGCCGTCAC	TCGCCATTCT	TCTCCAATA	CCGTCCACAG	700
	TTCTACTTCC	GTACCACCGA	TGTTACTGGC	GTTATCACCT	TGCCAGACGG	750
	CATCGAAATG	GTTCAGCCAG	GCGATCACGC	AACCTTCACT	GTTGAGTTGA	800
15	TCCAGGCTAT	CGCAATGGAA	GAG			823

2) INFORMATION FOR SEQ ID NO: 1724

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Listeria innocua*
 (B) STRAIN: ATCC 33090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
40	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
45	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTT	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
50	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1725

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACATAT	TCTTACTTTC	ACGTCAAGTT	GGTGTTCAT	ACATCGTTGT	100
	ATTCATGAAC	AAATGTGACA	TGGTTGACGA	TGAAGAATTA	CTTGAATTAG	150
20	TTGAAATGGA	AATTCGTGAT	CTATTAAGT	AATATGAATT	CCCTGGCGAC	200
	GACATTCCTG	TAATCAAAGG	TTCAGCTCTT	AAAGCACTTC	AAGGTGAAGC	250
	TGATTGGGAA	GCTAAAATTG	ACGAGTTAAT	GGAAGCTGTA	GATTCTTACA	300
	TTCCAAGTCC	AGAACGTGAT	ACTGACAAAC	CATTCATGAT	GCCAGTTGAG	350
	GATGTATTCT	CAATCACTGG	TCGTGGAACA	GTTGCAACTG	GACGTGTTGA	400
25	ACGTGGACAA	GTTAAAGTTG	GTGACGAAGT	AGAAGTTATC	GGTATTGAAG	450
	AAGAAAGCAA	AAAAGTAGTA	GTAAGTGGAG	TAGAAATGTT	CCGTAAATTA	500
	CTAGACTACG	CTGAAGCTGG	CGACAACATT	GGCGCACTTC	TACGTGGTGT	550
	TGCTCGTGAA	GATATCCAAC	GTGGTCAAGT	ATTAGCTAAA	CCAGGTTCGA	600
	TTACTCCACA	TACTAACTTC	AAAGCTGAAA	CTTATGTTTT	AACTAAAGAA	650
30	GAAGGTGGAC	GTCATACTCC	ATTCTTCAAC	AACTACCGCC	CACAATTCTA	700
	TTTCCGTACT	ACTGACGTAA	CTGGTATTGT	TACACTTCCA	GAAGGTACTG	750
	AAATGGTAAT	GCCTGGTGAT	AACATTGAGC	TTGCAGTTGA	ACTAATTGCA	800
	CCAATCGCTA	TCGAAGAC				818

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2) INFORMATION FOR SEQ ID NO: 1726

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: LSPQ 5093202

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
5	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCCW	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATCGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAACTGGAGT	AGAAATGTTC	CGTAAATTAC	500
10	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTT	550
	GCTCGTGAAG	ATATCCAACR	TGGTCAAGTA	TTAGCTAAAC	CAGGTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
15	AATGGTAAYG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1727

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria seeligeri*
 (B) STRAIN: ATCC 35967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGTGATG	200
40	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
45	AGAAAGCAAA	AAAGTAATAG	TAACTGGAGT	AGAAATGTTC	CGTAAATTAC	500
	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTT	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTCGAT	600
	TACTCCACAT	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
50	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1728

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 25923

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728

	CGGTGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
20	AGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAR	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTARTG	GAAGCTGTAG	ATACTTACAT	300
	TCCAACCTCCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
25	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
	CACATCTAAA	ACAACTGTTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	650
30	GTGGACGTCA	CACTCCATTC	TTCTCAAAC	ATCGTCCACA	ATTCTATTTC	700
	CGTACTACTG	ACGTAAC	TGTTGTTTAC	TTACCAGAAG	GTACTGAAAT	750
	GGTAATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCAA	800
	TCGCGATTGA	AGAC				814

35

2) INFORMATION FOR SEQ ID NO: 1729

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 15305

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACACAT	TCTTTTATCA	CGTRACGTTG	GTGYTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAY	GAAGAATTAT	TAGAATTRGT	150
	AGAAATGGAA	GTTCGTGRCT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACGCT	250
5	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTYCAT	300
	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAATC	GARATCATCG	GTATGCAAGA	450
	AGAATCAAGC	AAAACAACCTG	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
10	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCATTATT	ACGTGGTGTT	550
	TCACGTGATG	ATGTACAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTACTAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGATGT	TTACGTTTTA	TCTAAAGATG	650
	AAGGTGGTCG	TCATACGCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTGTTGTT	AACTTACCAG	AAGGTACTGA	750
15	AATGGTTATG	CCTGGCGATA	ACGTTGAAAT	GGATGTTGAA	TTAATTTCTC	800
	CAATCGCTAT	TGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1730

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus simulans*
 (B) STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730

35	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
40	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
45	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGTT	550
	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
50	TTCCGTACTA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTGATCGCTC	800
	CAATCGCGAT	TGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1731

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591
 (C) ACCESSION NUMBER:

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731

	CGGAGCTATC	CTTGTAGTTG	CTTCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTAAACA	CCTTATCGTA	100
20	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTCAGA	ATACGACTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCACTTGA	AGGCGACGAA	250
	AAATACGAAG	ACATCATCAT	GGAATTGATG	AGCACTGTTG	ATGAGTACAT	300
	TCCAGAACCA	GAACGTGATA	CTGACAAACC	TTTACTTCTT	CCAGTTGAAG	350
25	ATGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTCGTGTCAA	CGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
	AGATATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTT	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
30	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAAGTTCCAG	CAGGAACAGA	750
	AATGGTTATG	CCTGGTGATA	ACGTTACTAT	CGAAGTTGAA	TTGATTCACC	800
	CAATCGCCGT	AGAACAA				817

35

2) INFORMATION FOR SEQ ID NO: 1732

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 50 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732

	CGGAGCTATC	CTTGTAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TATTGTCAGA	ATACGACTTC	CCAGGTGACG	200
5	ATCTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATACGAAG	ACATCGTTAT	GGAATTGATG	AACACAGTTG	ATGAGTATAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTATCG	TTAAAGTCAA	CGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
10	AGAAACTCRA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTAG	GTGTCCTTCT	TCGTGGTGTT	550
	CAACGTGATG	AAATCGAACG	TGGACAAGTT	ATCGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	CTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
15	TTCCGTACTA	CTGACGTTAC	AGGTTCAATC	GAAGTTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTGACAAT	CGACGTTGAG	TTGATTCACC	800
	CAATCGCCGT	AGAACAA				817

20

2) INFORMATION FOR SEQ ID NO: 1733

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733

	CGGTGCGATC	CTTGTAGTAG	CATCTACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGATTCT	250
	AAATACGAAG	ACATCATCAT	GGACTTGATG	AACACTGTTG	ACGAATACAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGTTGCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTGTTG	TTCGTGTCAA	TGACGAAGTT	GAAATCGTTG	GTCTTAAAGA	450
	AGACATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGRAGG	TATTGCCGGA	GATAACGTCG	GTGTTCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTGCAC	CTGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAAGTTCTTG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAA				817

2) INFORMATION FOR SEQ ID NO: 1734

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Agrobacterium tumefaciens*
 (C) ACCESSION NUMBER: x99673

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734

	AACATGATCA	CCGGTGCTGC	CGAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
	GGCTGCCGAC	GGCCCGATGC	CACAGACCCG	CGAGCACATC	CTGCTTGCCC	100
	GTCAGGTGGG	CGTTCCGGCC	ATCGTCGTGT	TCCTCAACAA	GGTCGACCAG	150
20	GTTGACGACG	CCGAGCTTCT	CGAGCTCGTC	GAGCTTGAAG	TTCGCGAACT	200
	TCTGTCGTCC	TACGACTTCC	CGGGCGACGA	TATCCCGATC	ATCAAGGGTT	250
	CGGCACTTGC	TGCTCTTGAA	GATTCTGACA	AGAAGATCGG	TGAAGACGCG	300
	ATCCGCGAGC	TGATGGCTGC	TGTCGACGCC	TACATCCCGA	CGCCTGAGCG	350
	TCCGATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
25	CGGGTCGTGG	TACGGTTGTG	ACGGGTCGCG	TTGAGCGCGG	TATCGTCAAG	450
	GTTGGTGAAG	AAGTCGAAAT	CGTCGGCATC	CGTCCGACCT	CGAAGACGAC	500
	TGTTACCGGC	GTTGAAATGT	TCCGCAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACAT	CGGTGCACTC	GTTCGCGGCG	TTACCCGTGA	CGGCGTCGAG	600
	CGTGGTCAGA	TCCTGTGCAA	GCCGGGTTCG	GTCAAGCCGC	ACAAGAAGTT	650
30	CATGGCAGAA	GCCTACATCC	TGACGAAGGA	AGAAGGCGGC	CGTCATACGC	700
	CGTTCTTCAC	GAActACCGT	CCGCAGTTCT	ACTTCCGTAC	GAActGACGTT	750
	ACCGGTATCG	TTTCGCTTCC	TGAAGGCACG	GAAATGGTTA	TGCCTGGCGA	800
	CAACGTCACT	GTTGAAGTCG	AGCTGATCGT	TCCGATCGCG	ATGGAAGAAA	850
	AGCTGCGCTT	CGCTATCCGC	GAAGGCGGCC	GTACCGTCGG	CGCCGGC	897

35

2) INFORMATION FOR SEQ ID NO: 1735

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*
 50 (B) STRAIN: 168
 (C) ACCESSION NUMBER: Z99104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735

	ATGATCACTG	GTGCTGCGCA	AATGGACGGA	GCTATCCTTG	TAGTATCTGC	50
	TGCTGATGGC	CCAATGCCAC	AAACTCGTGA	GCACATCCTT	CTTTCTAAAA	100
	ACGTTGGTGT	ACCATACATC	GTTGTATTCT	TAAACAAATG	CGACATGGTA	150
5	GACGACGAAG	AGCTTCTTGA	ACTAGTTGAA	ATGGAAGTTC	GCGATCTTCT	200
	TAGCGAATAC	GACTTCCCTG	GTGATGATGT	ACCAGTTGTT	AAAGGTTCTG	250
	CTCTTAAAGC	TCTTGAAGGA	GACGCTGAGT	GGGAAGCTAA	AATCTTCGAA	300
	CTTATGGATG	CGGTTGATGA	GTACATCCCA	ACTCCAGAAC	GCGACACTGA	350
	AAAACCATTC	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	400
10	GTACAGTTGC	TACTGGCCGT	GTAGAACGCG	GACAAGTTAA	AGTCGGTGAC	450
	GAAGTTGAAA	TCATCGGTCT	TCAAGAAGAG	AACAAGAAAA	CAACTGTTAC	500
	AGGTGTTGAA	ATGTTCCGTA	AGCTTCTTGA	TTACGCTGAA	GCTGGTGACA	550
	ACATTGGTGC	CCTTCTTCGC	GGTGTATCTC	GTGAAGAAAT	CCAACGTGGT	600
	CAAGTACTTG	CTAAACCAGG	TACAATCACT	CCACACAGCA	AATTCAAAGC	650
15	TGAAGTTTAC	GTTCTTTCTA	AAGAAGAGGG	TGGACGTCAT	ACTCCATTCT	700
	TCTCTAACTA	CCGTCCTCAG	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	750
	ATCATCCATC	TTCCAGAAGG	CGTAGAAATG	GTTATGCCTG	GAGATAACAC	800
	TGAAATGAAC	GTTGAACTTA	TTTCTACAAT	CGCTATCGAA	GAAGGAACTC	850
	GTTTCTCTAT	TCGTGAAGGC	GGACGTACTG	TTGGT		885
20						

2) INFORMATION FOR SEQ ID NO: 1736

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*
 35 (B) STRAIN: DSM 2151
 (C) ACCESSION NUMBER: P33165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736

40	ATGGTTACTG	GTGCTGCTCA	GATGGACGGT	GCTATCATTG	TAGTTGCTGC	50
	TACTGATGGT	CCGATGCCTC	AGACTCGTGA	GCACATCCTT	TTGGCTCGTC	100
	AGGTAAACGT	TCCGAAGCTG	GTTGTATTCA	TGAACAAGTG	CGATATGGTT	150
	GAAGATGCTG	AGATGTTGGA	ACTTGTTGAA	ATGGAAATGA	GAGAATTGCT	200
	TTCATTCTAT	GATTTCGACG	GTGACAATAC	TCCGATCATT	CAGGGTTCTG	250
45	CTCTTGGTGC	ATTGAACGGC	GTAGAAAAAT	GGGAAGACAA	AGTAATGGAA	300
	CTGATGGAAG	CTGTTGATAC	TTGGATTCCA	CTGCCTCCGC	GCGATGTTGA	350
	TAAACCTTTC	TTGATGCCGG	TAGAAGACGT	GTTCTCTATC	ACAGGTCGTG	400
	GTAATGTAAG	TACAGGTCGT	ATCGAAACTG	GTGTTATCCA	TGTAGGTGAT	450
	GAAATCGAAA	TCCTCGGTTT	GGGTGAAGAT	AAGAAATCAG	TTGTAACAGG	500
50	TGTTGAAATG	TTCCGCAAAC	TTCTGGATCA	GGGTGAAGCT	GGTGACAACG	550
	TAGGTCTGTT	GCTTCGTGGT	GTTGACAAGA	ACGAAATCAA	ACGTGGTATG	600
	GTTCTTTGTA	AACCGGGTCA	GATTAAACCT	CACTCTAAAT	TCAAAGCAGA	650
	GGTTTATATC	CTGAAGAAAG	AAGAAGGTGG	TCGTCACACT	CCATTCCATA	700

ACAAATATCG	TCCTCAGTTC	TACCTGCGTA	CTATGGACTG	TACAGGTGAA	750
ATCACTCTTC	CGGAAGGAAC	TGAAATGGTA	ATGCCGGGTG	ATAACGTAAC	800
TATCACTGTA	GAGTTGATCT	ATCCGGTTGC	ACTGAACATC	GGTCTTCGTT	850
TCGCTATCCG	CGAAGGTGGA	CGTACAGTAG	GT		882

5

2) INFORMATION FOR SEQ ID NO: 1737

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
 20 (B) STRAIN: U78183
 (C) ACCESSION NUMBER: U78183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737

25	AATATGATTA	CAGGAGCAGC	TCAAATGGAT	GCAGCGATAC	TTTtagTTGC	50
	TGCTGATAGT	GGTGCTGAGC	CTCAAACAAA	AGAGCATTTG	CTTCTTGCTC	100
	AAAGAATGGG	AATAAGAAA	ATAATAGTTT	TTTTAAATAA	ATTGGACTTA	150
	GCAGATCCTG	AACTTGTTGA	GCTTGTTGAA	GTTGAAGTTT	TAGAACTTGT	200
	TGAAAAATAT	GGCTTTTCAG	CTGATACTCC	AATAATCAAA	GGTTCAGCTT	250
30	TTGGGGCTAT	GTCAAATCCA	GAAGATCCTG	AATCTACAAA	ATGCGTTAAA	300
	GAACTTCTTG	AATCTATGGA	TAATTATTTT	GATCTTCCAG	AAAGAGATAT	350
	TGACAAGCCA	TTTTTGCTTG	CTGTTGAAGA	TGTATTTTCT	ATTCAGGAA	400
	GAGGCACTGT	TGCTACTGGG	CGTATTGAAA	GAGGTATTAT	TAAAGTTGGT	450
	CAAGAAGTTG	AAATAGTTGG	AATTAAAGAA	ACCAGAAAAA	CTACTGTTAC	500
35	TGGTGTTGAA	ATGTTCCAGA	AAATTCTTGA	GCAAGGTCAA	GCAGGGGATA	550
	ATGTTGGTCT	TCTTTTGAGA	GGCGTTGATA	AAAAAGACAT	TGAGAGGGGG	600
	CAAGTTTTGT	CAGCTCCAGG	TACAATTACT	CCACACAAGA	AATTTAAAGC	650
	TTCAATTTAT	TGTTTGACTA	AAGAAGAAGG	CGGTAGGCAC	AAGCCATTTT	700
	TCCCAGGGTA	TAGACCACAG	TTCTTTTTTA	GAACAACCGA	TGTTACTGGA	750
40	GTTGTTGCTT	TAGAGGGCAA	AGAAATGGTT	ATGCCTGGTG	ATAATGTTGA	800
	TATTATTGTT	GAGCTGATCT	CTTCAATAGC	TATGGATAAG	AATGTAGAAT	850
	TTGCTGTTCG	AGAAGGTGGA	AGAACCGTTG	CTTCAGGA		888

45

2) INFORMATION FOR SEQ ID NO: 1738

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Brevibacterium linens*
 (B) STRAIN: DSM 20425
 (C) ACCESSION NUMBER: X76863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738

10	AACATGATCA	CCGGTGCCGC	TCAGATGGAC	GGTGCGATCC	TCGTGTCGCGC	50
	CGCTACCGAC	GGACCGATGC	CCCAGACCCG	TGAGCACGTG	CTGCTCGCGC	100
	GTCAGGTCGG	CGTTCCCTAC	ATCGTCGTGG	CTCTGAACAA	GTCCGACATG	150
	GTCGATGACG	AGGAGCTCCT	CGAGCTCGTC	GAATTCGAGG	TCCGCGACCT	200
	GCTCTCGAGC	CAGGACTTCG	ACGGAGACAA	CGCTCCGGTC	ATTCCGGTGT	250
15	CCGCTCTCAA	GGCGCTGGAA	GGCGACGAGA	AGTGGGTCAA	GAGCGTTCAG	300
	GATCTCATGG	CTGCCGTCGA	TGACAACGTT	CCGGAGCCGG	AGCGCGATGT	350
	CGACAAGCCG	TTCCTCATGC	CCGTGAGGA	CGTCTTCACG	ATCACCGGTC	400
	GTGGAACCGT	CGTCACCGGT	CGTGTCGAGC	GCGGCGTGCT	CCTGCCTAAC	450
	GACGAAATCG	AAATCGTCGG	CATCAAGGAG	AAGTCGTCCA	AGACGACTGT	500
20	CACCGCTATC	GAGATGTTCC	GCAAGACCCT	GCCGGATGCC	CGTGCAGGTG	550
	AGAACGTCGG	TCTGCTCCTC	CGCGGCACCA	AGCGCGAGGA	TGTTGAGCGC	600
	GGTCAGGTCA	TCGTGAAGCC	GGGTTCGATC	ACCCCGCACA	CCAAGTTCGA	650
	GGCTCAGGTC	TACATCCTGA	GCAAGGACGA	GGGCGGACGT	CACAACCCGT	700
	TCTACTCGAA	CTACCGTCCG	CAGTTCTACT	TCCGGACCAC	GGACGTCACC	750
25	GGTGTTCATCA	CGCTGCCCCGA	GGGCACCGAG	ATGGTCATGC	CCGGCGACAA	800
	CACCGATATG	TCGGTCGAGC	TCATCCAGCC	GATCGCTATG	GAGGACCGCC	850
	TCCGCTTCGC	AATCCGCGAA	GGTGGCCGCA	CCGTGCGCGC	CGGT	894

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2) INFORMATION FOR SEQ ID NO: 1739

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: F/IC-Cal-13
 (C) ACCESSION NUMBER: L22216

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739

	ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
	AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
50	AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
	GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
	CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300

	ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
	AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	AGCGCGGCAT	CGTGAAGGTC	450
	GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
5	CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
	GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
10	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
	CGTGTCGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
	TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCGGC		888

15

2) INFORMATION FOR SEQ ID NO: 1740

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*
 (B) STRAIN: S85
 (C) ACCESSION NUMBER: X76866

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740

	AACATGGTGA	CTGGTGCTGC	TCAGATGGAC	GGCGCTATCC	TCGTTGTTGC	50
	CGCTACTGAC	GGTCCGATGC	CGCAGACTCG	CGAACACATC	CTTCTCGCTC	100
35	ACCAGGTTGG	CGTGCCGAAG	ATCGTCGTGT	TCATGAACAA	GTGCGACATG	150
	GTTGACGATG	CTGAAATTCT	CGACCTCGTC	GAAATGGAAG	TTCGCGAACT	200
	CCTCTCCAAG	TATGACTTCG	ACGGTGACAA	CACCCCGATC	ATCCGTGGTT	250
	CCGCTCTCAA	GGCCCTCGAA	GGCGATCCGG	AATACCAGGA	CAAGGTCATG	300
	GAATCATGA	ACGCTTGCGA	CGAATACATC	CCGCTCCCGC	AGCGCGATAC	350
40	CGACAAGCCG	TTCCTCATGC	CGATCGAAGA	CGTGTTACAG	ATTACTGGCC	400
	GCGGCACTGT	CGCTACTGGC	CGTATCGAAC	GCGGTGTCGT	TCGCTTGAAC	450
	GACAAGGTTG	AACGTATCGG	TCTCGGTGAA	ACCACCGAAT	ACGTCATCAC	500
	CGGTGTTGAA	ATGTTCCGTA	AGCTCCTCGA	CGACGCTCAG	GCAGGTGACA	550
	ACGTTGGTCT	CCTCCTCCGT	GGTGCTGAAA	AGAAGGACAT	CGTCCGTGGC	600
45	ATGGTTCTCG	CAGCTCCGAA	GTCTGTCACT	CCGCACACCG	AATTTAAGGC	650
	TGAAATCTAC	GTTCTCACGA	AGGACGAAGG	TGGCCGTCAC	ACGCCGTTCA	700
	TGAATGGCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTTACTGGT	750
	ACGATCCAGC	TCCCGGAAGG	TGTCGAAATG	GTTACTCCGG	GTGACACGGT	800
	CACGATCCAC	GTGAACCTCA	TCGCTCCGAT	CGCTATGGAA	AAGCAGCTCC	850
50	GCTTCGCTAT	CCGTGAAGGT	GGACGTACTG	TTGGTGCTGG	C	891

2) INFORMATION FOR SEQ ID NO: 1741

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Flavobacterium ferrugineum*
 (B) STRAIN: DSM 13524
 (C) ACCESSION NUMBER: X76867

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741

	AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGTGCTATCT	TAGTTGTGGC	50
	TGCATCAGAC	GGTCCTATGC	CTCAAACAAA	AGAACACATC	CTGCTTGCTG	100
20	CCCAGGTAGG	TGTACCTAAA	ATGGTTGTGT	TTCTGAATAA	AGTTGACCTC	150
	GTTGACGACG	AAGAGCTCCT	GGAGCTGGTT	GAGATCGAGG	TTCGCGAAGA	200
	ACTGACTAAA	CGCGGTTTCG	ACGGCGACAA	CACTCCAATC	ATCAAAGGTT	250
	CCGCTACAGG	CGCCCTCGCT	GGTGAAGAAA	AGTGGGTTAA	AGAAATTGAA	300
	AACCTGATGG	ACGCTGTTGA	CAGCTACATC	CCACTGCCTC	CTCGTCCGGT	350
25	TGATCTGCCG	TTCCTGATGA	GCGTAGAGGA	CGTATTCTCT	ATCACTGGTC	400
	GTGGTACTGT	TGCTACCGGT	CGTATCGAGC	GTGGCCGTAT	CAAAGTTGGT	450
	GAGCCTGTTG	AGATCGTAGG	TCTGCAGGAG	TCTCCCCTGA	ACTCTACCGT	500
	TACAGGTGTT	GAGATGTTCC	GCAAACCTCCT	CGACGAAGGT	GAAGCTGGTG	550
	ATAACGCCGG	TCTCCTCCTC	CGTGGTGTTG	AAAAAACACA	GATCCGTCGC	600
30	GGTATGGTAA	TCGTTAACCC	CGGTTCCATC	ACTCCGCACA	CGGACTTCAA	650
	AGGCGAAGTT	TACGTACTGA	GCAAAGACGA	AGGTGGCCGT	CACACTCCAT	700
	TCTTCAACAA	ATACCGTCCT	CAATTCTACT	TCCGTACAAC	TGACGTTACA	750
	GGTGAAGTAG	AACTGAACGC	AGGAACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CACCAACCTG	ACCGTTAAAC	TGATCCAACC	GATCGCTATG	GAAAAAGGTC	850
35	TGAAATTCGC	GATCCGCGAA	GGTGGCCGTA	CCGTAGGTGC	AGGA	894

2) INFORMATION FOR SEQ ID NO: 1742

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: 26695
 (C) ACCESSION NUMBER: AE000626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742

	AACATGATCA	CCGGTGCGGC	GCAAATGGAC	GGAGCGATTT	TGGTTGTTTC	50
	TGCAGCTGAT	GGCCCTATGC	CTCAAAC TAG	GGAGCATATC	TTATTGTCTC	100
5	GTCAAGTAGG	CGTGCCCTCAC	ATCGTTGTTT	TCTTAAACAA	ACAAGACATG	150
	G TAGATGACC	AAGAATTGTT	AGAACTTGTA	GAAATGGAAG	TGCGCGAATT	200
	GTTGAGCGCG	TATGAATTTT	CTGGCGATGA	CACTCCTATC	G TAGCGGGTT	250
	CAGCTTTAAG	AGCTTTTAGAA	GAAGCAAAGG	CTGGTAATGT	GGGTGAATGG	300
	GGTGAAAAAG	TGCTTAAACT	TATGGCTGAA	GTGGATGCCT	ATATCCCTAC	350
10	TCCAGAAAGA	GACACTGAAA	AAACTTTCTT	GATGCCGGTT	GAAGATGTGT	400
	TCTCTATTGC	GGGTAGAGGG	ACTGTGGTTA	CAGGTAGGAT	TGAAAGAGGC	450
	GTGGTGAAAG	TAGGCGATGA	AGTGGAATC	GTTGGTATCA	GACCTACACA	500
	AAAAACGACT	GTAACCGGTG	TAGAAATGTT	TAGGAAAGAG	TTGGAAAAAG	550
	GTGAAGCCGG	CGATAATGTG	GGCGTGCTTT	TGAGAGGAAC	TAAAAAAGAA	600
15	GAAGTGGAAC	GCGGTATGGT	TCTATGCAAA	CCAGGTTCTA	TCACTCCGCA	650
	CAAGAAATTT	GAGGGAGAAA	TTTATGTCCT	TTCTAAAGAA	GAAGGCGGGA	700
	GACACACTCC	ATTCTTCACC	AATTACCGCC	CGCAATTCTA	TGTGCGCACA	750
	ACTGATGTGA	CTGGCTCTAT	CACCCTTCCT	GAAGGCGTAG	AAATGGTTAT	800
	GCCTGGCGAT	AATGTGAAAA	TCACTGTAGA	GTTGATTAGC	CCTGTTGCGT	850
20	TAGAGTTGGG	AACTAAATTT	GCGATTCGTG	AAGGCGGTAG	GACCGTTGGT	900
	GCTGGT					906

25 2) INFORMATION FOR SEQ ID NO: 1743

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*
 (B) STRAIN: IFO 3333
 (C) ACCESSION NUMBER: M17788

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743

	AACATGATCA	CCGGCGCCGC	TCAGATGGAC	GGCGCGATCC	TCGTGGTCGC	50
	CGCTACCGAC	GGCCCGATGG	CCCAGACCCG	TGAGCACGTG	CTCCTGGCCC	100
	GCCAGGTCGG	CGTGCCGGCC	CTGCTCGTGG	CCCTGAACAA	GTCGGACATG	150
45	GTGGAGGACG	AGGAGCTCCT	CGAGCGTGTC	GAGATGGAGG	TCCGGCAGCT	200
	GCTGTCCTCC	AGGAGCTTCG	ACGTCGACGA	GGCCCCGGTC	ATCCGCACCT	250
	CCGCTCTGAA	GGCCCTCGAG	GGCGACCCCC	AGTGGGTCAA	GTCCGTCGAG	300
	GACCTCATGG	ATGCCGTGGA	CGAGTACATC	CCGGACCCGG	TGCGCGACAA	350
	GGACAAGCCG	TTCCTGATGC	CGATCGAGGA	CGTCTTCACG	ATCACC GGCC	400
50	GTGGCACC GT	GGTGACCGGT	CGCGCCGAGC	GCGGCACCCT	GAAGATCAAC	450
	TCCGAGGTCG	AGATCGTCGG	CATCCGCGAC	GTGCAGAAGA	CCACTGTCAC	500
	CGGCATCGAG	ATGTTCCACA	AGCAGCTCGA	CGAGGCCTGG	GCCGGCGAGA	550
	ACTGCGGTCT	GCTCGTGCGC	GGTCTGAAGC	GCGACGACGT	CGAGCGCGGC	600

	CAGGTGCTGG	TGGAGCCGGG	CTCCATCACC	CCGCACACCA	ACTTCGAGGC	650
	GAACGTCTAC	ATCCTGTCCA	AGGACGAGGG	TGGGCGTCAC	ACCCCGTTCT	700
	ACTCGAACTA	CCGCGCGCAG	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	750
	GTCATCACGC	TGCCCCGAGGG	CACCGAGATG	GTCATGCCCCG	GCGACACCAC	800
5	CGAGATGTCG	GTCGAGCTCA	TCCAGCCGAT	CGCCATGGAG	GAGGGCCTCG	850
	GCTTCGCCAT	CCGCGAGGGT	GGCCGCACCG	TGGGCTCCGG	C	891

10 2) INFORMATION FOR SEQ ID NO: 1744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: Erdmann
 (C) ACCESSION NUMBER: X63539

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744

	AACATGATCA	CCGGCGCCGC	GCAGATGGAC	GGTGCGATCC	TGGTGGTCGC	50
	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	CGAGCACGTT	CTGCTGGCGC	100
	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	CGCTGAACAA	GGCCGACGCA	150
30	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	GAGATGGAGG	TCCGCGAGCT	200
	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	CCCGGTTGTG	CGGGTCTCGG	250
	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	GGGTTGCCTC	TGTCGAGGAA	300
	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	GACCCGGTCC	GCGAGACCGA	350
	CAAGCCGTTC	CTGATGCCGG	TCGAGGACGT	CTTCACCATT	ACCGGCCGCG	400
35	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	GCGTGATCAA	CGTGAACGAG	450
	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	ACCACCAAGA	CCACCGTCAC	500
	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	CCAGGGCCAG	GCGGGCGACA	550
	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	GCGAGGACGT	CGAGCGTGGC	600
	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	CCGCACACCG	AGTTCGAAGG	650
40	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	CGGCCGGCAC	ACGCCGTTCT	700
	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTGACCGGT	750
	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	GTGATGCCCCG	GTGACAACAC	800
	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	CGCCATGGAC	GAAGGTCTGC	850
45	GTTTCGCGAT	CCGCGAGGGT	GGCCGCACCG	TGGGCGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1745

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(B) STRAIN: G37

(C) ACCESSION NUMBER: U39732

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745

	AATATGATCA	CAGGTGCTGC	ACAAATGGAT	GGAGCTATTC	TAGTTGTTTC	50
	AGCAACTGAT	AGTGTGATGC	CCCAAACCCG	CGAGCACATC	TTACTTGCCC	100
	GCCAAGTAGG	GGTTCCTAAA	ATGGTAGTTT	TTCTAAACAA	GTGTGATATT	150
15	GCTAGTGATG	AAGAGGTACA	AGAACTTGTT	GCTGAAGAAG	TACGTGATCT	200
	GTAACTTCC	TATGGTTTTG	ATGGTAAGAA	CACTCCTATT	ATTTATGGCT	250
	CAGCTTTAAA	AGCATTGGAA	GGTGATCCAA	AGTGGGAGGC	TAAGATCCAT	300
	GATTTGATTA	AAGCAGTTGA	TGAATGGATT	CCAACCTCCTA	CACGTGAAGT	350
	AGATAAACCT	TTCTTATTAG	CAATTGAAGA	TACGATGACC	ATTACTGGTA	400
20	GAGGTACAGT	TGTTACAGGA	AGAGTTGAAA	GAGGTGAACT	CAAAGTAGGT	450
	CAAGAAGTTG	AAATTGTTGG	TTTAAACCA	ATTAGAAAAG	CAGTTGTTAC	500
	TGGAATTGAA	ATGTTCAAAA	AGGAACTTGA	TTCAGCAATG	GCTGGTGACA	550
	ATGCTGGGGT	ATTATTACGT	GGTGTTGAAC	GTAAAGAAGT	TGAAAGAGGT	600
	CAAGTTTTAG	CAAAACCAGG	CTCTATTAAA	CCGCACAAGA	AATTTAAAGC	650
25	TGAGATCTAT	GCTTTAAAGA	AAGAAGAAGG	TGGTAGACAC	ACTGGTTTTT	700
	TAAACGGTTA	CCGTCCTCAA	TTCTATTTCC	GTACCACTGA	TGTAACGGT	750
	TCTATTGCTT	TAGCTGAAAA	TACTGAAATG	GTTCTACCTG	GTGATAATGC	800
	TTCTATTACT	GTTGAGTTAA	TTGCTCCTAT	CGCTTGTGAA	AAAGGTAGTA	850
	AGTTCTCAAT	TCGTGAAGGT	GGTAGAACTG	TAGGGGCAGG	C	891

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2) INFORMATION FOR SEQ ID NO: 1746

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

45 (B) STRAIN: MS11

(C) ACCESSION NUMBER: L36380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746

50	AACATGATTA	CCGGCGCCGC	ACAAATGGAC	GGTGCAATCC	TGGTATGTTC	50
	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	CGAACACATC	CTGCTGGCCC	100
	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	TCATGAACAA	ATGCGACATG	150
	GTCGACGATG	CCGAGCTGTT	CCAACCTGGT	GAAATGGAAA	TCCGCGACCT	200

	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	CTGCCCCGATC	GTACAAGGTT	250
	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	CTTACGAAGA	AAAAATCTTC	300
	GAAGTGGCTA	CCGCATTGGA	CAGATACATC	CCGACTCCCG	AGCGTGCCGT	350
	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	CGTGTTCTCC	ATTTCCGGCC	400
5	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	GAGGTATCAT	CCACGTTGGT	450
	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	ACCCAAAAAA	CCACCTGTAC	500
	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAG	GCGGGCGACA	550
	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	GTGAAGACGT	AGAACGCGGT	600
	CAGGTATTGG	CCAAACGGGG	TACTATCACT	CCTCACACCA	AGTTCAAAGC	650
10	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	CGGCCCCCAT	ACCCCGTTTT	700
	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	GTACCACTGA	CGTAACCGGC	750
	ACGATTACTT	TGGAAAAAGG	TGTGGAAATG	GTAATGCCGG	GTGAGAACGT	800
	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	CGCTATGGAA	GAAGGTCTGC	850
15	GCTTTGCGAT	TCGCGAAGGC	GGCCGTACCG	TGGGTGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1747

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*
 30 (B) STRAIN: Madrid E
 (C) ACCESSION NUMBER: Z54170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747

35	AATATGATAA	CTGGTGCCGC	TCAGATGGAT	GGTGCTATAT	TAGTAGTTTC	50
	TGCTGCTGAT	GGTCCTATGC	CTCAAACCTAG	AGAACATATA	TTACTGGCAA	100
	AACAGGTAGG	TGTACCTGCT	ATGGTAGTAT	TTTTGAATAA	AGTAGATATG	150
	GTAGATGATC	CTGACCTATT	AGAATTAGTT	GAGATGGAAG	TAAGAGAATT	200
	ATTATCAAAA	TATGGTTTCC	CTGGTAATGA	AATACCTATT	ATTAAAGGTT	250
40	CTGCACTTCA	AGCTTTAGAA	GGAAAACCTG	AAGGTGAAAA	AGCTATTAAT	300
	GAGTTAATGA	ATGCAGTAGA	TACGTATATA	CCTCAGCCTA	TAGAGCTACA	350
	AGATAAACCT	TTTTTAATGC	CAATAGAGGA	TGTATTTTCT	ATTTTCAGGCA	400
	GAGGTACCGT	TGTAACCTGG	AGAGTGGAGT	CAGGCATAAT	TAAGGTGGGT	450
	GAAGAAATTG	AAATAGTAGG	TCTAAAAAAT	ACGCAAAAAA	CGACTTGTAC	500
45	AGGTGTAGAA	ATGTTTCAGAA	AATTACTTGA	TGAAGGACAA	TCTGGAGATA	550
	ATGTCGGTAT	ATTACTACGT	GGTACAAAAA	GAGAAGAAGT	AGAAAGAGGA	600
	CAAGTACTTG	CAAAACCTGG	GAGCATAAAA	CCGCATGATA	AATTTGAAGC	650
	TGAAGTGTAT	GTGCTTAGTA	AAGAGGAAGG	TGGACGTCAT	ACCCCATTTA	700
	CTAATGATTA	TCGCCACAG	TTCTATTTTA	GAACAACAGA	TGTTACCGGC	750
50	ACAATAAAAT	TGCCTTCTGA	TAAGCAGATG	GTTATGCCTG	GAGATAATGC	800
	TACTTTTTCA	GTAGAATTAA	TTAAGCCGAT	TGCTATGCAA	GAAGGGTTAA	850
	AATTCTCTAT	ACGTGAAGGT	GGTAGAACAG	TAGGAGCCGG	T	891

2) INFORMATION FOR SEQ ID NO: 1748

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 891 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Typhimurium
- (B) STRAIN: LT2 trpE91
- (C) ACCESSION NUMBER: X55116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748

	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	GGCGCGATCC	TGGTTGTTGC	50
20	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	TGAGCACATC	CTGCTGGGTC	100
	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	ATGCGACATG	150
	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	TTCGCGAACT	200
	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	GTTCGTGGTT	250
	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	GAAAATCATC	300
25	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	CCGGAACCAG	AGCGTGCGAT	350
	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	ATCTCCGGTC	400
	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	CAAAGTGGGC	450
	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	CTACCTGTAC	500
	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	GCCGGTGAGA	550
30	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	CGAACGTGGT	600
	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	AGTTCGAATC	650
	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	ACTCCGTTCT	700
	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	CGTGACTGGT	750
	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	800
35	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	GACGGTCTGC	850
	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	TTGGCGCGGG	C	891

40 2) INFORMATION FOR SEQ ID NO: 1749

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: DSM 50426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749

	ATGATCACTG	GTGCTGCACA	GATGGACGGC	GCGATTCTGG	TAGTCGCTTC	50
	AACAGACGGT	CCAATGCCAC	AGACTCGTGA	GCACATCCTG	CTTTCTCGTC	100
5	AGGTTGGCGT	ACCATTCATC	ATCGTATTCA	TGAACAAATG	TGACATGGTA	150
	GATGACGAAG	AGCTGTTAGA	GCTAGTTGAG	ATGGAAGTGC	GTGAACTGTT	200
	ATCAGAATAC	GATTTCCCAG	GTGATGACTT	ACCGGTAATC	CAAGGTTTCAG	250
	CTCTGAAAGC	GCTAGAAGGC	GAGCCAGAGT	GGGAAGCAAA	AATCCTTGAA	300
	TTAGCAGCGG	CGCTGGATTC	TTACATTCCA	GAACCACAAC	GTGACATCGA	350
10	TAAGCCGTTT	CTACTGCCAA	TCGAAGACGT	ATTCTCAATT	TCAGGCCGTG	400
	GTACAGTAGT	AACAGGTCGT	GTGAGCGTG	GTATTGTACG	CGTAGGCGAC	450
	GAAGTTGAAA	TCGTTGGTGT	ACGTGCGACA	ACTAAGACAA	CGTGTACTGG	500
	TGTAGAAATG	TTCCGTAAAC	TGCTTGACGA	AGGTCGTGCA	GGTGAGAACT	550
	GTGGTATTTT	GTTACGTGGT	ACTAAGCGTG	ATGACGTAGA	ACGTGGTCAA	600
15	GTATTAGCGA	AGCCAGGTTC	AATCAACCCA	CACACTACTT	TTGAATCAGA	650
	AGTTTACGTA	CTGTCAAAAG	AAGAAGGTGG	TCGTCACACG	CCATTCTTCA	700
	AAGGCTACCG	TCCACAGTTC	TACTTCCGTA	CAACTGACGT	AACCGGTACT	750
	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	ATGCCAGGCG	ATAACATCAA	800
	GATGGTAGTG	ACACTGATTT	GCCCAATCGC	GATGGACGAA	GGTTTACGCT	850
20	TCGCAATCCG	TGAAGGCGGT	CGTACAGTGG	T		881

2) INFORMATION FOR SEQ ID NO: 1750

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*
 (B) STRAIN: DW4
 (C) ACCESSION NUMBER: X82820

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750

40

	AACATGATCA	CGGGCGCGGC	GCAGATGGAC	GGAGCGATTTC	TGGTGGTGTC	50
	CGCGGCCGAC	GGCCCGATGC	CCCAGACGCG	TGAGCACATC	CTGCTGGCCA	100
	GGCAGGTGGG	CGTGCCCTAC	ATCGTCGTCT	TCCTGAACAA	GGTGGACATG	150
	CTGGACGATC	CGGAGCTGCG	CGAGCTGGTG	GAGATGGAGG	TGCGCGACCT	200
45	GCTCAAGAAG	TACGAGTTCC	CGGGCGACAG	CATCCCCATC	ATCCCTGGCA	250
	GCGCGCTCAA	GGCGCTGGAG	GGAGACACCA	GCGACATCGG	CGAGGGAGCG	300
	ATCCTGAAGC	TGATGGCGGC	GGTGGACGAG	TACATCCCGA	CGCCGCAGCG	350
	TGCGACGGAC	AAGCCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCCATCG	400
	CAGGCCGAGG	AACGGTGGCG	ACGGGCCGAG	TGGAGCGCGG	CAAGATCAAG	450
50	GTGGGCGAGG	AAGTGGAGAT	CGTGGGGATC	CGTCCGACGC	AGAAGACGGT	500
	CATCACGGGG	GTGGAGATGT	TCCGCAAGCT	GCTGGACGAG	GGCATGGCGG	550
	GAGACAACAT	CGGAGCGCTG	CTGCGAGGCC	TGAAGCGCGA	GGACCTGGAG	600
	CGTGGGCAGG	TGCTGGCGAA	CTGGGGGAGC	ATCAACCCGC	ACACGAAGTT	650

	CAAGGCGCAG	GTGTACGTGC	TGTCGAAGGA	AGAGGGAGGG	CGGCACACGC	700
	CGTTCTTCAA	GGGATACCGG	CCGCAGTTCT	ACTTCCGGAC	GACGGACGTG	750
	ACCGGAACGG	TGAAGCTGCC	GGACAACGTG	GAGATGGTGA	TGCCGGGAGA	800
	CAACATCGCC	ATCGAGGTGG	AGCTCATTAC	TCCGGTCGCC	ATGGAGAAGG	850
5	AGCTGCCGTT	CGCCATCCGT	GAGGGTGGCC	GCACGGTGGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1751

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiomonas cuprina*
 (B) STRAIN: Hoe5
 (C) ACCESSION NUMBER: x76871

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1751

25

	AACATGATCA	CCGGTGCGGC	CCAGATGGAC	GGCGCCATCC	TGGTCGTGTC	50
	CGCCGCCGAC	GGCCCCATGC	CCCAAACCCG	CGAGCACATC	CTGCTGGCGC	100
	GTCAGGTGGG	CGTGCCCTAC	ATCATCGTGT	TCCTCAACAA	GTGCGACATG	150
	GTCGACGACG	CCGAGCTGCT	CGAACTCGTC	GAGATGGAAG	TGCGCGAGCT	200
30	GCTGTCCAAG	TACGACTTCC	CCGGTGACGA	CACCCCCATC	ATCAAGGGCT	250
	CGGCCAAGCT	GGCCCTCGAA	GGCGACAAGG	GCGAACTGGG	CGAAGGCGCC	300
	ATTCTCAAGC	TGGCCGAGGC	CCTGGACACC	TACATCCCCA	CGCCCGAGCG	350
	GGCCGTCGAC	GGCGCGTTCC	TCATGCCCGT	GGAAGACGTG	TTCTCCATCT	400
	CCGGGCGCGG	CACGGTGGTC	ACCGGGCGTG	TGGAGCGCGG	CATCATCAAG	450
35	GTCGGCGAGG	AAATCGAGAT	TGTCGGCCTC	AAGCCCACCC	TCAAGACCAC	500
	CTGCACCGGC	GTGGAAATGT	TCAGGAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACGT	CGGCATCTTG	CTGCGCGGCA	CCAAGCGCGA	GGAAGTCGAG	600
	CGCGGCCAGG	TGCTGTGCAA	ACCGGGCTCG	ATCAAGCCCC	ACACCCACTT	650
	CACCGCCGAG	GTGTACGTGC	TGAGCAAGGA	CGAGGGCGGC	CGCCACACCC	700
40	CCTTCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGCAC	CACCGACGTC	750
	ACCGGCGCCA	TCGAACTGCC	CAAGGACAAG	GAAATGGTCA	TGCCCGGCGA	800
	TAATGTGAGC	ATCACCGTCA	AGCTCATCGC	CCCCATCGCC	ATGGAAGAAG	850
	GCCTGCGCTT	CGCCATCCGC	GAAGGCGGCC	GCACCGTCGG	CGCCGGC	897

45

2) INFORMATION FOR SEQ ID NO: 1752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: AE001202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752

```

10 AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC      50
   TGC GCCTGAC GGC GTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC      100
   GTCAGGTTGG TGTTCCTCC ATCATTGTTT TTTTGAACAA GGTTGATTTG      150
   GTTGATGATC CTGAGTTGCT AGAGCTGGTG GAAGAAGAGG TCGGTGATGC      200
15 GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC AAGGGGTCTG      250
   CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGTATT      300
   GAGGAACTGC TTGCGGCCAT GGATTCCTAC TTTGAAGACC CAGTGCGTGA      350
   CGACGCAAGA CCTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTTCTG      400
   GGC GTGGTAC CGTTGTCACG GGGCGCATCG AATGTGGGGT AATTAGTCTG      450
20 AATGAAGAGG TCGAGATCGT CGGGATTAAG CCCACTAAGA AAACAGTGGT      500
   TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA ATTGCAGGTG      550
   ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAAGA GGTTGAGCGC      600
   GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA      650
   GGCGCAGATC TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCTT      700
25 TTTTTC AAGG TTATCGTCCG CAGTTTTATT TTAGA ACTAC TGACATTACC      750
   GGTACGATTT CTCTTCCTGA AGGGGTAGAC ATGGTGAAGC CGGGGGATAA      800
   CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG GACAAGGGTC      850
   TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT          894
  
```

30

2) INFORMATION FOR SEQ ID NO: 1753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ureaplasma urealyticum*
 (B) STRAIN: ATCC 33697
 45 (C) ACCESSION NUMBER: Z34275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753

```

50 AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC      50
   TGCATCTGAT GGGGTTATGG CTCAA ACTAA AGAACATATT TTATTAGCAC      100
   GTCAAGTTGG TGTTC CAAAA ATCGTTGTTT TCTTAAACAA ATGTGATTTT      150
   ATGACAGATC CAGATATGCA AGATCTTGTT GAAATGGAAG TTCGTGAATT      200
   ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT ATTCGTGGTT      250
  
```

	CAGGTCTTAA	GGCTTTAGAA	GGAGATCCAG	TTTGAGAAGC	AAAAATTGAT	300
	GAATTAATGG	ACGCAGTTGA	TTCATGAATT	CCATTACCAG	AACGTAGTAC	350
	TGACAAACCA	TTCTTATTAG	CAATTGAAGA	TGTATTCACA	ATTTCAGGAC	400
	GTGGTACAGT	AGTAACTGGA	CGTGTTGAAC	GTGGTGTATT	AAAAGTTAAT	450
5	GATGAGGTTG	AAATTGTTGG	TCTAAAAGAC	ACTCAAAAAA	CTGTTGTTAC	500
	AGGAATTGAA	ATGTTTAGAA	AATCATTAGA	TCAAGCTGAA	GCTGGTGATA	550
	ATGCTGGTAT	TTTATTACGT	GGTATTAAAA	AAGAAGATGT	TGAACGTGGT	600
	CAAGTACTTG	TAAAACCAGG	ATCAATTAAA	CCTCACCGTA	CTTTTACTGC	650
	TAAAGTTTAT	ATTCTTAAAA	AAGAAGAAGG	TGGACGTCAT	ACACCTATTG	700
10	TTTCAGGATA	CCGTCCACAA	TTCTATTTTA	GAACAACAGA	TGTAACAGGT	750
	GCTATTTCAT	TACCTGCTGG	TGTTGATTTG	GTTATGCCAG	GTGATGACGT	800
	TGAAATGACT	GTAGAATTAA	TTGCTCCAGT	TGCGATTGAA	GATGGATCTA	850
	AATTCTCAAT	CCGTGAAGGT	GGTAAAAC TG	TAGGTCATGG	T	891

15

2) INFORMATION FOR SEQ ID NO: 1754

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 909 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wolinella succinogenes*
 (B) STRAIN: DSM 1740
 30 (C) ACCESSION NUMBER: X76862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754

	AACATGATTA	CAGGTGCTGC	TCAAATGGAT	GGCGCGATTC	TTGTTGTTTC	50
35	TGCGGCGGAT	GGCCCCATGC	CCCAAAC TAG	GGAGCACATT	CTTCTTTCTC	100
	GACAAGTAGG	CGTTCCTTAC	ATCGTGGTTT	TCTTGAACAA	AGAAGATATG	150
	GTTGATGACG	CTGAGCTTCT	TGAGCTTGTT	GAAATGGAAG	TTAGAGAACT	200
	TCTTAGCAAC	TACGACTTCC	CTGGAGATGA	CACTCCTATC	GTTGCAGGTT	250
	CCGCTCTTAA	AGCTCTTGAA	GAGGCTAACG	ACCAGGAAAA	TGTTGGCGAG	300
40	TGGGGCGAGA	AAGTATTGAA	GCTTATGGCT	GAGGTTGACC	GATATATTCC	350
	TACGCCTGAG	CGAGATGTGG	ATAAGCCTTT	CCTTATGCCT	GTTGAAGACG	400
	TATTCTCCAT	CGCGGGTCGT	GGAACCGTTG	TGACAGGAAG	AATTGAAAGA	450
	GGCGTGTTTA	AAGTCGGTGA	CGAAGTAGAA	ATCGTTGGTA	TCCGAAACAC	500
	ACAAAAACA	ACCGTAACTG	GCGTTGAGAT	GTTCCGAAAA	GAGCTCGACA	550
45	AGGGTGAGGC	GGGTGACAAC	GTTGGTGTTT	TTTTGAGAGG	CACCAAGAAA	600
	GAAGATGTTG	AGAGAGGTAT	GGTTCTTTGT	AAAATAGGTT	CTATCACTCC	650
	TCACACTAAC	TTTGAAGGTG	AAGTTTACGT	TCTTTCCAAA	GAGGAAGGCG	700
	GACGACACAC	TCCATTCTTC	AATGGATACC	GACCTCAGTT	CTATGTTAGA	750
	ACTACAGACG	TTACCGGTTT	TATCTCTCTT	CCTGAGGGCG	TAGAGATGGT	800
50	TATGCCTGGT	GACAACGTTA	AGATCAATGT	TGAGCTTATC	GCTCCTGTAG	850
	CCCTCGAAGA	GGGAACACGA	TTGCGGATCC	GTGAAGGTGG	TCGAACCGTT	900
	GGTGCGGGT					909

2) INFORMATION FOR SEQ ID NO: 1755

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755

15

15	ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
	AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
	AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
	GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
20	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
	CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300
	ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
	AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCTG	AGCGCGGCAT	CGTGAAGGTC	450
25	GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
	CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
	GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
30	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
	CGTGTCGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
	TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCGGC		888

35

2) INFORMATION FOR SEQ ID NO: 1756

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756

TGAAAGTTCA GGTAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50

AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 5 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1757

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 20
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: ATCC 4229

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757

TGAAAGTTCA GGTAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 30 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388
 35

2) INFORMATION FOR SEQ ID NO: 1758

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 45
 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 50 (B) STRAIN: ATCC 7064
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758

5 TGAAAGTTCA GGTAAAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 5 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388
 10

2) INFORMATION FOR SEQ ID NO: 1759

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 25 (B) STRAIN: ATCC 13472
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759

30 TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC 50
 AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT 100
 CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC 150
 ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 35 CCGAAAGCAG AGATTGAAGG TGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA 350
 AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT 388

40 2) INFORMATION FOR SEQ ID NO: 1760

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760

```

5  AAACGACAGT TTCATTACAT GCAATTGCAG AAGTACAACG TCAAGGTGGA      50
   CAAGCAGCAT TCATCGATGC GGAGCACGCA ATGGATCCTG TATATGCACA      100
   AAAATTAGGC GTTAACATAG ATGAATTACT ATTATCACAG CCTGATACAG      150
   GGGAGCAAGG ATTAGAAATC GCAGAAGCAC TTGTACGAAG TGGTGCGGTT      200
   GACATTATCG TAATTGACTC TGTAGCAGCT CTTGTACCGA AAGCAGAGAT      250
   TGAAGGAGAC ATGGGTGACT CACACGTAGG TTTACAAGCA CGTTTAATGT      300
10  CACAAGCACT TCGTAAGCTT TCAGGAGCAA TCAACAAATC AAAACAATT      350
   GCAATCTTTA TTAACCAAAT TCGT                                374

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15 2) INFORMATION FOR SEQ ID NO: 1761

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
 (B) STRAIN: NRRL BD-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761

```

30  GGAAAGTTCA GGTAACAAAC CGGTTTCCTT ACATGCGATT GCAGAAGTGC      50
   AACGTCAAGG TGGACAAGCG GCATTTATTG ATGCGGAGCA TGCGATGGAT      100
   CCTGTATATG CACAAAAGTT AGGTGTTAAT ATTGATGAGT TACTATTATC      150
   GCAGCCTGAT ACAGGAGAAC AAGGTTTAGA AATCGCAGAA GCATTAGTAC      200
35  GAAGCGGTGC GATTGATATC ATTGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CCAAAGCAG AAATCGAAGG GGAAATGGGT GACTCCCACG TTGGTTTACA      300
   AGCGCGTTTA ATGTCACAAG CACTTCGTAA GCTTTCTGGT GCGATTAACA      350
   AATCAAAAAC AATTGCAATC TTCATTAACC A                                381

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40

2) INFORMATION FOR SEQ ID NO: 1762

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762

5	TGAAAGTTCA	GGTAAAACGA	CAGTTTCATT	ACATGCAATT	GCAGAAGTAC	50
	AACGTCAAGG	TGGACAAGCA	GCATTCATCG	ATGCGGAGCA	CGCAATGGAT	100
	CCTGTATATG	CACAAAAATT	AGGCGTTAAC	ATAGATGAAT	TACTATTATC	150
	ACAGCCTGAT	ACAGGGGAGC	AAGGATTAGA	AATCGCGGAA	GCACTTGTAC	200
	GAAGTGGTGC	GGTTGACATT	ATCGTAATTG	ACTCTGTAGC	AGCTCTTGTA	250
10	CCGAAAGCAG	AGATTGAAGG	CGACATGGGT	GACTCACACG	TAGGTTTACA	300
	AGCACGTTTA	ATGTCACAAG	CACTTCGTAA	GCTTTCAGGA	GCAATCAACA	350
	AATCAAAAAC	AATTGCAATC	TTTATTAACC	AAATTCGT		388

15

2) INFORMATION FOR SEQ ID NO: 1763

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 388 bases
20	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Bacillus thuringiensis</i>
	(B) STRAIN: HER 1418

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763

	TGAAAGTTCA	GGTAAAACGA	CAGTTTCATT	ACATGCAATT	GCAGAAGTAC	50
	AACGTCAAGG	TGGACAAGCA	GCATTCATTG	ATGCGGAGCA	CGCAATGGAT	100
	CCTGTATATG	CACAAAAATT	AGGCGTTAAC	ATAGATGAAT	TACTATTATC	150
35	ACAGCCTGAT	ACAGGGGAGC	AAGGATTGGA	AATCGCGGAA	GCACTTGTAC	200
	GAAGTGGTGC	GGTTGACATT	ATCGTAATTG	ACTCTGTAGC	AGCTCTTGTA	250
	CCGAAAGCAG	AGATTGAAGG	CGATATGGGT	GACTCACACG	TAGGTTTACA	300
	AGCACGTTTA	ATGTCACAAG	CACTTCGTAA	GCTTTCAGGA	GCAATCAACA	350
	AATCAAAAAC	AATTGCAATC	TTTATTAACC	AAATTCGT		388

40

2) INFORMATION FOR SEQ ID NO: 1764

(i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH: 358 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764

5 CTCCTATCTG GATTATGCGA TGTCGGTCAT TGTGCGCCGT GCGCTGCCGG 50
 ATGTCCGAGA TGGCCTGAAG CCGGTACACC GTCGCGTACT ATACGCCATG 100
 AACGTATTGG GCAATGACTG GAACAAAGCC TATAAAAAAT CTGCCCCTGT 150
 CGTGGGTGAC GTCATCGGTA AATACCACCC TCATGGTGAT ACTGCCGTAT 200
 10 ACGACACCAT TGTACGTATG GCGCAGCCCT TCTCCCTGCG TTACATGCTG 250
 GTAGATGGCC AGGGTAACTT TGGTTCGGTC GACGGCGACT CCGCCGCAGC 300
 GATGCGTTAT ACGGAAATCC GTATGTCGAA GATCGCCCAT GAACTGATGG 350
 CCGACCTC 358

15

2) INFORMATION FOR SEQ ID NO: 1765

- (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 365 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765

TTAAGAACTC TTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG 50
 CTGCCGGATG TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTTTA 100
 35 CGCCATGAAC GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCAG 150
 CCCGTGTCGT TGGTGACGTA ATCGGTAAAT ACCACCCGCA CGGCGACTCC 200
 GCGGTATACG ACACCATCGT GCGTATGGCG CAGCCGTTCT CGCTGCGTTA 250
 CATGCTGGTG GACGGCCAGG GTAACCTTGG TTCCATCGAC GGC GACTCCG 300
 CCGCGGCGAT GCGTTATACC GAAATTCGTC TGGCGAAAAT CGCTCATGAG 350
 40 CTGATGGCCG ATCTT 365

2) INFORMATION FOR SEQ ID NO: 1766

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766

	AAGAGCTCGT	ATCTGGATTA	TGCGATGTCG	GTCATTGTTG	GCCGTGCGCT	50
	GCCGGATGTC	CGAGATGGCC	TGAAACCGGT	ACACCGTCGC	GTA CTTTACG	100
	CCATGAACGT	ATTGGGCAAT	GACTGGAACA	AAGCCTATAA	AAAATCCGCC	150
10	CGTGTCGTTG	GTGACGTAAT	CGGTAAATAC	CACCCTCATG	GTGATACCGC	200
	CGTTTATGAC	ACCATTGTAC	GTATGGCACA	GCCATTCTCC	TTGCGTTATA	250
	TGCTGGTCGA	TGGCCAGGGT	AACTTCGGTT	CTGTCGATGG	CGACTCCGCC	300
	GCAGCGATGC	GTTATACGGA	AATCCGTATG	TCGAAAATCG	CCCA	344

15

2) INFORMATION FOR SEQ ID NO: 1767

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 345 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(B) STRAIN: ATCC 27336

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767

	AACTCTTATC	TGGATTATGC	GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	50
	GGATGTCCGA	GATGGCCTGA	AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	100
35	TGAACGTATT	GGGCAATGAC	TGGAACAAAG	CCTATAAAAA	ATCAGCCCGT	150
	GTCGTTGGTG	ACGTAATCGG	TAAATACCAC	CCGCACGGCG	ACTCCGCGGT	200
	ATACGACACC	ATCGTGCGTA	TGGCGCAGCC	GTTCTCGCTG	CGTTACATGC	250
	TGGTGGACGG	CCAGGGTAAC	TTTGGTTCCA	TCGACGGCGA	CTCCGCCGCG	300
	GCGATGCGTT	ATACCGAAAT	TCGTCTGGCG	AAAATCGCTC	ATGAG	345

40

2) INFORMATION FOR SEQ ID NO: 1768

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 356 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
(B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768

5 CTTATCTGGA TTATGCGATG TCGGTCATTG TTGGCCGTGC GCTGCCGGAT 50
GTCCGAGATG GCCTGAAGCC GGTACACCGT CGCGTACTTT ACGCCATGAA 100
CGTATTGGGC AATGACTGGA ACAAAGCCTA TAAAAAATCA GCCCGTGTCTG 150
TTGGTGACGT AATCGGTAAA TACCACCCGC ACGGCGACTC CGCGGTATAC 200
10 GACACCATCG TCGGTATGGC GCAGCCGTTT TCGCTGCGTT ACATGCTGGT 250
GGACGGCCAG GGTAACCTTTG GTTCCATCGA CGGCGACTCC GCCGCGGCCGA 300
TGC GTTATAC CGAAATTCGT CTGGCGAAAA TCGCTCATGA GCTGATGGCC 350
GATCTT 356

15

2) INFORMATION FOR SEQ ID NO: 1769

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 361 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
(B) STRAIN: ATCC 29011

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769

TAAGAACTCT TATCTGGATT ATGCGATGTC GGTCATTGTT GGCCGTGCGC 50
TGCCGGATGT CCGAGATGGC CTGAAGCCGG TACACCGTCG CGTACTTTAC 100
35 GCCATGAACG TATTGGGCAA TGACTGGAAC AAAGCCTATA AAAAATCAGC 150
CCGTGTCGTT GGTGACGTAA TCGGTAAATA CCACCCGCAC GGCGACTCCG 200
CGGTATACGA CACCATCGTG CGTATGGCGC AGCCGTTCTC GCTGCGTTAC 250
ATGCTGGTGG ACGGCCAGGG TAACTTTGGT TCCATCGACG GCGACTCCGC 300
CGCGGCGATG CGTTATACCG AAATTCGTCT GGCGAAAATC GTCATGAGC 350
40 TGATGGCCGA T 361

45

2) INFORMATION FOR SEQ ID NO: 1770

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
 (B) STRAIN: ATCC 13824

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770

	TAAGAACTCT	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	50
	TGCCGGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	100
10	GCCATGAACG	TATTGGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCAGC	150
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCACCCGCAC	GGCGACTCCG	200
	CGGTATACGA	CACCATCGTG	CGTATGGCGC	AGCCGTTCTC	GCTGCGTTAC	250
	ATGCTGGTGG	ACGGCCAGGG	TAACTTTGGT	TCCATCGACG	GCGATTCCGC	300
	CGCGGCGATG	CGTTATACCG	AAATTCGTCT	GGCGAAAATC	GCTCATGAGC	350
15	TGATGGCCGA	TCTTG				365

2) INFORMATION FOR SEQ ID NO: 1771

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Klebsiella terrigena*
 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771

35	TCGTATCTGG	ATTATGCGAT	GTCGGTCATT	GTTGGCCGTG	CGCTGCCGGA	50
	TGTCCGAGAT	GGGTTGAAAC	CGGTACACCG	TCGCGTACTT	TACGCCATGA	100
	ACGTATTGGG	CAATGACTGG	AACAAAGCCT	ATAAAAAATC	CGCCCGTGTC	150
	GTTGGTGACG	TAATCGGTAA	ATATCACCCCT	CACGGTGATA	CCGCCGTTTA	200
	TGACACCATT	GTACGTATGG	CGCAGCCATT	CTCCTTGCGT	TATATGCTGG	250
40	TCGATGGCCA	GGGTAAC TTC	GGTTCTGTCG	ATGGCGACTC	CGCCGCAGCG	300
	ATGCGTTATA	CGGAAATCCG	TATGTCGAAA	ATCGCCCACG	AGCTGATGGC	350
	CGACCTC					357

45

2) INFORMATION FOR SEQ ID NO: 1772

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 5 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772

	CAGTACACAG	GCGAGTTCTT	TTTGCGATGA	GTGAGTTAAG	TAATGATTGG	50
10	AATAAGCCGT	ATAAAAAATC	TGCTCGTGTA	GTAGGGGATG	TCATTGGTAA	100
	ATATCATCCT	CATGGGGATA	CAGCTGTTTA	TGACACTATT	GTTCGTATGG	150
	CTCAGCCCTT	TTCCATGCGT	TATATGCTGA	TTGATGGGCA	GGGTAATTTT	200
	GGCTCTGTAG	ATGGAGATGC	TCCAGCTGCC	ATGCGTTACA	CTGAAGTAAG	250
	AATGTCCAAA	GTGGCGCATG	CTTTACTGGC	TGATTTGGAT	AAGGAAACCG	300
15	TTGATTTTAG	TCCTAACTAT	GATGAAACAG	AATTTGCTCC	AGTGGTATTG	350
	CCATCGAGAA	TTCCCAATTT	ACTAGTTAAT	GGCTCTTCCG	GTATTGCGGT	400
	AGGGATGGCT	ACTAATATTC	CACCACATAA	TCTTACCGAA	GTAATCAATG	450
	CATGTATTGC	TTTAGTGGAT	GAACCTGACA	CGAGTCTTGA	AGATTTAATG	500
	GAAATTATTC	CTGGCCCTGA	TTTTCCTACA	GCCGCAATTA	TTAATGGTCG	550
20	TGCTGGAATT	ATTGAAGGTT	ATCGTACTGG	AAAAGGGCGG	GTTGTTATCA	600
	GGGCACGCAC	AGAAATTGAA	ACGGATGAAA	G TTCAGGCCG	TCAGTCAATT	650
	ATTATTCAGG	AATTACCCTA	TCAGGTGAAT	AAAGCGCGTT	TGATCGAGCG	700
	TATTGCTGAA	TTGGTAAGGG	ACAAGAAAAT	CGAAGGAATT	TCCGGCTTGA	750
	GAGATGAGTC	AGACAAGCAA	GGAATGAGAG	TAGTCATTGA	ATTAAAACGC	800
25	AATGAAGTAG	CAGATGTGGT	ATTGAATAAC	CTGTTCGCTC	ATACTCAAAT	850
	GCAAAATGTA	TTCGGAATTA	ATATGGTTGC	TCTGGTGGAT	GGCCAACCGC	900
	GTACTTTGAA	TTTGAAGCAA	ATACTGGAAT	ATTTTATAAA	ACATCGAAGA	950
	GAGGTTGTTA	CCAGACGC				968

30

2) INFORMATION FOR SEQ ID NO: 1773

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 967 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
 45 (B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773

	CACCGCCGAG	TGCTATTTGC	GATGAATGTA	CTGGGAAACG	ATTGGAATAA	50
	ACCTTATAAA	AAATCAGCCC	GTGTTGTTGG	GGATGTAATC	GGTAAATATC	100
50	ACCCGCACGG	TGACAGTGCT	GTCTATGAAA	CGATTGTTCG	TTTAGCACAG	150
	CCTTTTTCTA	TGCGCTACAT	GTTGGTTGAC	GGTCAGGGTA	ACTTCGGGTC	200
	AGTTGATGGT	GACTCCGCGG	CGGCTATGCG	TTATACCGAA	GTTCGTATGG	250
	CGAAGATCGC	CCATGAACTG	CTGGCGGATT	TGGAAAAAGA	GACGGTCGAC	300

TTTGTTCTTA ACTATGATGG AACAGAAAAT ATACCGGCTG TTATGCCAAC 350
 CCGTATTCCA AACTTGTTAG TTAATGGCTC TTCAGGTATT GCCGTTGGGA 400
 TGGCAACGAA TATCCCTCCG CATAACCTCG GTGAAGTTAT CGACGGTTGT 450
 CTTGCCTATG TTGATAATGA AGACATCACC ATAGAAGAAT TAATGGAATA 500
 5 TATTACCGGG CCTGATTTTC CGACTGCTGC GATTATTAAT GGTCGCAGAG 550
 GAATATTAGA TGCTTATCGT ACAGGGCGTG GAAAGATTTA TATCCGTGCT 600
 CAGGCTGATA TTGAAACTGA TGAGAAAACA GGTCGCGAAA CCATTATCGT 650
 GACAGAAATT CCTTATCAGG TGAATAAAGC CCGTTTAATT GAAAAAATTG 700
 CGGAGCTTGT AAAAGATAAA CGTATTGAAG GTATCAGCGG ATTACGTGAC 750
 10 GAGTCTGATA AAGACGGTAT GCGTATTGTT GTTGAGATCA AACGTGATGC 800
 AGTCGGTGAA GTAGTATTAA ATCACCTCTT TTCACAACT CAAATGCAAG 850
 TCTCTTTTGG TATTAATATG GTTGCGCTTC ATCAAGGCCA ACCAAAATTA 900
 TTGAACCTAA AAGAAATTAT CGCAGCCTTT ATTCGCCATC GTCGTGAAGT 950
 GGTGACTCGC CGTACCA 967
 15

2) INFORMATION FOR SEQ ID NO: 1774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 30 (B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774

CCAGTACACC GCAGAGTATT GTATGCGATG AATGTATTGG GAAATGATTG 50
 35 GAATAAACCC TATAAAAAAT CTGCCCCTAT TGTTGGGGAC GTCATCGGTA 100
 AATACCATCC ACATGGTGAT AGCGCTGTTT ACGAGACAAT CGTTCGTCTT 150
 GCTCAGCCTT TCTCAATGCG TTACATGCTG GTTGATGGTC AGGGAAACTT 200
 CGGTTCTGTT GACGGAGACT CCGCAGCGGC AATGCGTTAT ACGGAAATCC 250
 GTATGGCGAA AATTGCCCAT GAACTACTTG CTGACCTTGA AAAAGAAACC 300
 40 GTTGATTTTCG TTCCTAACTA TGACGGAACA GAGCACATTC CTGAAGTTAT 350
 GCCAACGAAA ATCCCAAACC TTTTGGTTAA TGGGTCGTCA GGTATTGCTG 400
 TTGGGATGGC AACCAATATC CCACCTCACA ATTTAGGGGA GGTGATTAAT 450
 GGTGTCTTG CCTATATAGA AGACGAAGAC ATCAGCATTG ATGGTTTAAT 500
 GGAACACATT CCAGGGCCTG ATTTCCCAAC CGCAGCTATT ATTAATGGCC 550
 45 GTCGTGGGAT TATTGATGCG TATCGCACAG GCGGTGGCAA GGTCTATATC 600
 CGTGCAAGCG CTGAAGTGGA AGTCGATGAG AAAAATGGTC GCGAAACCAT 650
 TATTGTCAGC GAAATTCCTT ATCAAGTGAA TAAAGCTCGC TTGATTGAAA 700
 AAATTGCTGA GTTAGTTAAA GACAAGCGTG TTGAAGGTAT CAGTGCACTG 750
 CGTGACGAGT CTGATAAAGA CGGTATGCGT ATTGTTATTG AAATCAAACG 800
 50 CGATGCGGTG GGTGAAGTTG TACTGAACAA CTTATATTCC CTGACCCAAT 850
 TGCAAGTTTC TTTTGGTATC AATATGGTAG CTCTACACCA AGGGCAGCCG 900
 AAAATACTGA ATTTAAAAGA TATCATTGCT GCTTTTGTGC GTCACCGCCG 950
 TGAAGTCGTC ACTCGTCGTA CGATTTTC 978

2) INFORMATION FOR SEQ ID NO: 1775

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775

	CCAGTACACC	GTCGCGTTCT	TTTCGCGATG	AATGTATTAG	GAAACGATTG	50
	GAATAAACCT	TATAAAAAAT	CAGCCCGTGT	TGTTGGGGAT	GTTATCGGTA	100
	AATATCACCC	GCACGGTGAC	AGTGCTGTTT	ATGAAACGAT	AGTTCGTTTA	150
20	GCACAGCCTT	TTTCTATGCG	TTACATGTTG	GTTGACGGGC	AGGGTAACTT	200
	CGGGTCAGTT	GATGGTGACT	CGGCGGCTGC	AATGCGTTAT	ACCGAAGTTC	250
	GTATGGCGAA	AATCGCCCAT	GAAGTGTGG	CGGATTTGGA	AAAAGAAACG	300
	GTTGATTTTG	TTCCTAACTA	TGATGGAACA	GAGCATATCC	CGGCAGTCAT	350
	GCCAACCCGT	ATTCCAAACT	TATTAGTCAA	TGGTTCCTCA	GGTATCGCAG	400
25	TCGGGATGGC	AACAAACATT	CCTCCGCATA	ACCTAGGTGA	AGTTATCGAC	450
	GGCTGTCTTG	CTTATGTTGA	TAACGAAGAC	ATCACTATTG	AAGAGTTGAT	500
	GGAGCATATC	ACGGGGCCTG	ATTTCCCAAC	TGCCGCTATT	ATTAATGGCC	550
	GCAGAGGAAT	TTTAGATGCT	TACCGTACTG	GGCGCGGAAA	AATTTATATT	600
	CGTGACACAAG	CTGATGTAGA	AACCGATGAG	AAAAGTGGTC	GCGAAACAAT	650
30	TATCGTGACG	GAAATTCCTT	ATCAGGTGAA	CAAAGCTCGC	TTAATTGAAA	700
	AAATTGCAGA	GCTTGTTAAA	GATAAACGTA	TTGAAGGCAT	TAGCGGATTA	750
	CGTGATGAGT	CAGATAAAGA	TGGTATGCGC	ATTGTTGTTG	AAATTAAGCG	800
	TGATGCTGTT	GGTGAAGTTG	TACTAAATCA	CTTATTTTCT	CAGACTCAGA	850
	TGCAGGTTTC	TTTTGGTATT	AACATGGTTG	CACTGCATCA	AGGTCAACCG	900
35	AAAGTGTTAA	ACCTGAAAGA	AATTATTTCA	GCCTTTATTC	GTCACCGTCG	950
	TGAAGTGGTG	ACTCGTCGTA	CTATTTTT			978

40 2) INFORMATION FOR SEQ ID NO: 1776

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 940 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776

	TGGGTAATGA	CTGGAATAAG	CCATACAAAA	AATCGGCCCG	TGTAGTCGGG	50
	GACGTTATCG	GTAAATATCA	CCCGCATGGT	GACAGCGCGG	TCTACGACAC	100
5	AATTGTGCGT	ATGGCCCAGC	CGTTCTCACT	GCGCTATATG	CTGGTGGATG	150
	GGCAGGGCAA	CTTCGGTTCC	GTTGATGGCG	ACTCCGCCGC	AGCGATGCGT	200
	TATACCGAAA	TCCGTATGTC	TAAAATTGCT	CACGAATTGT	TGGCGGACTT	250
	AGAAAAAGAT	ACCGTCGACT	TCGTGCCGAA	CTATGACGGT	ACGGAGCAAA	300
	TTCCTGCCGT	AATGCCAACC	CGAATCCCTA	ACTTGCTGGT	TAACGGCTCG	350
10	TCAGGTATTG	CTGTCGGTAT	GGCAACCAAT	ATTCCGCCGC	ATAACCTTTC	400
	TGAGGTATT	GATGGCTGTC	TGGCCTATAT	CGAAGATGAA	AACATCACCA	450
	TTGAAGGGTT	GATGGAGTAC	ATCCCGGGGC	CAGATTTCCC	AACTGCTGCG	500
	ATTATCAATG	GTCGCCGTGG	TATTGAAGAA	GCTTATCGTA	CTGGCCGTGG	550
	CAAGGTGTAT	ATCCGTGCCC	GTGCTGAAGT	TGAGGCTGAC	GCTTAAACCG	600
15	GTCGCGAAAC	CATTATTGTT	CACGAGATCC	CGTATCAGGT	GAACAAGGCG	650
	CGGTTGATTG	AAAAAATCGC	CGAGCTGGTT	AAAGAAAAAC	GCGTAGAAGG	700
	CATCAGTGCG	TTGCGTGATG	AGTCTGATAA	AGACGGCATG	CGTATCGTGA	750
	TTGAAATCAA	ACGTGATGCT	GTCGGGGAAG	TGGTTCTGAA	CAACCTCTAT	800
	TCTCTGACGC	AATTGCAGGT	GACTTTCGGT	ATCAATATGG	TGGCTCTGTC	850
20	TCAAGGGCAG	CCTAAGTTGC	TTAACCTGAA	AGACATTTTG	GTTGCTTTTCG	900
	TGCGCCACCG	CCGTGAAGTG	GTGACTCGCC	GTACCATTTT		940

25 2) INFORMATION FOR SEQ ID NO: 1777

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777

40	CCGTTTATTG	GCGATGGCCT	GAAGCCGGTC	CAGCGTCGCA	TCGTCTATGC	50
	GATGTCTGAA	CTGGGTCTGA	ACGCCAGCGC	GAAGTTCAAA	AAGTCCGCCC	100
	GCACCGTCGG	TGACGTGCTG	GGTAAATACC	ATCCCCACGG	CGACAGCGCG	150
	TGCTATGAAG	CCATGGTGCT	GATGGCTCAG	CCCTTCTCCT	ACCGCTATCC	200
45	GCTGGTTGAC	GGTCAGGGAA	ACTGGGGGGC	GCCGGACGAT	CCTAAATCCT	250
	TCGCCGCAAT	GCGTTATACC	GAATCCCGTT	TGTCGAAGTA	TGCTGAACTG	300
	CTGCTGAGCG	AACTGGGGCA	AGGCACCGTT	GACTGGGTAC	CAAACCTCGA	350
	CGGCACTTTG	CAGGAGCCGA	AGATGCTGCC	TGCGCGCCTG	CCCAATATTC	400
	TGCTAAACGG	TACTACCGGC	ATTGCCGTTG	GGATGGCGAC	GGACATTCCG	450
50	CCGCACAACC	TGCGTGAAGT	GGCCCGGGCG	GCCATTACCC	TGATTGAAAA	500
	GCCGCAAAC	TCGCTGGATG	ACCTGCTGGA	TATCGTGCA	GGGCCGGATT	550
	ATCCTACCGA	AGCGGAAATC	ATTACCCCCC	GTGCCGAAAT	CCGCAAAATC	600
	TACCAGAATG	GCCGCGGTTT	GGTGCGGATG	CGCGCGGTAT	GGGCCAAAGA	650

AGACGGCGCG GTGGTGAT

668

5 2) INFORMATION FOR SEQ ID NO: 1778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778

20 GTTTATTGGC GATGGCCTGA AGCCGGTCCA GCGTCGCATC GTCTATGCGA 50
 TGTCTGAACT GGGTCTGAAC GCCAGCGCGA AGTTCAAAAA GTCCGCCCGC 100
 ACCGTCGGTG ACGTGCTGGG TAAATACCAT CCCCACGGCG ACAGCGCGTG 150
 CTATGAAGCC ATGGTGCTGA TGGCTCAGCC CTTCTCCTAC CGCTATCCGC 200
 25 TGGTTGACGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC TAAATCCTTC 250
 GCCGCAATGC GTTATAACCGA ATCCCGTTTG TCGAAGTATG CTGAACTGCT 300
 GCTGAGCGAA CTGGGGCAAG GCACCGTTGA CTGGGTACCA AACTTCGACG 350
 GCACTTTGCA GGAGCCGAAG ATGCTGCCTG CGCGCCTGCC CAATATTCTG 400
 CTAAACGGTA CTACCGGCAT TGCCGTTGGG ATGGCGACGG ACATTCCGCC 450
 30 GCACAACCTG CGTGAAGTGG CCCGGGCGGC CATTACCCTG ATTGAAAAGC 500
 CGCAAACCTC GCTGGATGAC CTGCTGGATA TCGTGCAGGG GCCGGATTAT 550
 CCTACCGAAG CGGAAATCAT TACCCCCCGT GCCGAAATCC GCAAAATCTA 600
 CCAGAATGGC CGCGGTTCGG TGC GGATGCG CGCGGTATGG GCCAAAGAAG 650
 ACGGCGCGGT GGTGATTAGC GCGCTGCCGC ATCAGGTTTC CGGCGCCCGC 700
 35 GTGCTTGAGC AGAT 714

2) INFORMATION FOR SEQ ID NO: 1779

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779

```

5  TTGGCGATGG CTTAAAACCG GTCCAGCGTC GCATCGTCTA TGCGATGTCC      50
   GAGCTGGGGC TGAACGCCAG CGCGAAATTC AAAAAGTCCG CCCGCACCGT      100
   CGGCGACGTG TTGGGTAAAT ATCACCCGCA CGGCGACAGC GCCTGCTATG      150
   AAGCGATGGT GCTGATGGCG CAGCCGTTCT CTTACCGCTA TCCGCTGGTG      200
   GATGGTCAGG GAAACTGGGG GGCGCCGGAC GATCCCAAAT CTTTCGCCGC      250
   CATGCGTTAC ACCGAATCCC GCCTGTGCGAA GTATGCCGAG CTGCTGCTCA      300
   GCGAGCTGGG GCAGGGGACG GTCGACTGGG TGCCAAACTT TGACGGTACG      350
   CTGCAGGAGC CGAAAATGCT GCCAGCGCGT TTGCCGAACA TCCTGCTGAA      400
10  CGGCACCACC GGCATCGCGG TAGGTATGGC GACCGATATT CCTCCGCACA      450
   ACCTGCGGGA AGTGGCCAAA GCGGCGATTA CGCTGATTGA GCAGCCGAAA      500
   ACCACCCTCG ACGAACTGCT GGATATCGTA CAGGGGCCGG ATTTCCCGAC      550
   CGAGGCGGAG ATCATCACCT CGCGGGCGGA AATTCGAAAA ATCTACCAGA      600
   ACGGGCGCGG CTCAGTGCGC ATGCGCGCGG TGTGGAGTAA AGAGGACGGC      650
15  GCGGTGGTGA TCAGCGCGCT GCCGCATCAG GTCTCCGGCG CCAAAGTGCT      700
   GGAGCAGATT GCGGCGCAGA TG                                     722

```

20 2) INFORMATION FOR SEQ ID NO: 1780

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780

```

35  GTCCAGCGTC GCATCGTTTA TGCGATGTCT GAGCTGGGGC TGAACGCCAG      50
   CGCGAAGTTC AAAAAGTCCG CCCGCACCGT GGGTGATGTG CTGGGTAAAT      100
   ATCACCCGCA CGGCGATAGC GCATGCTATG AAGCTATGGT GCTGATGGCG      150
   CAGCCATTCT CCTACCGCTA CCCGCTGGTG GATGGGCAGG GGAAGTGGGG      200
40  GGCACCGGAC GATCCTAAAT CCTTCGCCGC GATGCGTTAT ACCGAATCCC      250
   GTTTGTGCGAA GTATGCGGAA CTGCTGCTGG GCGAACTGGG GCAGGGAACC      300
   GTCGACTGGG TGCCGAACTT CGACGGGACG ATGCAGGAGC CGAAAATGCT      350
   GCCTGCGCGT CTGCCGAATA TTCTGCTGAA CGGCACTACC GGCATCGCCG      400
   TCGGTATGGC AACCGATATT CCTCCGCACA ACCTGCGTGA AGTGGCGCAG      450
45  GCGGCGATTA CCCTGATCGA AAAACCGCAG ACCTCGCTCG ACGAACTGCT      500
   GGATATCGTT CACGGACCCG ACTACCCGAC CGAAGCCGAA ATCATTACTC      550
   CACGCGCGGA GATCCGCAA AATCTACCAGA ACGGCCGCGG TTCGGTGCGG      600
   ATGCGCGCGG TATGGAAAAA AGAGGACGGC GCGGTCGTGA TTACGGCGTT      650
   GCCGCATCAG GTTTCCGGCG CCCGCGTGCT GGAGCAAATT GC               692
50

```

2) INFORMATION FOR SEQ ID NO: 1781

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781

15
 GTTTATTGGC GATGGCTTAA AACCGGTCCA GCGTCGCATC GTCTATGCGA 50
 TGTCCGAGCT GGGGCTGAAC GCCAGCGCGA AATTCAAAAA GTCCGCCCGC 100
 ACCGTCGGCG ACGTGTGGG TAAATATCAC CCGCACGGCG ACAGCGCCTG 150
 CTATGAAGCG ATGGTGCTGA TGGCGCAGCC GTTCTCTTAC CGCTATCCGC 200
 20 TGGTGGATGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC CAAATCTTTC 250
 GCCGCCATGC GTTACACCGA ATCCCGCCTG TCGAAGTATG CCGAGCTGCT 300
 GCTCAGCGAG CTGGGGCAGG GGACGGTCGA CTGGGTGCCA AACTTTGACG 350
 GCACGCTGCA GGAGCCGAAA ATGCTGCCAG CGCGTTTGCC GAACATCCTG 400
 CTGAACGGCA CCACCGGCAT CGCGGTAGGC ATGGCGACCG ATATTCCTCC 450
 25 GCACAACCTG CGGGAAGTGG CCAAAGCGGC GATTACGCTG ATTGAGCAGC 500
 CGAAAACCAC CCTCGACGAA CTGCTGGATA TCGTACAGGG GCCGGATTTC 550
 CCGACCGAGG CGGAGATCAT CACCTCGCGG GCGGAAATTC GCAAAATCTA 600
 CCAAAACGGG CGCGGCTCAG TGCGCATGCG CGCGGTGTGG AGTAAAGAGG 650
 ACGGCGCGGT GGTGATCAGC GCGCTGCCGC ATCAGGTCTC CGGCGCCAAA 700
 30

2) INFORMATION FOR SEQ ID NO: 1782

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 45 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782

ATTGGCGATG GCTTAAAACC GGTCCAGCGT CGCATCGTCT ATGCGATGTC 50
 50 CGAGCTGGGG CTGAACGCCA GCGCGAAATT CAAAAAGTCC GCCCGCACCG 100
 TCGGCGACGT GTTGGGTAAA TATCACCCGC ACGGCGACAG CGCCTGCTAT 150
 GAAGCGATGG TGCTGATGGC GCAGCCGTTC TCTTACCGCT ATCCGCTGGT 200
 GGATGGTCAG GGAAACTGGG GGGCGCCGGA CGATCCCAA TCTTTCGCCG 250

	CCATGCGTTA	CACCGAATCC	CGCCTGTCGA	AGTATGCCGA	GCTGCTGCTC	300
	AGCGAGCTGG	GGCAGGGGAC	GGTCGACTGG	GTGCCAAACT	TTGACGGCAC	350
	GCTGCAGGAG	CCGAAAATGC	TGCCAGCGCG	TCTGCCGAAC	ATCCTGCTGA	400
	ACGGCACCAC	CGGCATCGCG	GTAGGCATGG	CGACCGATAT	TCCTCCGCAC	450
5	AACCTGCGGG	AAGTGGCCAA	AGCGGCGATT	ACGCTGATTG	AGCAGCCGAA	500
	AACCACCCTC	GACGAACTGC	TGGATATCGT	ACAGGGGCCG	GATTTCCCGA	550
	CCGAGGCGGA	GATCATCACC	TCGCGGGCGG	AAATTCGCAA	AATCTACCAG	600
	AACGGGCGCG	GCTCAGTGCG	CATGCGCGCG	GTGTGGAGTA	AAGAGGACGG	650
	CGCGGTGGTG	ATCAGTGCGC	TGCCGCATCA	GGTCTCTGGC	GCCAAAGTGC	700
10	TGGAGCAGAT	TGCGGCGCAG	ATGCGC			726

2) INFORMATION FOR SEQ ID NO: 1783

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 29011

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783

30	GGCTTAAAC	CGGTCCAGCG	TCGCATCGTC	TATGCGATGT	CCGAGCTGGG	50
	GCTGAACGCC	AGCGCGAAAT	TCAAAAAGTC	CGCCCGCACC	GTCGGCGACG	100
	TGTTGGGTAA	ATATCACCCG	CACGGCGACA	GCGCCTGCTA	TGAAGCGATG	150
	GTGCTGATGG	CGCAGCCGTT	CTCTTACCGC	TATCCGCTGG	TGGATGGTCA	200
	GGGAAACTGG	GGGGCGCCGG	ACGATCCCAA	ATCTTTTGCC	GCCATGCGTT	250
35	ACACCGAATC	CCGCCTGTCG	AAGTATGCCG	AGCTGCTGCT	CAGCGAGCTG	300
	GGGCAGGGGA	CGGTCGACTG	GGTGCCAAAC	TTTGACGGCA	CGCTGCAGGA	350
	GCCGAAAATG	CTGCCAGCGC	GTCTGCCGAA	CATCCTGCTG	AACGGCACCA	400
	CCGGCATCGC	GGTAGGCATG	GCGACCGATA	TTCTCCGCA	CAACCTGCGG	450
	GAAGTGGCCA	AAGCGGCGAT	TACGCTGATT	GAGCAGCCGA	AAACCACCCT	500
40	CGACGAACTG	CTGGATATCG	TACAGGGGCC	GGATTTCCCG	ACCGAGGCGG	550
	AGATCATCAC	CTCGCGGGCG	GAAATTCGCA	AAATCTACCA	GAACGGGCGC	600
	GGCTCAGTGC	GCATGCGCGC	GGTGTGGAGT	AAAGAGGACG	GCGCGGTGGT	650
	GATCAGTGCG	CTGCCGCATC	AGGTCTCCGG	CGCCAAAGTG	CTGGAGCAGA	700
	TTGCGG					706

45

2) INFORMATION FOR SEQ ID NO: 1784

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

(B) STRAIN: ATCC 13884

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784

	TTGGCGATGG	CTTAAAACCG	GTCCAGCGTC	GCATCGTCTA	TGCGATGTCC	50
	GAGCTGGGGC	TGAACGCCAG	CGCGAAATTC	AAAAAGTCCG	CCCGCACCGT	100
	CGGCGACGTG	TTGGGTAAAT	ATCACCCGCA	CGGCGACAGC	GCCTGCTATG	150
15	AAGCGATGGT	GCTGATGGCG	CAGCCGTTCT	CTTACCGCTA	TCCGCTGGTG	200
	GATGGTCAGG	GAAACTGGGG	GGCGCCGGAC	GATCCCAAAT	CTTTCGCCGC	250
	CATGCGTTAC	ACCGAATCCC	GCCTGTCTGAA	GTATGCCGAG	CTGCTGCTCA	300
	GCGAGCTGGG	GCAGGGGACG	GTCGACTGGG	TGCCAAACTT	TGACGGCACG	350
	CTGCAGGAGC	CGAAAATGCT	GCCAGCGCGT	CTGCCGAACA	TCCTGCTGAA	400
20	CGGCACCACC	GGCATCGCGG	TAGGCATGGC	GACCGATATT	CCTCCGCACA	450
	ACCTGCGGGA	AGTGGCCAAA	GCGGCGATTA	CGCTGATTGA	GCAGCCGAAA	500
	ACCACCCTCG	ACGAACTGCT	GGATATCGTA	CAGGGGCCGG	ATTTCCCGAC	550
	CGAGGCGGAG	ATCATCACCT	CGCGGGCGGA	AATTCGCAAA	ATCTACCAGA	600
	ACGGGCGCGG	CTCA				614

25

2) INFORMATION FOR SEQ ID NO: 1785

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella terrigena*

40 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785

	GCCTGAAACC	GGTCCAGCGG	CGCATCGTTT	ATGCGATGTC	CGAACTGGGT	50
45	CTGAACGCCA	CCGCTAAATT	CAAAAAATCC	GCGCGCACCG	TCGGCGACGT	100
	GCTGGGTAAA	TATCACCCGC	ACGGCGATAG	CGCCTGCTAT	GAGGCGATGG	150
	TGCTGATGGC	GCAGCCGTTC	TCTTACCGCT	ACCCGCTGGT	GGACGGTCAG	200
	GGCAACTGGG	GCGCCCCGGA	CGATCCCAA	TCCTTCGCCG	CGATGCGTTA	250
	TACCGAATCC	CGCCTGTCAA	AGTATGCGGA	GCTGCTGCTG	GGCGAGCTGG	300
50	GTCAGGGAAC	CGTTGACTGG	GTACCTAACT	TTGACGGTAC	GATGCAGGAG	350
	CCGAAAATGC	TGCCTGCGCG	TTTGCCGAAT	ATTCTGCTCA	ACGGCACCCAC	400
	CGGTATCGCC	GTGGGGATGG	CCACCGATAT	TCCGCCGCAC	AACCTGCGCG	450
	AAGTGGCCAA	AGCGGCCATC	ACCCTGATTG	AAAAGCCGCA	GACCTCGCTC	500

GACGAACTGC	TGGATATCGT	TCACGGGCCG	GACTACCCCA	CCGAAGCTGA	550
AATCATCACC	CCGCGCGCCG	AGATCCGCAA	AATCTATCAG	AACGGTCGCG	600
GCTCGGTTCG	CATGCGTGCG	GTGTGGAAAA	AAGAGGACGG	CGCGGTGGTG	650
ATTAGCGCCC	TGCCGCAT				668

5

2) INFORMATION FOR SEQ ID NO: 1786

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 7064

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786

CATTACGTTT	TAACACTCAA	GGACGCGGAA	CATTCTCTAT	GGTGTTTGAC	50
CACTATGAAG	AAGTACCAAA	GTCTGTTTCT	GAAGAAATTA	TCAAAAAAAAA	100
TAAAGGTGAA	TAA				113

25

30 2) INFORMATION FOR SEQ ID NO: 1787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787

AACGTCATTA	CGTTCTAACA	CTCAAGGACG	CGGAACATTC	TCTATGGTGT	50
TTGACCACTA	TGAAGAAGTA	CCAAAGTCTG	TTTCTGAAGA	AATTATCAAA	100
AAAAATAAAG	GTGAATAA				118

45

50

2) INFORMATION FOR SEQ ID NO: 1788

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788

15 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
 GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
 AAAAAATAA AGGTGAATAA 120

20

2) INFORMATION FOR SEQ ID NO: 1789

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789

 AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT 50
 TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAAA 100
 AAAAATAAAG GTGAATAA 118

40

2) INFORMATION FOR SEQ ID NO: 1790

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790

5 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1791

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
(B) STRAIN: NRRL B-617

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791

GCAACGTCAT TACGTTCTAA CACGCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATCA 100
30 AAAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1792

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792

50 CGTCATTACG TTCTAACACT CAAGGACGCG GAACATTCTC TATGGTGTTT 50
GACCACTATG AAGAAGTACC AAAGTCTGTT TCTGAAGAAA TTATCAAAAA 100
AAATAAAGGT GAATAA 116

2) INFORMATION FOR SEQ ID NO: 1793

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
10
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1794

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
35 (B) STRAIN: ATCC 15816
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794

CACTCAAGGA CGCGGAACAT TCTCTATGGT GTTTGATCAC TATGAAGAAG 50
40 TACCAAAGTC TGTTTCTGAA GAAATTATCA AAAAAAATAA AGGTGAATAA 100

2) INFORMATION FOR SEQ ID NO: 1795

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus weihenstephanensis*

(B) STRAIN: WSBC 10204

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795

GCAACGGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCTGAA GAAATTATTA 100
AAAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1796

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

25 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796

GCGACAGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
30 ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATTA 100
AAAAAAATAA AGGCGAATAA 120

35 2) INFORMATION FOR SEQ ID NO: 1797

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797

50

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1798

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCCATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1799

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

45 2) INFORMATION FOR SEQ ID NO: 1800

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
10 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1801

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Bacillus pseudomycoides*
(B) STRAIN: NRRL B-617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801

30 TTGATTTTTA TCGATTGTTT AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACTTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

35

2) INFORMATION FOR SEQ ID NO: 1802

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100

CTAAGGAGGA ATTTAGA

117

5 2) INFORMATION FOR SEQ ID NO: 1803

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803

20 TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

25

2) INFORMATION FOR SEQ ID NO: 1804

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM *Bacillus cereus*
(B) STRAIN: ATCC 49064

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCACCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
45 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1805

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
- (B) STRAIN: ATCC 6462

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805

TTGATTTT	TA	TCAATTG	TTC	GAGTATA	ACT	ACTTATG	TAA	GCTTAGA	AAAG	50
TGGGACG	TAA	GTTTCG	CTTT	CTAGTCT	AAA	TATAAA	AATAA	CCTATAT	ATAAA	100
CTAAGG	A	GGA	ATT	AGA						117

15

2) INFORMATION FOR SEQ ID NO: 1806

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806

TTGATTTT	TA	TCGATTG	TTC	AAGTATA	ACT	ACTTATG	TAA	GCTTAGA	AAAG	50
TGGGACG	TAA	GTTTCA	CTTT	CTAGTCT	AAA	TATAAA	AATAA	CCTATAT	ATAAA	100
CTAAGG	A	GGA	ATT	AGA						117

40 2) INFORMATION FOR SEQ ID NO: 1807

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
5 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1808

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808

25 TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

30

2) INFORMATION FOR SEQ ID NO: 1809

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAG 117

50

2) INFORMATION FOR SEQ ID NO: 1810

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810

15 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GACGCTGCTC CAGAAGAAAG AGAGCGCGGA ATCACAATCT CAACTGCACA 200
 20 CGTTGAGTAC GAAACTGAAA CTCGTCAC TA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

25 2) INFORMATION FOR SEQ ID NO: 1811

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811

40 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 45 CGTTGAGTAC GAAACTGAAA CTCGTCAC TA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

50 2) INFORMATION FOR SEQ ID NO: 1812

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
15 CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
GTCACGCTGA	CTATGTTAAA				270

20

2) INFORMATION FOR SEQ ID NO: 1813

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10204

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
40 CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GACGCTGCTC	CAGAAGAAAG	AGAGCGCGGA	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
GTCATGCTGA	CTATGTTAAA	AACATGAT			278

45

2) INFORMATION FOR SEQ ID NO: 1814

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 266 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814

10	ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC	50
	AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA	100
	CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC	150
	GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA	200
	CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG	250
15	GTCACGCTGA CTATGT	266

2) INFORMATION FOR SEQ ID NO: 1815

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815

35	ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC	50
	AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA	100
	CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC	150
	GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA	200
	CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG	250
40	GTCACGCTGA CTATGTTAA	269

2) INFORMATION FOR SEQ ID NO: 1816

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 13472

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816

	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTGCT	GCGATCACTA	100
	CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
10	GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCACGCTGA	CTATGTGA				268

15

2) INFORMATION FOR SEQ ID NO: 1817

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 278 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817

	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTGCT	GCGATCACTA	100
	CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
35	GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCACGCTGA	CTATGTAAA	AACATGAT			278

40

2) INFORMATION FOR SEQ ID NO: 1818

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 268 bases
45	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818

5 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTGCT GCGATCACTA 100
CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
GTCACGCTGA CTATGTTA 268

10

2) INFORMATION FOR SEQ ID NO: 1819

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- 25 (B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819

30 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTGCT GCGATCACTA 100
CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
GTCACGCTGA CTATGTTAAA AACATGAT 278

35

2) INFORMATION FOR SEQ ID NO: 1820

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- 50 (B) STRAIN: NRRL B-617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820

	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTGCT	GCGATCACTA	100
	CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGACCAAATC	150
	GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
5	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCACGCTGA	CTATGTTAAA	AACATGAT			278

10 2) INFORMATION FOR SEQ ID NO: 1821

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821

25	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTGCT	GCGATCACTA	100
	CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
	GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
30	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCACGCTGA	CTA				263

35 2) INFORMATION FOR SEQ ID NO: 1822

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822

50	CAATCGAAGT	ACAACGTTCT	CTTCGWGTAT	TGGACGGTGC	GGTTACTGTT	50
	CTTGACTCAC	AATCAGGTGT	TGAGCCTCAA	ACTGAAACAG	TTTGGCGTCA	100
	AGCAACTGAG	TACGGAGTTC	CACGTATCGT	ATTGCTAAC	AAAATGGACA	150

	AAATCGGTGC	TGACTTCCTT	TACTCAGTAA	GCACACTTCA	CGACCGTCTT	200
	CAAGCAAACG	CACACCCAAT	CCAATTGCCA	ATCGGTGCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGATA	TTCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGGTT	GAAGCAGTCG	CTGAAACTGA	400
	TGAAGACTTG	ATGATGAAAT	ACCTTGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGCTATCCGT	AAAGCAACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GTTCTGCCTT	CAAGAACAAG	GGTGTTCAT	TGATGCTTGA	550
	TGCGGTTATC	GACTACCTTC	CAAGCCCACT	TGATATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGACGAA	650
	GAGCCATTCT	CAGCTCTTGC	CTTCAAGATC	ATGACGGACC	CATTTGTAGG	700
	TCGTTTGACA	TTCTTCCGTG	TATACTCARG	TGTTCTCCAA	TCARGKTCTT	750
	ACGTATTGAA	CACATCTAAA	GGTAAACGTG	AACGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CTAACAGCCG	TCAAGAAATT	GACACTGTTT	ACTCAGGTGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TYCAACTGGT	GACTCATTGM	900
	CAGATGAAAA	AGCTAAAATC	ATCCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGATAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCAGGTAT	GGGTGAGCTT	1100
20	CACTTGGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTGGAAGC	1150
	GAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTCTA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	TCTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	CGCGGCTTCA	CTTGCCCTTA	1500
	AAGAAGCTGC	TAAGTCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACCATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTC	TGCTTACG				1668

35 2) INFORMATION FOR SEQ ID NO: 1823

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823

50	AGACCTGCGT	TCACAAACAC	AGGGTCGTGC	TTCTTACTCT	ATGGAGTTCT	50
	TGAAGTACAA	CGAAGCGCCA	AACAACGTTG	CTACAGCAAT	CATTGAAGCT	100
	CGTAAGGCTA	GATAA				115

2) INFORMATION FOR SEQ ID NO: 1824

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 107 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
10
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Buttiauxella agrestis*
(B) STRAIN: ATCC 33320
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824

CTGCGTTCAC TGACCAAGGT CGTGCATCTT ACTCCATGGA ATTCCTGAAG 50
TATGATGACG CGCCAAACAA CGTAGCTCAG GCCGTAATCG AAGCTCGCGG 100
TAAATAA 107

20

2) INFORMATION FOR SEQ ID NO: 1825

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
35 (B) STRAIN: ATCC 13182
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825

TTACTCCATG GAGTTCCTGA AGTATGATGA TGCGCCGAAC AACGTTGCTC 50
40 AGGCCGTAAT CGAAGCCCGT GGTAATAA 79

2) INFORMATION FOR SEQ ID NO: 1826

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

5. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826

CAGCTGCGTT CTCTGACCAA AGGTCGTGCA TCATACACTA TGG AATT CCT 50
GAAGTATGAT GATGCGCCAA ACAACGTTGC TCAGGCCGTT ATTGAAGCCC 100
GTGGTAAGTA A 111

10

2) INFORMATION FOR SEQ ID NO: 1827

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shewanella putrefaciens*

25 (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827

GATTTGCGCT CTGCAACTCA TGGGCGTGCT TCGTACTCCA TGGAGTTCTT 50
30 GAAGTACTCT GATGCACCGC AAAACATTGC GAAAGCGATT ATTGAATCTC 100
GTAGCTAA 108

35 2) INFORMATION FOR SEQ ID NO: 1828

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Obesumbacterium proteus*

(B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828

50

CTCAGCTGCG TTCTCTGACC AAAGGTCGTG CATCTTACTC CATGGAATTC 50
CTGAAGTATG ATGATGCGCC TAACAACGTT GCTCAGGCCG TTATTGAAGC 100
TCGTGGCAAA TAA 113

2) INFORMATION FOR SEQ ID NO: 1829

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
10
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829

GCCGCAGGGT TAAAACCAAA GTCCCGTGCT CTCTCCTGAA GGGGAGAGCA 50
CTATAGTAAG GAATATAGCC 70

20

2) INFORMATION FOR SEQ ID NO: 1830

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 66 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
30
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Budvicia aquatica*
(B) STRAIN: ATCC 35567
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830

GCCTCGGGTA AACTTATAT CCCAGTCCCC CTCGTATAGA GGGGGATAGA 50
GTAAAGGAAG ATAATC 66

40

2) INFORMATION FOR SEQ ID NO: 1831

- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 81 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
(B) STRAIN: ATCC 14029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831

5

TCCACAGGAT TAAACCCAG GTTTAAACCT AAGTCCCGTG CTCTCTCCTC 50
AGGGGAGAGC ACAATAGTAA GGAATATAGC C 81

10

2) INFORMATION FOR SEQ ID NO: 1832

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
(B) STRAIN: ATCC 12841

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832

GCTACTAGTT TAAACATTG ATCCCGTGCT CTCTCTATGA AGGGAGAGCA 50
CAAGAGTAAG GAATAAAGCC 70

30

2) INFORMATION FOR SEQ ID NO: 1833

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 72 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
(B) STRAIN: ATCC 8071

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833

TTTCCAGTTA CGACATAAAT GTTATTATGG TCCAGCTTTG ACTGGACTAT 50
TCTGAAAAGA AAGGAATATA TC 72

50

2) INFORMATION FOR SEQ ID NO: 1834

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Buttiauxella agrestis*
 (B) STRAIN: ATCC 33320

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834
 15

GCCCCGGGTT TTAAAAACA TTGATCCCGT GCTCTCTCCA GAAGGGGAGA 50
 GCGCAACAGT AAGGAATATA GCC 73

- 20 2) INFORMATION FOR SEQ ID NO: 1835

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 795 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear.

(ii) MOLECULE TYPE: Genomic DNA
 30

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter coli*
 (B) STRAIN: ATCC 43479

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835

	CTGCAGCTGA	TGGTCCTATG	CCACAAACTA	GAGAGCACAT	CCTTCTATCA	50
	CGCCAAGTAG	GTGTTCCATA	TATCGTTGTA	TTTATGAATA	AAGCAGATAT	100
	GGTTGATGAT	GCTGAACTTT	TAGAATTGGT	TGAAATGGAA	ATTAGAGAAT	150
40	TATTAAGCTC	TTATGATTTT	CCAGGTGATG	ACACACCTAT	TATTTTCAGGT	200
	TCTGCTTTAA	AAGCTCTTGA	AGAAGCAAAA	GCTGGACAAG	ATGGCGAATG	250
	GTCAGCGAAA	ATTATGGATC	TTATGGCTGC	TGTTGATAGC	TATATTCCAA	300
	CTCCAACCTG	TGACACTGAA	AAAGATTTCT	TAATGCCAAT	TGAAGATGTT	350
	TTCTCAATTT	CAGGTCGTGG	TACTGTTGTT	ACAGGTAGAA	TTGAAAAAGG	400
45	TATTGTAAAA	GTTGGTGATA	CTATAGAAAT	CGTTGGTATT	AAAGATACTC	450
	AAACAACAAC	TGTAACCTGG	GTTGAAATGT	TTAGAAAAGA	AATGGACCAA	500
	GGTGAAGCAG	GGGATAATGT	TGGTGTCTT	CTTCGTGGTA	CAAAAAAAGA	550
	AGAAGTTATC	CGCGGTATGG	TTCTTGCTAA	ACCAAATCA	ATTACTCCAC	600
	ATACTGATTT	CGAAGCTGAA	GTTTATATCC	TAAATAAAGA	TGAGGGTGGT	650
50	AGACATACTC	CATTCTTTAA	TAACATAGA	CCGCAATTCT	ATGTAAGAAC	700
	AACAGATGTA	ACAGGTTCTA	TTAAATTAGC	TGATGGCGTT	GAAATGGTTA	750
	TGCCTGGTGA	AAATGTAAGA	ATTACTGTAA	GCTTGATTGC	ACCAG	795

2) INFORMATION FOR SEQ ID NO: 1836

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
- (B) STRAIN: ATCC 25936
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836

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GCCATACTAG TTGTTTCTGC AGCTGATGGC CCAATGCCAC AAAC TAGAGA      50
GCACATTTTG CTATCTCGTC AAGTTGGTGT TCCATATATA GTTGTTTTTA      100
TGAACAAAGC TGATATGGTA GATGACGCAG AGTTGCTAGA ATTAGTTGAA      150
ATGGAGATCA GAGAGTTATT AAGCGAATAT GACTTCCCTG GTGATGATAC      200
TCCTATTATA AGCGGATCAG CACTTCAAGC TCTTGAAGAA GCTAAAGCTG      250
GTAATGATGG CGAATGGTCA GCTAAGATTA TGGATCTTAT GGCTGCTGTT      300
GATAGCTACA TACCAACTCC AGTTCGTGCT ACTGATAAAG ATTTCTTAAT      350
GCCGATTGAA GACGTATTCT CAATTTCTGG CCGTGGTACT GTTGTTACTG      400
GTAGAATTGA AAAAGGTATA GTTAAAGTTG GTGATACTAT CGAAATCGTA      450
GGTATTAGAG ATACACAAAC TACAACAGTT ACCGGCGTTG AAATGTTTAG      500
AAAAGAAATG GATCAAGGCG AGGCTGGTGA TAACGTTGGT GTTCTTTTAC      550
GCGGTACAAA GAAAGAAGAC GTTGAAAGAG GTATGGTTCT TTGTAAGCCA      600
AAATCAATTA CTCCTCATAC TAAATTTGAG GGAGAAGTTT ATATCTTGAC      650
TAAGGAAGAG GCGGGTAGAC ATACTCCATT CTTCAACAAC TATAGACCAC      700
AATTTTATGT AAGAACAACA GATGTTACTG GATCAATCAC TCTTCCAGAG      750
GGTACTGAGA TGGTTATGCC TGGTGATAAC TTAAAAATCA CTGTTGAGTT      800
AATCAACCCA GTTGCTC                                     817

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35

2) INFORMATION FOR SEQ ID NO: 1837

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
- (B) STRAIN: ATCC 33561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837

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CCATACTAGT TGTTTCTGCA GCTGATGGCC CAATGCCACA AAAC TAGAGAG      50

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	CACATTTTGC	TATCTCGTCA	AGTTGGTGTT	CCATATATAG	TTGTTTTTAT	100
	GAACAAAGCT	GATATGGTAG	ATGACGCAGA	GTTGCTAGAA	TTAGTTGAAA	150
	TGGAGATCAG	AGAGTTATTA	AGCGAATATG	ACTTCCCTGG	TGATGATACT	200
	CCTATTATAA	GCGGATCAGC	ACTTCAAGCT	CTTGAAGAAG	CTAAAGCTGG	250
5	TAATGATGGC	GAATGGTCAG	CTAAGATTAT	GGATCTTATG	GCTGCTGTTG	300
	ATAGCTACAT	ACCAACTCCA	GTTCGTGCTA	CTGATAAAGA	TTTCTTAATG	350
	CCGATTGAAG	ACGTATTCTC	GATTTCTGGC	CGTGGTACTG	TTGTTACTGG	400
	TAGAATTGAA	AAAGGTATAG	TTAAAGTTGG	TGATACTATC	GAAATCGTAG	450
	GTATTAGAGA	TACACAAACT	ACAACAGTTA	CCGGCGTTGA	AATGTTTAGA	500
10	AAAGAAATGG	ATCAAGGCGA	GGCTGGTGAT	AACGTTGGTG	TTCTTTTACG	550
	CGGTACAAAG	AAAGAAGACG	TTGAAAGAGG	TATGGTTCTT	TGTAAGCCAA	600
	AATCAATTAC	TCCTCATACT	AAATTTGAGG	GAGAAGTTTA	TATCTTGACT	650
	AAGGAAGAGG	GCGGTAGACA	TACTCCATTC	TTCAACAACT	ATAGACCACA	700
	ATTTTATGTA	AGAACAACAG	ATGTTACTGG	ATCAATCACT	CTTCCAGAGG	750
15	GTACTGAGAT	GGTTATGCCT	GGTGATAACT	TAAAAATCAC	TGTTAGTT	798

2) INFORMATION FOR SEQ ID NO: 1838

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Buttiauxella agrestis*
- (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838

35	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
	TATCGGCCAC	GTTGACCATG	GTAAACTACT	TCTGACTGCA	GCAATCACTA	100
	CCGTTCTGGC	TAAACCTAC	GGCGGTTCTG	CACGCGCATT	CGACCAGATC	150
	GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
	CGTTGAATAT	GACACCCCGA	CTCGTCACTA	CGCGCACGTT	GACTGCCCGAG	250
40	GGCACGCCGA	CTACGTTAAA	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCGATGC	CACAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATTC	ATGATCGTGT	400
	TCATGAACAA	ATGTGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	450
	GAAATGGAAG	TTCGTGAAC	TCTGTCTGCT	TATGATTTCC	CGGGCGACGA	500
45	CATCCCAGTG	GTTCGTGGTT	CAGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	TAAATCATC	GAGCTGGCTG	GTCACCTGGA	TAAGTACATC	600
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCA	TTCTGCTGCT	CAATCGAAGA	650
	CGTATTCTCC	ATCTCCGGCC	GTGGTACTGT	TGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	TAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAT	750
50	ACCGTGAAAT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATTAAAC	850
	GTGAAGATAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCTATCAAG	900
	CCGCACACTC	AGTTCGAATC	AGAAGTTTAT	ATCCTGTCCA	AAGATGAAGG	950

CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	1050
GTAATGCCGG	GCGACAACAT	TCAAATGGTT	GTTACCCTGA	TCCACCCAAT	1100
CGCAATGGAC	GACGGT				1116

5

2) INFORMATION FOR SEQ ID NO: 1839

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 20 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
25 TATCGGCCAC	GTTGACCATG	GTAAACTAC	TCTGACCGCT	GCAATCACTA	100
CCGTTCTGGC	TAAACCTAC	GGTGGTGCTG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GACTGCCCGG	250
GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
30 GCGCGCATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	350
TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	400
TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGT	450
GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	500
CACTCCGATC	GTTCTGTGGT	CTGCTCTGAA	AGCTCTGGAA	GGCGACGCTG	550
35 AGTGGGAATC	TAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	600
CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	650
CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	700
GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	750
ACTGCTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
40 CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	850
GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	900
CCGCACACCA	AGTTCGAATC	TGAAGTTTAT	ATCCTGTCCA	AAGACGAAGG	950
CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	1050
45 GTTATGCCGG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCGAT	1100
CGCGATGGA					1109

50 2) INFORMATION FOR SEQ ID NO: 1840

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
- (B) STRAIN: ATCC 14029

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840

	GTGTCTAAAG	AAAAATTTGA	ACGTACTAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAACTAC	CCTGACTGCA	GCTATCACTA	100
15	CCGTACTGTC	TAAAGTATAC	GGTGGTCAGG	CTCGTGCATT	CGATCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTAGAGTAC	GACACCCCAA	CTCGTCACTA	CGCGCACGTT	GACTGCCCAG	250
	GTCACGCCGA	CTACGTGAAG	AACATGATCA	CTGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTAGTAGC	TGCGACTGAC	GGCCCAATGC	CTCAGACTCG	350
20	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	450
	GAAATGGAAG	TACGTGAGCT	GCTGTCTCAG	TACGACTTCC	CAGGCGACGA	500
	TACTCCAGTT	GTTCGCGGTT	CTGCACTGAA	AGCGCTGGAA	GGCGATGCTC	550
	AGTGGAAGA	GAAGATTGTT	GAAGTGGCAG	GCTACCTGGA	CAGCTACATC	600
25	CCTGAGCCAG	AGCGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATCTCCGGCC	GTGGTACTGT	AGTAACTGGT	CGTGTAGAGC	700
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	750
	ACTACCAAGA	CTACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGCTGCTGGA	800
	CGAAGGTCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	850
30	GTGATGACGT	AGAGCGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCAATCAAC	900
	CCACACACCA	ACTTTGTAGC	AGAAGTTTAT	ATTCTGTCCA	AAGATGAAGG	950
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050
	GTAATGCCAG	GTGACAACAT	TCAAATGGTT	GTTACCCTGA	TTGCACCAAT	1100
35	CGCGATGG					1108

2) INFORMATION FOR SEQ ID NO: 1841

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841

	TGGCAAAAGC	TAAATTTGAA	CGTATTAAGC	CTCACGTAAA	CGTGGGCACC	50
	ATTGGTCACG	TTGACCATGG	TAAAACCACT	CTGACTGCAG	CTATCTCTCA	100
	CGTACTGGCT	AAGACCTACG	GTGGCGAAGC	TAAAGACTTC	TCTCAAATCG	150
5	ATAACGCTCC	AGAAGAGCGT	GAGCGCGGTA	TTACCATCAA	TACCTCTCAC	200
	ATCGAATATG	ACACGCCATC	ACGCCACTAC	GCCCACGTAG	ACTGCCCAGG	250
	CCACGCTGAC	TATGTTAAAA	ACATGATCAC	TGGTGCTGCA	CAGATGGACG	300
	GCGCGATTCT	GGTAGTCGCT	TCAACAGACG	GTCCAATGCC	ACAGACTCGT	350
	GAGCACATCC	TGCTTTCTCG	TCAGGTTGGC	GTACCATTCA	TCATCGTATT	400
10	CATGAACAAA	TGTGACATGG	TAGATGACGA	AGAGCTGTTA	GAGCTAGTTG	450
	AGATGGAAGT	GCGTGAAGT	TTATCAGAAT	ACGATTTCCT	AGGTGATGAC	500
	TTACCGGTAA	TCCAAGGTTT	AGCTCTGAAA	GCGCTAGAAG	GCGAGCCAGA	550
	GTGGGAAGCA	AAAATCCTTG	AATTAGCAGC	GGCGCTGGAT	TCTTACATTC	600
	CAGAACCACA	ACGTGACATC	GATAAGCCGT	TCCTACTGCC	AATCGAAGAC	650
15	GTATTCTCAA	TTTCAGGCCG	TGGTACAGTA	GTAACAGGTC	GTGTTGAGCG	700
	TGGTATTGTA	CGCGTAGGCG	ACGAAGTTGA	AATCGTTGGT	GTACGTGCGA	750
	CAACTAAGAC	AACGTGTACT	GGTGTAGAAA	TGTTCCGTAA	ACTGCTTGAC	800
	GAAGGTCGTG	CAGGTGAGAA	CTGTGGTATT	TTGTTACGTG	GTACTAAGCG	850
	TGATGACGTA	GAACGTGGTC	AAGTATTAGC	GAAGCCAGGT	TCAATCAACC	900
20	CACACACTAC	TTTTGAATCA	GAAGTTTACG	TACTGTCAAA	AGAAGAAGGT	950
	GGTCGTCACA	CGCCATTCTT	CAAAGGCTAC	CGTCCACAGT	TCTACTTCCG	1000
	TACAACTGAC	GTAACCGGTA	CTATCGAACT	GCCAGAAGGC	GTAGAGATGG	1050
	TAATGCCAGG	CGATAACATC	AAGATGGTAG	TGACACTGAT	TTGCCCAATC	1100
	GCGATGG					1107
25						

2) INFORMATION FOR SEQ ID NO: 1842

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1116 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Obesumbacterium proteus*
 - 40 (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1842

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
45	AATCGGCCAC	GTTGACCACG	GTAAAACTAC	CCTGACTGCT	GCAATCACTA	100
	CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CACGTGCATT	CGACCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
	GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
50	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAGCTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CAGGCAATGA	500

	TACTCCAATC	ATCCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCGTA	GAAGTGGCTG	AAACTCTGGA	TTCTTACATC	600
	CCAGAACCAG	AACGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTTACCGGT	CGTGTAGAGC	700
5	GCGGTATCGT	TAAAGTTGGT	GAAGAAGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTTAAAT	CAACTTGTAC	CGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	800
	CGAAGGTCGT	GCAGGCGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	850
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAA	900
	CCACACACCA	AGTTCGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
10	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTGGAAATG	1050
	GTAATGCCAG	GCGATAACAT	CAAAATGATC	GTTACCCTGA	TCCACCCAAT	1100
	CGCAATGGAC	GATGGT				1116

15

2) INFORMATION FOR SEQ ID NO: 1843

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1129 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Budvicia aquatica*

(B) STRAIN: ATCC 35567

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAACAAC	TCTGACTGCT	GCTATCACCA	100
35	GCGTTTTAGC	TAAAACTTAT	GGCGGTAACG	CTCGTGCAAT	CGATCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCACGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAGTAT	GATACTCCTG	CTCGCCACTA	CGCACACGTA	GACTGCCCCAG	250
	GACACGCCGA	CTATGTGAAA	AACATGATCA	CCGGTGCTGC	TCAAATGGAC	300
	GGCGCGATCT	TAGTTGTTGC	GGCAACTGAT	GGTCCTATGC	CACAGACTCG	350
40	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAACTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAGCT	TCTTTCTGCT	TATGATTTCC	CTGGTGACGA	500
	TACTCCAGTT	GTTCGTGGTT	CTGCGCTGAA	AGCGTTAGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCATT	GAATTAGCCG	GATATCTGGA	TAGCTACATC	600
45	CCAGAGCCAG	AGCGTGCGAT	TGACCGTCCG	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATTTCAGGCC	GTGGTACAGT	TGTTACCGGT	CGTGTAGAGC	700
	GCGGAATCGT	TAAAGTCGGT	GAAGCCGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTACAAA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGTTACTTGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	850
50	GTGAAGAAAT	CGAACGCGGT	CAAGTACTGG	CTAAGCCAGG	TTCAATCAAC	900
	CCGCACACCA	ACTTTGTATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050

GTGATGCCTG GTGACAACAT TCAGATGACT GTAACCTCTGA TTGCACCAAT 1100
 CGCGATGGAC GAAGGTTTAC GCTTCGCTA 1129

5

2) INFORMATION FOR SEQ ID NO: 1844

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844

ATATTCATAA TGCATTACAA GTTGTGAAAA CAACAAGTGA CGGAAGTGAA 50
 AAGACTGTTA CATTGGAAAC TGCTGTAGAA TTAGGGGATG GTGCAGTTCG 100
 TACGATTGCC ATGGAATCTA CAGATGGTTT GCAACGTGGC ATGAAAGTAG 150
 25 TGGACTTAGG ACGCACAATT AGCGTTCCTG TGGGACCTGA AACATTAGGT 200
 CGTGTATTCA ACGTTTTTAGG AGATACAATC GACTTGAAAG AACCATTTCCC 250
 AGAAGACTTT ACAAGACATG AAATCCATAA ACCAGCACCA AAATTTGAAG 300
 AATTAAACAG TCAATATGAA ATTCTACAAA CAGGGATTAA AGTTATTGAC 350
 CTTTTAGCAC CTTATCTTAA AGGTGGTAAA ATCGGTTTAT TCGGTGGTGC 400
 30 CGGTGTAGGG AAAACCGTAT TAATTCAAGA ATTAATTCAT AATATCGCTG 450
 AAGAACTTGG TGGTATTTCA GTATTTACAG GGGTAGGGGA ACGTACTCGT 500
 GAAGGGAATG ACCTTTACCA TGAAATGCAA GAATCAGGCG TATCTGCTAA 550
 AACAGCGATG GTGTTTGGGC AAATGAACGA ACCACCAGGA GCTCGTATGC 600
 GTGTAGCACT AACAGGGTTA ACTATTGCGG AATACTTCCG TGATATGGAA 650
 35 AAACAAGACG TGCTTTTATT CATCGATAAC ATTTATCGTT TCACGCAAGC 700
 AGGTTCAGAA GTGTCAGCGT TACTTGGTCG TATGCCTTCT GCCGTAGGGT 750
 ATCAACCAAC ATTAGCGACA GAAATGGGTC AATTACAAGA ACGTATCAGT 800
 TCAACTAAAG 810

40

2) INFORMATION FOR SEQ ID NO: 1845

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*

(B) STRAIN: ATCC 9345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845

5	TGCTCTGCCA	GAAATTAACA	ACGCCCTCCT	CACCGAAGTA	GACCTCTCCG	50
	GCCAAGGCGA	AGGCGAAAGC	GTTCTCAAGA	TGACTCTTGA	GGTTGCTCAG	100
	CACCTCGGCG	ATAACATCGT	CCGTACCATC	GCCATGAAGC	CAACCGACGG	150
	TCTGGTTCGC	GGCGCCACCG	TTATCGATAC	CGGCGCCCCA	ATCACCGTGC	200
	CAGTTGGCGA	CGCAACTAAA	GGTCATGTTT	TCAACGTGAC	CGGTGATGTC	250
10	CTAAACTTGG	GCGAAGGCGA	AACCCTTGAC	GTCAAGGAAC	GGTGGCCAAT	300
	CCACCGCAAG	GCTCCACAGT	TCGACGAACT	CGAACCGGAA	ACCAAGATGT	350
	TCGAAACAGG	CATCAAGGTG	ATCGATCTCC	TCACCCCATTA	CGTACAGGGC	400
	GGCAAGATCG	GTCTGTTTGG	CGGTGCTGGT	GTTGGTAAGA	CCGTTCTTAT	450
	CCAGGAAATG	ATCCAGCGTG	TTGCACAGGA	TCATGGCGGT	GTGTCCGTGT	500
15	TCGCGGGTGT	GGGTGAACGT	ACCCGTGAAG	GTAACGATCT	TATCCACGAA	550
	ATGGAAGATG	CGGGCGTTCT	TGATAAGACC	GCGCTTGTGT	TCGGCCAGAT	600
	GGATGAACCG	CCAGGGGTTC	GTTTGCGTAT	TGCACTTTCC	GGCCTGACCA	650
	TGGCGGAATA	CTTCCGTGAC	GTGCAAAACC	AGGACGTGCT	TTTGTTCATC	700
	GATAACATCT	TCCGCTTCAC	CCAGGCAGGT	TCGGAAGTGT	CCACGTTGCT	750
20	TGGCCGTATG	CCATCAGCAG	TGGGCTACCA	GCCGACCTTG	GCAGATKAAA	800
	TGGGCGCATT	GCAGG				815

25 2) INFORMATION FOR SEQ ID NO: 1846

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|--------------------------|
| | (A) LENGTH: 1073 bases |
| | (B) TYPE: Nucleic acid |
| 30 | (C) STRANDEDNESS: Double |
| | (D) TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- | | |
|--|-------------------------------------------|
| | (A) ORGANISM: <i>Basidiobolus ranarum</i> |
| | (B) STRAIN: ATCC 24670 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846

40	ACCTTCCTCC	TATCTTGAAG	GCCCTGGAGG	TCCAAAACCA	CAGCTCTCGY	50
	TTAGTTTGTAG	AGGTGTCCCA	GCATTTGGGT	GAAAACACCG	TTCGTACTAT	100
	TGCTATGGAC	GGTACTGAAG	GATTGGTTCG	TGGTCAAAAT	GTCGTAGATA	150
	CCGGATATCC	TATTAGAGTT	CCTGTCGGTC	CTGAATGTTT	GGGTCGTATC	200
45	ATGAACGTTA	TTGGCGAGCC	TGTTGATGAG	CGCGGYCCTA	TCAAGACCAA	250
	GAAGCTTGCA	CCCATCCACG	CTTCTCCCCC	CGAGTTCGTY	GACCAATCCA	300
	CCACCCCCGA	AATCTTGGAG	ACTGGTATTA	AGGTTGTCGA	TTTGTGCGCC	350
	CCTTACGCTC	GTGGTGGTAA	GATCGGTCTT	TTCGGTGGTG	CCGGTGTCCG	400
	TAAGACTGTG	TTTATCCAGG	AGTTGATYAA	CAACGTTGCC	AAGGCCACG	450
50	GTGGTTACTC	CGTGTTGCTC	GGTGTTGGTG	AGCGTACTCG	TGAGGGTAAC	500
	GATTTGTACC	ACGAGATGAT	TCAAACCTGGT	GTCATCAAGC	TTGATGGCCA	550
	ATCCAAGGCT	GCCCTTGTCT	ACGGMCAAAT	GAACGAGCCC	CCAGGTGCTC	600
	GTGCCCGMGT	CGCTTTGACC	GGTCTTACCG	TTGCTGAATA	CTTCCGTGAT	650

GAGGAAGGHC AAGATGTGTT GCTCTTCATT GACAACATTT TCCGTTTCAC 700
 CCAAGCTGGT TCTGAAGTGT CYGCCTTGTT GGGTCGTATC CCCTCCGCTG 750
 TCGGTTACCA ACCCACCTTG GCCACCGATA TGGGTGTCAT GCAAGAGCGT 800
 ATTACCACCA CCAAGAAGGG TTCCATTACC TCTGTCCAGG CCATTTACGT 850
 5 CCCTGCTGAT GATTTGACCG ATCCCGCTCC TGCCACTACT TTTGCCCATC 900
 TTGACGCCAC CACCGTGTTG TCTCGTTCCA TCTCTGAGTT GGGTATTTAC 950
 CCCGCTGTCG ATCCCCTCGA CTCCAAGTCT CGTATGTTGG ATCCYCGTAT 1000
 TGTCGGTGAA GAGCACTACG ACATCGCCAC TGGTGTTCAG AAGATTCTCC 1050
 ARTCTTACAA GTCTCTCCAG GAT 1073
 10

2) INFORMATION FOR SEQ ID NO: 1847

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Blastomyces dermatitidis*
 25 (B) STRAIN: ATCC 56220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847

TGTCTTTATC CAGGAGTTGA TTGTACGTCT TGCCTCACCC TTTGGGTATT 50
 30 TTGCGAATAC TAATTATAGT AGAACAACAT TGCCAAGGCT CACGGTGGTT 100
 ACTCTGTCTT CACTGGTGTC GGTGAACGTA CTCGTGAGGG TAACGATTTG 150
 TACCACGAAA TGCAGGAAAC TGGTGTCAAT CAGCTCGAGG GTGAATCCAA 200
 GGTCGCCCTC GTGTTTCGGTC AGATGAACGA GCCCCCTGGT GCCCGTGCCC 250
 GTGTCGCTCT TACTGGTTTG ACCATTGCCG AGTACTTCCG TGACGAGGAG 300
 35 GGTCAAGATG TGCTTCTCTT CATTGACAAC ATTTTCCGTT TCACTCAGGC 350
 CGGTTCTGAG GTGTCTGCCC TTTTGGGTCG TATCCCCTCT GCCGTCGGTT 400
 ACCAGCCCAC TCTCGCCGTC GACATGGGTG TCATGCAGGA GCGTATTACC 450
 ACCACCACCA AGGGTTCCAT CACCTCCGTC 480
 40

2) INFORMATION FOR SEQ ID NO: 1848

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 566 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 50 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848

5	TGTCTTCATT	CAGGAGTTGA	TTGTACGTCC	CTTCCTCTCT	ACAAATGACG	50
	GGCGAGGAAA	ATTTTGGCT	TTTTCTAATA	GCTCGTTATA	GAACAACATT	100
	GCCAAAGCCC	ACGGTGGTTA	CTCCGTTTTC	ACTGGTGTCTG	GCGAGCGGAC	150
	CCGTGAAGGA	AACGATTTGT	ACCACGAGAT	GCAGGAAACC	CGTGTTATCC	200
	AGCTCGATGG	CGAGTCTAAG	GTCGCACTCG	TCTTCGGTCA	GATGAACGAG	250
10	CCCCCGGAG	CCCGTGCCCG	TGTTGCCCTC	ACTGGCCTGA	CCATTGCTGA	300
	ATATTTCCGT	GACGAGGAAG	GTCAAGACGG	TATGTATTCA	TATAAATTAC	350
	TCCGGGCAAA	TTGACTCAGA	ACCGCACTCA	CTCACACATA	TATTAGTGCT	400
	TCTCTTTATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	TCCGAAGTGT	450
	CCGCCCTGCT	TGGTCGTATT	CCCTCCGCCG	TCGGTTACCA	ACCCACTCTC	500
15	GCCGTCGACA	TGGGTGGTAT	GCAGGAACGT	ATCACAACCA	CCACCAAGGG	550
	CTCCATTACC	TYCGTG				566

20 2) INFORMATION FOR SEQ ID NO: 1849

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 817 bases
	(B) TYPE: Nucleic acid
25	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Campylobacter coli</i>
	(B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849

35	AATGAAGCCA	TTGTTGTAAA	TTTTGAAAGT	GAAGGC AAAA	AACAAAAACT	50
	TGTTTTAGAA	GTAGCAGCAC	ACTTGGGCGA	TAATAGAGTT	AGAACTATTG	100
	CTATGGATAT	GACAGATGGC	TTGGTAAGAG	GACTTAAAGC	AGAAGCTTTG	150
	GGTGCTCCTA	TTAGCGTTCC	TGTGGGTGAA	AAAGTTTTAG	GAAGAATTTT	200
40	TAATGTTACG	GGAGATTTGA	TCGATGAAGG	TGAAGAAATT	TCTTTTGATA	250
	AAAAATGGGC	AATTCATAGA	GATCCACCAG	CTTTTGAAGA	TCAAAGCACA	300
	AAAAGTGAGA	TTTTTGAAAC	AGGGATTAAA	GTTGTGGATT	TACTTGCTCC	350
	TTATGCAAAA	GGTGGTAAAG	TAGGTCTTTT	TGGTGGTGCA	GGTGTGGTA	400
	AAACTGTTAT	TATTATGGAG	CTTATTCACA	ATGTTGCATT	TAAACATAGC	450
45	GGCTATTCTG	TATTTGCAGG	TGTAGGTGAG	AGAACTCGTG	AAGGAAATGA	500
	CCTTTATAAT	GAAATGAAAG	AAAGTAATGT	TTTAGACAAA	GTTGCTCTAT	550
	GTTATGGACA	AATGAATGAA	CCACCAGGGG	CAAGAAATCG	TATTGCTTTA	600
	ACAGGTTTAA	CAATGGCTGA	GTATTTTAGA	GATGAAATGG	GTCTTGATGT	650
	GCTTATGTTT	ATTGATAATA	TCTTTAGATT	TTCACAATCA	GGTTCTGAAA	700
50	TGTCAGCACT	TTTAGGAAGA	ATTCCATCAG	CTGTGGGTTA	TCAACCAACC	750
	CTAGCAAGTG	AAATGGGTAA	ATTCCAAGAA	AGAATTACTT	CAACTAAAAA	800
	AGGATCAATT	ACTTCAG				817

2) INFORMATION FOR SEQ ID NO: 1850

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850

AAGGCAACAC GCATAAACTT ATTTTAGAGA CTGCTGCACA CCTTGGAGAT 50
 AATCGTGTA GAACATATCGC TATGGATATG AGCGAAGGAC TTACAAGAGG 100
 GTTAGATGCT ATAGCGCTTG GGTCGCCTAT CAGTGTTCCT GTTGGAGAAA 150
 20 AAGTTTTAGG AAGAATATTC AACGTAATTG GTGATCTTAT AGACGAAGGC 200
 GAAGAAGAAA AATTTGATAA AAAATGGTCG ATTCATAGAG ATCCGCCGGC 250
 ATTTGAAGAT CAAAGCACAA AAAGTGAAAT TTTTGAAACA GGTATAAAAG 300
 TCGTAGATCT TTTGGCTCCT TATGCAAAAG GCGGTAAAGT TGGACTATTT 350
 GGCGGTGCCG GCGTTGGTAA AACAGTTATC ATTATGGAAC TTATCCACAA 400
 25 CGTTGCATTC AAACACAGCG GCTATTCGGT ATTTGCCGGT GTCGGTGAAA 450
 GAACAAGAGA GGGTAACGAT CTTTATAATG AAATGAAAGA ATCCGGCGTT 500
 TTGGATAAAG TTGCCTTATG TTATGGACAA ATGAATGAAC CGCCGGGTGC 550
 AAGAAACCGT ATAGCGCTTA CTGGTCTTAC AATGGCTGAG TATTTTCGTG 600
 ACGAGATGGG ACTAGATGTT CTTATGTTTA TCGATAACAT CTTCCGTTTC 650
 30 TCACAATCAG GCTCAGAGAT GTCGGCTCTT CTTGGACGTA TCCCAAGTGC 700
 GGTTGGTTAT CAACCAACGT TAGCTAGCGA AATGGGAAGA CTTCAAGAAA 750
 GAATCACATC AACTAAAAAA GTTTC 775

35

2) INFORMATION FOR SEQ ID NO: 1851

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851

CGAAGCTATT GAAGTAAATT TTACAGTAGA AGGCAACACG CATAAACTTA 50
 TTTTAGAGAC TGCTGCACAC CTTGGAGATA ATCGTGTAAG AACTATCGCT 100

	ATGGATATGA	GCGAAGGACT	TACAAGAGGG	TTAGATGCTA	TAGCGCTTGG	150
	GTCGCCTATC	AGTGTTTCCTG	TTGGAGAAAA	AGTTTTAGGA	AGAATATTCA	200
	ACGTAATTGG	TGATCTTATA	GACGAAGGCG	AAGAAGAAAA	ATTTGATAAA	250
	AAATGGTCGA	TTCATAGAGA	TCCGCCGGCA	TTTGAAGATC	AAAGCACAAA	300
5	AAGTGAAATT	TTTGAAACAG	GTATAAAAGT	CGTAGATCTT	TTGGCTCCTT	350
	ATGCAAAAGG	CGGTAAAGTT	GGACTATTTG	GCGGTGCCGG	CGTTGGTAAA	400
	ACAGTTATCA	TTATGGAAC	TATCCACAAC	GTTGCATTCA	AACACAGCGG	450
	CTATTCGGTA	TTTGCCGGTG	TCGGTGAAAG	AACAAGAGAG	GGTAACGATC	500
	TTTATAATGA	AATGAAAGAA	TCCGGCGTTT	TGGATAAAGT	TGCCTTATGT	550
10	TATGGACAAA	TGAATGAACC	GCCGGGTGCA	AGAAACCGTA	TAGCGCTTAC	600
	TGGTCTTACA	ATGGCTGAGT	ATTTTCGTGA	CGAGATGGGA	CTAGATGTTC	650
	TTATGTTTAT	CGATAACATC	TTCCGTTTCT	CACAATCAGG	CTCAGAGATG	700
	TCGGCTCTTC	TTGGACGTAT	CCCAAGTGCG	GTTGGTTATC	AACCAACGTT	750
	AGCTAGCGAA	ATGGGAAGAC	TTCAAGAAAG	AATCACATCA	ACT	793
15						

2) INFORMATION FOR SEQ ID NO: 1852

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter gracilis*

30 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852

	GGACTATTTA	CCGAAGATTA	ACGAAGCTAT	CGAGGTAA	TTTGACGTCG	50
35	AGGGCGCTCA	TCGCAGGCTG	ATCCTAGAGG	TAGCCGCGCA	CCTTGAGAGAC	100
	AATCGCGTCC	GCACGATCGC	TATGGATATG	AGCGATGGAC	TTAGGCGAGG	150
	GCTTGAGGCC	GTCGCTTTGG	GCGCGCCTAT	TACGGTGCCT	GTGGGCGAGA	200
	AAGTTTTTGGG	TAGAATTTTT	AATGTTACGG	GCGATCTGAT	CGACGAAGGC	250
	GAGGATGAAA	AATTTGAAAC	CCGCTGGTCG	ATCCACAGAG	ATCCGCCTAG	300
40	CTTTGAAAAT	CAAAGCACGA	AGAGTGAAAT	TTTTGAAACC	GGCATTAAGG	350
	TAGTCGATCT	GCTCGCCCCT	TATGCAAAGG	GCGGTAAGGT	AGGACTATTC	400
	GGCGGTGCTG	GCGTCGGTAA	GACCGTCATC	ATCATGGAAC	TGATTCACAA	450
	CGTCGCTTTC	AAACACAGCG	GCTACTCCGT	ATTTGCGGGT	GTCGGCGAGC	500
	GAACGAGAGA	GGGAAACGAC	CTTTATAACG	AGATGAAAGA	ATCGGGCGTT	550
45	TTGGATAAAG	TCGCCTTGAC	CTATGGTCAG	ATGAACGAAC	CGCCGGGAGC	600
	GAGAAACCGT	ATCGCGCTAA	CCGGTCTTAC	GATGGCCGAG	TATTTCCGCG	650
	ACGAGCTAGG	GCTTGACGTT	TTGATGTTTA	TTGATAATAT	CTTCCGCTTC	700
	TCGCAGTCGG	GTTCCGAGAT	GTCCGCGCTT	TTAGGACGAA	TTCCGTCGCG	750
	GGTCGGTTAT	CAGCCTACGC	TTGCCAGCGA	AATGGGTAAA	TTACAGGAGC	800
50	GCATTACTTC	TACTAAGAAG	GGCTC			825

2) INFORMATION FOR SEQ ID NO: 1853

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33560
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853

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TTTACCTCAA ATTAATGAAG CAATTGTTGT AAATTTTGAA AGCGAAGGAA      50
AAAAACATAA ACTTGTTTTA GAAGTAGCAG CTCATTTAGG AGATAATAGA      100
GTTAGAACTA TTGCTATGGA TATGACAGAT GGTTTGGTAA GGGGCTTAAA      150
20 AGCTGAGGCT TTAGGTGCTC CTATTAGTGT TCCTGTTGGT GAGAAAGTTT      200
TAGGAAGAAT TTTCAATGTT ACTGGAGATT TGATCGATGA AGGTGAAGAA      250
ATTTCTTTTG ATAAAAAATG GGCAATTCAT AGAGATCCGC CAGCTTTTGA      300
AGATCAAAGC ACAAAAAGTG AGATTTTGA AACAGGGATT AAAGTTGTAG      350
ATTTGCTTGC TCCTTATGCA AAAGGTGGTA AAGTAGGTCT TTTTGGTGGT      400
25 GCAGGTGTTG GTAAACTGT TATTATTATG GAGCTTATTC ACAATGTTGC      450
ATTTAAGCAT AGCGGCTATT CTGTATTGTC AGGTGTGGGT GAGAGAACTC      500
GTGAAGGAAA TGACCTTTAT AATGAAATGA AAGAAAGTAA TGTTTTAGAC      550
AAAGTTGCTC TATGTTATGG ACAAATGAAT GAACCACCAG GAGCAAGAAA      600
TCGTATTGCT TTAACAGGTT TAACAATGGC TGAGTATTTT AGAGATGAAA      650
30 TGGGTCTTGA TGTGCTTATG TTTATTGATA ATATCTTTAG ATTTTCACAA      700
TCAGGTTCTG AAATGTCAGC ACTTTTAGGA AGAATTCCAT CAGCTGTGGG      750
TTATCAACCA ACCCTAGCAA GTGAAATGGG TAAATTCCAA GAAAGAATTA      800
CTTCAACTAA AAAAGGCT                                     818

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35

2) INFORMATION FOR SEQ ID NO: 1854

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus cecorum*
- (B) STRAIN: ATCC 43198

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854

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ATTACCTGAT ATCAACAACG CCTTATTGGT CTATAAAAAT GATGAACAAA      50

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	AAAGTAAAAT	TGTGCTAGAA	GCTGCCTTAG	AATTAGGTGA	TGGCATCATT	100
	CGTACAATTG	CCATGGAATC	AACGGATGGT	TTACAACGTG	GGATGGAAGT	150
	TGTCGATACT	GGTAAACCAA	TTTCAGTTCC	AGTTGGTAAA	GAAACGCTAG	200
	GACGTGTCTT	TAACGTTTTA	GGGGATACGA	TTGATATGCA	AGAACCATTT	250
5	GCACAAGATG	CAGATCGTTC	TGCAATTCAT	AAAGCTGCAC	CAAAATTTGA	300
	AGACTTAAGT	ACAAGTACTG	AAATTTTAGA	AACAGGGATT	AAAGTTATCG	350
	ACTTATTAGC	ACCATATTTA	AAAGGTGGTA	AAGTCGGTCT	ATTCGGGGGT	400
	GCCGGAGTAG	GTAAAACCGT	TTTAATCCAA	GAATTAATCC	ATAATATTGC	450
	ACAAGAACAT	GGTGGGATTT	CTGTATTTAC	CGGTGTTGGT	GAACGTACAC	500
10	GTGAAGGAAA	TGACTTGTAT	CATGAAATGC	GTGATTTCAGG	AGTTATTGAA	550
	AAAAGTCCA	TGGTGTGTTG	TCAAATGAAC	GAACCACCTG	GAGCTCGTAT	600
	GCGTGTTGCT	TTAACTGGGT	TAACGATTGC	TGAATATTTT	CGTGATGTAG	650
	AAGGACAAGA	TGTGTTGCTA	TTTATTGATA	ACATCTTCCG	TTTCACTCAA	700
	GCGGGTTCTG	AAGTATCAGC	CTTGCTTGGT	CGTATGCCAT	CTGCCGTGGG	750
15	TTATCAACCT	ACATTGGCTA	CAGAAATGGG	TCAATTACAA	GAACGTATCA	800
	CTTCAACTAA	GAAGGGCTCT	ATCACTTCTA			830

20 2) INFORMATION FOR SEQ ID NO: 1855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855

35	TCTTTACCAG	ATATCAATAA	TGCGCTTATT	GTCTATAAAA	ATGATGAACA	50
	AAAAAGTAAA	ATCGTGCTTG	AAGCTGCTTT	AGAGCTAGGA	GATGGCATT	100
	TTCGTACGAT	TGCAATGGAA	TCAACTGATG	GATTGCAACG	TGGAATGGAA	150
	GTTTTTCGATA	CAGGTAAGCC	AATTTTCAGTA	CCAGTAGGTC	GTGAAACATT	200
40	AGGTCGTGTA	TTTAATGTTT	TAGGTGATAC	CATTGATACG	CAAGAAGCTT	250
	TTCCTGCTGA	TGCGAATCGT	GATGCGATT	ATAAATCAGC	TCCAGCTTTT	300
	GAAGAATTAA	GTACAAGTAC	TGAAATCCTA	GAAACAGGGA	TTAAAGTTAT	350
	CGACTTACTA	GCACCATACT	TAAAAGGTGG	GAAAGTTGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACC	GTATTAATTC	AAGAATTAAT	TCATAATATC	450
45	GCCCAAGAAC	ATGGGGGTAT	TTCAGTATTT	ACCGGTGTTG	GTGAACGTAC	500
	ACGTGAAGGA	AATGACTTGT	ATCACGAAAT	GCGTGATTCA	GGCGTTATCG	550
	AAAAAACTGC	TATGGTGTTT	GGGCAAATGA	ACGAACCACC	TGGAGCACGT	600
	ATGCGTGTTG	CGCTAACTGG	ACTAACTATT	GCGGAATACT	TCCGTGATGT	650
	TGAAGGCCAA	GACGTATTGC	TATTTATTGA	TAATATCTTC	CGTTTTACTC	700
50	AAGCAGGTTC	TGAAGTTTCT	GCCTTACTTG	GTCGTATGCC	TTCTGCGGTA	750
	GGTTATCAAC	CTACTTTGGC	TACTGAAATG	GGTCAATTGC	AAGAACGGAT	800
	TACATCAACG	AAGAAAGGTT	CGA			823

2) INFORMATION FOR SEQ ID NO: 1856

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856

TTACCAGACA TTAATAATGC CTTGGTTGTC TATAAAAATG ACGAACAAAA 50
 AACCAAGATT GTATTAGAAG CTGCCTTAGA ACTAGGAGAT GGTGTGATTC 100
 GAACTATCGC CATGGAATCT ACTGATGGCT TACAACGGGG AATGGAAGTT 150
 20 GTCGATACTG GCAGTTCCAT TTCTGTACCG GTAGGAAAAG AAACATTGGG 200
 TCGTGTATTT AACGTTTTAG GAAATACAAT TGACTTAGAA GAACCTTTTC 250
 CAGCGGATGC TAAACGTAGT GGTATCCATA AAAAAGCGCC TGATTTTGAT 300
 GAATTAAGCA CTAGTACAGA AATTTTAGAA ACAGGGATTA AAGTTATTGA 350
 CCTATTAGCC CCTTATTTAA AAGGTGGTAA AGTCGGATTA TTCGGTGGTG 400
 25 CCGGAGTTGG TAAAACCGTT TTAATTCAAG AATTAATTCA TAATATTGCC 450
 CAAGAACATG GTGGGATTTT TGTTTTTACT GGTGTTGGTG AAAGAACACG 500
 TGAAGGTAAT GACTTGTATT ATGAAATGAA AGAATCTGGC GTTATCGAAA 550
 AAAGTGCAT GGTATTTGGT CAAATGAATG AGCCACCTGG TGCCCGGATG 600
 CGGGTTGCTT TAACCGGACT TACCATTGCG GAATACTTCC GGGACGTTGA 650
 30 AGGACAAGAT GTATTGCTCT TTATCGATAA TATTTTCCGT TTTACCCAAG 700
 CTGGTTCAGA AGTATCTGCC TTATTAGGAC GGATGCCCTC TGCCGTTGGT 750
 TATCAACCAA CTTTGGCTAC TGAAATGGGA CAACTTCAAG AACGGATTAC 800
 CTCAACGAAA AAAGGTTCTA TTACAT 826

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2) INFORMATION FOR SEQ ID NO: 1857

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857

TCCTTACCAG ACATCAACAA TCGGTTGATT GTTTACAAAA AAAATAAAAC 50

	AAAAGTTGTT	CTTGAAGCTG	CTTTGGAAC	TGGTGATGGT	GTTATCCGCA	100
	CGATCTCTAT	GGAATCAACA	GATGGCTTGC	AACGTGGAAT	GGAAGTTGTC	150
	GATACAGGCA	AACCAATCTC	AGTTCCCGTT	GGTAAAGAAA	CTTTAGGTCG	200
	TGTGTTTAAC	GTATTAGGTG	AAACAATCGA	CAAAGAAGCG	CCTTTTCCAG	250
5	AAGATGCAGT	AAAAAGCGGT	ATTCATAAAA	AAGCGCCGGC	TTTTGAAGAA	300
	CTTAGTACCA	GTAATGAAAT	TTTAGAAACA	GGGATCAAAG	TTATCGACTT	350
	ATTAGCTCCT	TACTTAAAGG	GTGGTAAAGT	CGGACTATTT	GGTGGTGCCG	400
	GTGTTGGTAA	AACCGTCTTG	ATCCAAGAAT	TGATTCATAA	TATCGCCCAA	450
	GAACACGGTG	GTATTTTCAGT	GTTTACGGGT	GTTGGTGAAC	GTACTCGTGA	500
10	AGGGAACGAC	CTTTATTATG	AAATGAAGGA	ATCAGGCGTT	ATTGAGAAAA	550
	CTGCCATGGT	GTTTGGACAA	ATGAACGAGC	CGCCAGGTGC	GCGTATGCGT	600
	GTTGCCTTGA	CTGGTTTGAC	ATTGGCTGAA	TATTTCCGAG	ATGAAGAAGG	650
	ACAAGATGTG	CTGTTGTTTA	TCGACAACAT	CTTCCGTTTC	ACTCAAGCCG	700
	GTTCTGAAGT	TTCTGCCTTG	CTTGGCCGGA	TGCCTTCAGC	CGTTGGCTAC	750
15	CAACCAACTT	TGGCAACTGA	AATGGGTCAA	TTGCAAGAAC	GAATCACTTC	800
	AACGAAGAAG	GGCT				814

20 2) INFORMATION FOR SEQ ID NO: 1858

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 791 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus mundtii*
 - (B) STRAIN: ATCC 43186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858

35	CGCATTAGTT	GTTTATAAAA	ATGATGAGCA	AAAATCAAAA	GTTGTTCTTG	50
	AAGCAGCATT	AGAATTAGGT	GACGGTGTGA	TCCGTACGAT	CGCAATGGAA	100
	TCGACGGATG	GACTACAACG	TGGAATGGAA	GTCATCGACA	CAAGCAAAGC	150
	GATCTCTGTA	CCAGTTGGAA	CAGAAACATT	AGGTCGTGTG	TTCAACGTGT	200
40	TAGGTGAAAC	AATCGATTTG	GAAGCACCAT	TTCCAGAGGA	TGCCCAAAGA	250
	AGCGAGATCC	ACAAGAAAGC	ACCAAATTTT	GATGAATTAA	GCACAAGTAC	300
	AGAGATTCTT	GAAACTGGGA	TCAAAGTCAT	TGACTTATTA	GCACCTTATT	350
	TAAAAGGTGG	GAAAGTTGGA	TTGTTTGGGG	GTGCCGGTGT	TGGTAAAACC	400
	GTA CTGATCC	AAGAATTGAT	CCATAATATC	GCCCAAGAAC	ATGGGGGAAT	450
45	CTCAGTGTTT	ACCGGTGTAG	GGGAACGTAC	CCGTGAAGGA	AACGATCTGT	500
	ATTACGAAAT	GAAAGATTCA	GGCGTAATCG	AAAAAACAGC	GATGGTGTTT	550
	GGACAAATGA	ATGAGCCACC	AGGTGCTCGT	ATGCGTGTCG	CACTAACTGG	600
	ATTGACGATT	GCGGAATATT	TCCGTGATGT	CGAAGGACAA	GACGTGCTCT	650
	TATTTATTGA	TAATATTTTC	CGTTTCACCC	AAGCAGGTTC	AGAAGTATCT	700
50	GCCTTACTAG	GACGTATGCC	ATCAGCGGTT	GGTTATCAAC	CAACCTTAGC	750
	GACTGAAATG	GGACAACCTCC	AAGAACGGAT	CACTTCAACG	A	791

2) INFORMATION FOR SEQ ID NO: 1859

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859

TCCTTACCAG ACATCAACAA TCGGTTGATT GTTTATAAAA AAGATAAAAC 50
 AAAAGTTGTT CTTGAAGCTG CTTTGGAACT TGGTGATGGT GTTATTTCGCA 100
 CAATCGCCAT GGAATCAACG GATGGATTAC AACGTGGAAT GGAAGTTGTC 150
 20 GATACTGGCA AGCCTATTTC TGTTCCAGTA GGAAAAGAAA CTCTAGGTCG 200
 TGTATTTAAT GTATTAGGTG AAACAATCGA CAAGGAAGCG CCTTTTCCAG 250
 AAGATGCAGA AAAAAGTGGT ATTCACAAGA AAGCACCAAC TTTCGAAGAA 300
 CTTAGCACAA GTAATGAGAT CTTAGAAACA GGAATCAAAG TTATTGACTT 350
 GTTAGCTCCT TACTTAAAAG GTGGTAAAGT TGGATTATTT GGTGGTGCCG 400
 25 GTGTTGGTAA AACAGTCTTG ATTCAAGAGC TAATTCATAA TATCGCTCAA 450
 GAACATGGTG GTATTTCTGT GTTTACTGGT GTTGGTGAAC GTACTCGTGA 500
 AGGGAACGAC CTTTATTATG AAATGAAAGA TTCTGGTGTT ATTGAGAAAA 550
 CTGCTATGGT GTTCGGTCAA ATGAACGAGC CGCCAGGTGC ACGTATGCGT 600
 GTTGCCTTAA CTGGTTTAAAC CTTAGCCGAA TACTTCCGTG ATGAAGAAGG 650
 30 ACAAGATGTG TTGCTATTTA TTGACAACAT TTTCCGTTTC ACTCAAGCCG 700
 GATCAGAAGT TTCTGCCTTA CTTGGCCGTA TGCCGTCAGC AGTTGGTTAC 750
 CAACCGACTT TAGCAACTGA AATGGGTCAA TTACAAGAAC GTATTACGTC 800
 GACGAAAAAA GGTTCAA 817

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2) INFORMATION FOR SEQ ID NO: 1860

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Globicatella sanguis*
 (B) STRAIN: ATCC 51173

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860

CCTGACATTC ATAATGCATT AATTGTAACG AACGCTGATA TGGCGGATGT 50

	AATGCAAGAA	AATATTTTCGG	ATGAAGAAAA	ATTATTAACC	TTAGAAGTTG	100
	CACTGGATTT	AGGTCATGGA	ATGGTCCGGA	CAATTGCGAT	GGAATCAACC	150
	GATGGTTTGG	AACGCGGCAT	GACAGTTGTG	GATTATTTAA	CACCGATTAA	200
	AGTGCCAGTA	GGCGAAGCCA	CTTTAGGTAG	AGTATTCAAT	GTTTTAGGTG	250
5	AGACAATTGA	TGAACTAGAA	CCGGTTGGCG	ACGATGTTGA	ACTCAAAAGT	300
	ATTCATCGTG	AAGCCCCTAA	ATATGAGGAC	TTAGATAATA	GTTTTCATGT	350
	TTTAGAAACC	GGAATTAAGG	TCATCGATTT	ATTAGCTCCT	TATATTAAAG	400
	GGGGAAAAAT	CGGTTTATTC	GGTGGTGCCG	GAGTGGGTAA	AACGGTCTTA	450
	ATTCAAGAAT	TAATTCATAA	TATTGCAGAA	CAATTAGGAG	GTATCTCAGT	500
10	TTTCACTGGG	GTTGGAGAAC	GTACCCGTGA	AGGGAATGAC	CTCGTTTTTG	550
	AAATGCGAGA	GTCAGGTGTA	AGCAAGAAGA	CGGCCATGGT	TTTCGGTCAA	600
	ATGAATGAAC	CACCTGGAGC	ACGTATGCGT	GTTGTCTTAA	CAGGACTTAC	650
	AATGGCGGAA	TATTTCCGTG	ACGAATTGAA	ACAAGACGTC	TTATTATTTA	700
	TTGATAATAT	TTATCGTTTT	ACTCAAGCAG	GTTCCGAAGT	GTCAGCCTTA	750
15	TTAGGTCGTA	TGCCTTCAGC	AGTAGGGTAT	CAACCAACTT	TAGCAAGTGA	800
	AATGGGACAA	ATGCAAGAAC	GTATTACGTC	WACGAAGCRC	GGTTCCATTA	850
	CA					852

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2) INFORMATION FOR SEQ ID NO: 1861

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus garvieae*
 (B) STRAIN: ATCC 49156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861

	GCGCGACTCT	TCCTGAGATT	AATAACGCAC	TCATCGTTTA	CAAAGATGTA	50
	GACGGCGTTA	AAACTAAAAT	CGTCCTTGAA	GTGGCGTTGG	AACTTGGTGA	100
	TGGTGCCGTA	CGTACCATCG	CTATGGAATC	AACTGATGGC	TTGACACGTG	150
40	GACTTGAAGT	TCTCGATACA	GGTAAAGCAA	TCAGCGTACC	TGTTGGTCAA	200
	GAAACACTTG	GACGTGTCTT	CAATGTACTT	GGAGATGCTA	TTGATGGAGG	250
	GGAAGCATTT	GCTGAAAATG	CAGAACGCAG	CCCTATCCAT	AAAAAAGCCC	300
	CATCTTTTGA	TGAACTTTCA	ACAGCAAATG	AAATTCTGGT	GACAGGGATT	350
	AAAGTTATTG	ACTTGCTTGC	CCCATACCTT	AAAGGTGGTA	AGATTGGGTT	400
45	GTTCGGTGGT	GCCGGAGTTG	GTAAAACCGT	CCTTATCCAA	GAGTTGATTG	450
	ACAATATTGC	CCAAGAACAC	GGTGGTATTT	CCGTATTTAC	TGGTGTGGG	500
	GAACGTACAC	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AAGAATCAGG	550
	CGTTATCGAA	AAAACAGCCA	TGGTCTTCGG	TCAAATGAAT	GAACCACCTG	600
	GAGCACGTAT	GCGTGTTGCT	CTTACTGGTT	TGACAATTGC	TGAATATTTG	650
50	CGTGATGTAG	AAAAACAAGA	CGTTTTGCTT	TTCATTGATA	ATATCTTCCG	700
	TTTCACCCAA	GCCGGTTCAG	AAGTATCTGC	CCTCTTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	TTACCAACCT	ACGCTTGCAA	CTGAAATGGG	TCAACTTCAA	800
	GAACGTATCA	CTTCAACAAA	ACAAGGTT			828

2) INFORMATION FOR SEQ ID NO: 1862

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis*
 (B) STRAIN: ATCC 11454

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862

AATTGCCTGA RATTAACAAT GCCTTGATTG TCTACAAAGA TGTCAATGGC 50
 CTAAAAACAA AAATTACTCT TGAAGTTGCT TTGGAAGTTG GTGATGGTGC 100
 AGTTCGTACA ATCGCTATGG AATCTACTGA TGGCTTGACT CGTGGACTTG 150
 20 AAGTCCTTGA TACAGGTAAA GCAGTCAGCG TTCCTGTTGG GGAAGCCACT 200
 CTTGGTCGTG TTTTAAACGT TCTTGGTGAT GTTATTGACG GTGGGGAAGA 250
 ATTTGCTGCT GATGCAGAAC GTAATCCTAT CCATAAAAAA GCTCCAACAT 300
 TTGACGAATT GTCAACTGCA AACGAAGTTC TCGTAACTGG GATTAAAGTT 350
 GTCGATTTGC TTGCACCTTA CCTTAAAGGT GGTAAAGTTG GACTTTTCGG 400
 25 TGGTGCCGGA GTTGGTAAAA CCGTCCTTAT TCAAGAATTG ATTCACAACA 450
 TCGCCCAAGA ACACGGAGGT ATTTCTGTGT TTACCGGTGT TGGGGAACGT 500
 ACTCGTGAAG GGAATGACCT TTAAGTGGAA ATGAAAGAAT CAGGCGTTAT 550
 TGAAAAAAT GCCATGGTCT TTGGTCAAAT GAATGAACCA CCAGGAGCAC 600
 GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCTGAATA TTTCCGTGAT 650
 30 GTTCAAGGTC AAGACGTACT GCTTTTCATT GACAACATCT TCCGTTTCAC 700
 ACAAGCTGGT TCAGAAGTTT CTGCCCTTTT GGGACGTATG CCTTCTGCCG 750
 TTGGTTACCA ACCAACACTT GCTACTGAAA TGGGGCAATT GCAAGAACGT 800
 ATCACTTCTA CTAAGAAGGG TTCTGTTA 828

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2) INFORMATION FOR SEQ ID NO: 1863

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863

CTTACCTGAA ATCTACAACG CCCTAGTTAT TGAATATAAA TCTGATGCAG 50

	AAGAAGCACC	AACTAGCCAA	CTTACTTTAG	AAGTAGCCAT	TCAATTAGGT	100
	GATGACGTTG	TTCGTACAAT	TGCAATGGCA	TCAACTGATG	GTGTTCAAAG	150
	AGGTATGGAA	GTTATTGATA	CTGGGAGCCC	AATCACAGTT	CCAGTTGGTA	200
	CAGTAACACT	TGGTCGTGTA	TTTAACGTAT	TAGGAAACAC	TATCGATTTG	250
5	GATGAGCCAC	TTCCAAGCGA	TATCAAGCGT	AATAAAATTC	ACCGTGAAGC	300
	ACCAACATTT	GACCAATTAG	CAACAACACT	TGAAATTCTT	GAAACAGGAA	350
	TAAAAGTTGT	AGACTTGCTA	GCCCCATATT	TAAAAGGTGG	TAAAATTGGT	400
	TTGTTTCGGCG	GAGCGGGTGT	TGGTAAAACC	GTTTTAATCC	AAGAACTTAT	450
	TCATAATATC	GCTCAAGAAC	ATGGTGGTAT	TTCTGTGTTC	GCTGGTGTG	500
10	GAGAACGTAC	TCGTGAAGGG	AACGATCTTT	ACTTTGAAAT	GAAAGACTCT	550
	GGTGTAATTG	AAAAAACTGC	CATGGTATTC	GGTCAAATGA	ACGAACCACC	600
	AGGTGCTCGT	ATGCGTGTAG	CTTTAACAGG	TCTTACAATC	GCTGAATATT	650
	TCCGTGATGA	AGAACACCAA	GATGTACTTC	TATTCATTGA	TAATATTTTC	700
	CGCTTTACTC	AAGCTGGTTC	AGAGGTTTCG	GCTTTACTAG	GTCGTATGCC	750
15	ATCTGCAGTA	GGTTATCAAC	CAACTCTAGC	TACCGAAATG	GGACAATTAC	800
	AAGAACGTAT	TACTTCTACT	AATGT			825

20 2) INFORMATION FOR SEQ ID NO: 1864

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864

35	GTCATATTCC	AGAGCTTTAT	GACGCTCTGG	AGGTAAAGGG	CGATGGTAAG	50
	CATCGTTCAG	ACCTAGTTCT	TGAGGTTCAA	CAGCAGATTG	GCGGTGGTGT	100
	GGTACGCTGC	ATTGCCATGG	GTTCTTCTGA	CGGTTTGAGC	AGAGGAATTG	150
	AGGCTGTAAA	TACTGGTGCC	GGTGTTAAGG	TTCCAGTTGG	TCGTGAGACC	200
40	CTAGGACGTA	TTATGAACGT	TTTAGGTCAG	CCTGTAGATG	AGAGAGGTCC	250
	TATCGGACAG	AAAGAGGATT	GGGAAATTCA	CCGTCCAGCT	CCTACCTATG	300
	CTGAGCAGTC	ATCAACTACA	GAAATTCTAG	AAACCGGTAT	TAAGGTTATG	350
	GACCTTATCT	GCCCATTTGC	TAAGGGTGGT	AAAGTTGGTC	TGTTCGGTGG	400
	TGCCGGTGTG	GGTAAGACAG	TTAACATGAT	GGAGCTTATC	AATAACATTG	450
45	CTAAGGCTCA	CTCAGGTCTA	TCTGTATTTA	CCGGTGTGTTG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	CAGGAATCAA	AGGTTATCGA	550
	TAAGGTATCA	ATGATTTACG	GTCAGATGAA	CGAGCCTCCA	GGGAACCGTC	600
	TACGTGTTGC	TCTGACAGGT	CTGACTGTTG	CTGAGAAGTT	CCGTGACGAA	650
	GGTCTGGATG	TGCTTCTGTT	CATCGATAAC	ATCTATCGTT	ATACACTGGC	700
50	TGGTACAGAG	GTATCTGCTC	TGTTAGGCCG	TATGCCTTCA	GCTGTGGGTT	750
	ACCAGCCTAC	ACTGGCTGAG	GAAATGGGTG	TATTACAGGA	GCGTATTGCT	800
	TCAACTAAGA	AAGGTTCTAT	T			821

2) INFORMATION FOR SEQ ID NO: 1865

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tetragenococcus halophilus*
- (B) STRAIN: ATCC 33315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865

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TGATACTTTA CCAGATATCA ATAATGCATT AGCCGTATAT AAAAATGATG      50
AGAACAAGAC GCGTGTTGTA TTGGAAGCTA CTTTAGAACT TGGAGATGGG      100
GTAATTCGTG CCATTTCTAT GGGGTCTACT GACGGCTTGC AACGTGGCAT      150
GGAAGTTGTG GATACACAAG AACCTATTTC TGTTCCGGTA GGAAATGATA      200
CTTTAGGTCG TGTATTTAAT GTGTTAGGAG AAACAATAGA TAATCAGGAG      250
CCATTTCTTG AAGATGCTGA AAAAAGTGGT ATTCACAAAA AAGCCCCTAG      300
TTTTGATGAA TTAAGTACTA GTTCGGAAAT ATTAGAAACA GGGATCAAAG      350
TGATTGATTT ATTAGAACCT TATCTAAGAG GCGGTAAAGT CGGATTGTTT      400
GGAGGCGCCG GTGTTGGAAA AACGGTGCTA ATTCAAGAAT TGATCAATAA      450
TGTTGCCCAA GAACACGGGG GTATTTCCTG GTTTAATGGT GTAGGTGAAC      500
GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGCAGGA TTCAGGCGTT      550
ATCGAAAAAA CAGCCATGGT GTTTGGTCAA ATGAACGAAC CACCAGGTGC      600
TCGTATGCGT GTTGCTTTAA CTGGCCTAAC ACTGGCAGAA TATTTTCGAG      650
ATGTTGAAGG TCAAGACGTA TTATTATTTA TTGATAATAT TTTCCGTTTT      700
ACACAAGCAG GTACCGAAGT TTCCGCTTTA CTTGGTAGAA TGCCATCTGC      750
TGTTGGCTAT CAACCCACAC TAGCAACTGA AATGGGGCAA CTGCAAGAAC      800
GGATTACGTC AACGGATAAG GG                                     822

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2) INFORMATION FOR SEQ ID NO: 1866

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
- (B) STRAIN: ATCC 25936
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866

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ATCTCCTCAG GATCKATAGG ACTTGATATA GCTCTTGGTA TAGGCGGCGT      50

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	ACCAAAAGGA	AGAATAGTCG	AAATTTATGG	GCCAGAAAGC	TCTGGTAAAA	100
	CAACTCTTAC	TTTGCAATTA	ATAGCAGAAT	CTCAAAAAGT	CGGCGGAGTT	150
	TGCGCGTTTG	TAGATGCAGA	GCATGCACTT	GATGTTAAAT	ATGCTAAAAA	200
	TTTAGGCGTT	GATACGGATA	ACTTATATAT	TTCTCAACCG	GACTTCGGAG	250
5	AGCAAGCTCT	TGATATAGTA	GAAACTCTAG	CTAGAAGCGG	CGCCGTTGAT	300
	CTTATAGTAA	TAGATAGCGT	AGCAGCTYTA	ACACCAAAAA	GCGAAATAGA	350
	AGGCGATATG	GGAGATCAGC	ACGTAGGGCT	GCAAGCAAGA	CTCATGAGTC	400
	AAGCACTTAG	AAAATTAACC	GGAGTTGTCC	ATAAAATGGG	AACTACAGTT	450
	GTATTTATAA	ACCAAATTCG	TATGAAAATC	GGCGCTATGG	GCTATGGCAC	500
10	TCCTGAAACT	ACTACTGGCG	GAAATGCGCT	TAAATTTTAC	GCTTCAGTTA	550
	GACTTGACGT	ACGTAAAATA	GCTACTTTAA	AACAGAGCGA	TGAGCCAATC	600
	GGAAACCGCG	TAAAAGTAAA	AGTAGTAAAA	AACAAAGTCG	CTCCTCCTTT	650
	TAGACAAGCC	GAATTTGATA	TCATGTTTGG	AGAAGGTATC	AGCAAAGAAG	700
	GAGAGATAAT	AGATTACGGC	GTAAAACTTG	ATATTATCGA	TAAAAGCGGC	750
15	GCTTGGTTTA	GCTATGATAA	TTCAAAATTA	GGTCAAGGCA	GAGAAAAC TC	800
	AAAAGCGTTT	TTAAAAGA				818

20 2) INFORMATION FOR SEQ ID NO: 1867

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867

35	TCTCCTCAGG	ATCKATAGGA	CTTGATATAG	CTCTTGGTAT	AGGCGGCGTA	50
	CCAAAAGGAA	GAATAGTCGA	AATTTATGGG	CCAGAAAGCT	CTGGTAA AAC	100
	AACTCTTACT	TTGCATTTAA	TAGCAGAATC	TCAAAAAGTC	GGCGGAGTTT	150
	GCGCGTTTGT	AGATGCAGAG	CATGCACTTG	ATGTTAAATA	TGCTAAAAAT	200
40	TTAGGCGTTG	ATACGGATAA	CTTATATATT	TCTCAACCGG	ACTTCGGAGA	250
	GCAAGCTCTT	GATATAGTAG	AAACTCTAGC	TAGAAGCGGC	GCCGTTGATC	300
	TTATAGTAAT	AGATAGCGTA	GCAGCTYTAA	CACCAAAAAG	CGAAATAGAA	350
	GGCGATATGG	GAGATCAGCA	CGTAGGGCTG	CAAGCAAGAC	TCATGAGTCA	400
	AGCACTTAGA	AAATTAACCG	GAGTTGTCCA	TAAAATGGGA	ACTACAGTTG	450
45	TATTTATAAA	CCAAATTCGT	ATGAAAATCG	GCGCTATGGG	CTATGGCACT	500
	CCTGAAACTA	CTACTGGCGG	AAATGCGCTT	AAATTTTACG	CTTCAGTTAG	550
	ACTTGACGTA	CGTAAAATAG	CTACTTTAAA	ACAGAGCGAT	GAGCCAATCG	600
	GAAACCGCGT	AAAAGTAAAA	GTAGTAAAAA	ACAAAGTCGC	TCCTCCTTTT	650
	AGACAAGCCG	AATTTGATAT	CATGTTTGGG	GAAGGTATCA	GCAAAGAAGG	700
50	AGAGATAATA	GATTACGGCG	TAAAAC TTGA	TATTATCGAT	AAAAGCGGCG	750
	CTTGGTTTAG	CTATGATAAT	TCAAAATTAG	GTCAAGGCAG	AGAAAAC TCA	800
	AAAGCGTTTT	TAAA				814

2) INFORMATION FOR SEQ ID NO: 1868

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter jejuni jejuni*
- (B) STRAIN: ATCC 33560
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868

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5      GATAGCATAG GCWCAGGTTT AGTTGGACTT GATCTTGCTT TAGGTATAGG      50
      CGGTGTTCCA AAAGGAAGAA TTATAGAAAT TTATGGGCCT GAAAGTTCAG      100
      GTAAACTACT TCTAACTCTA CACATTATCG CAGAATGCCA AAAAGCAGGT      150
20     GGGGTTTGTG CTTTATCGA TGCAGAACAT GCACTTGATG TGAAATATGC      200
      TAAAAATTTA GGTGTAAATA CAGATGATTT GTATGTTTCT CAACCTGATT      250
      TTGGAGAGCA AGCCTTAGAA ATTGTAGAAA CTATAGCWAG AAGTGGTGCA      300
      GTAGATCTTA TWGTAGTAGA TAGCGTTGCA GCWCTTACCC CAAAAGCAGA      350
      AATTGAAGGC GATATGGGCG ATCARCATGT AGGACTTCAA GCAAGACTTA      400
25     TGTCTCAAGC TCTAAGAAAA CTTACAGGTA TAGTTCATAA AATGAATACC      450
      ACAGTAATTT TCATCAACCA AATTCGTATG AAAATCGGTG CTATGGGTTA      500
      TGGTACTCCT GAAACCACAA CAGGTGGAAA TGCATTAAAA TTTTATGCTT      550
      CTGTGCGTTT AGATGTTAGA AAAGTAGCAA CCTTAAAMCA AAACGWAGAM      600
      CCTATAGGAA ACCGCGTTAA AGTAAAAGTA GTTAAAAATA AAGTTGCTCC      650
30     TCCATTCAGM CAAGCTGAAT TTGATGTGAT GTTTGGAGAG GGTTTAAGCC      700
      GTGAAGGTGA ATTGATCGAT TATGGTGTA AACTTGATAT CGTAGATAAA      750
      AGTGGTGCGT GGTTTTCTTA TAAAGATAAA AACTTGGAC AAGGTAGAGA      800
      AAATTCAAAA GCTTTCTTAA AAGA                                     824

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35

2) INFORMATION FOR SEQ ID NO: 1869

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 388 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus avium*
- (B) STRAIN: ATCC 14025
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869

50

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AGAAAGTTCT GGTAAAACAA CGGTTGCACT GCATGCGATT GCAGAAGTTC      50

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AAAAACATGG CGGGACGGCA GCCTTTATTG ATGCCGAGCA CGCGTTGGAC 100
 CCTCAATACG CACAACGTCT AGGTGTAAAC ATTGATGAAT TGCTGCTATC 150
 ACAACCAGAT ACTGGGGAAC AAGGCTTAGA AATTGCAGAT GCTTTAGTTT 200
 CAAGTGGCGC AGTCGATATT ATCGTTATTG ACTCGGTGGC CGCGCTAGTC 250
 5 CCCC GTGCTG AAATCGATGG CGAGATGGGT GATGCGCACG TTGGTCTGCA 300
 GGCTCGTTTG ATGTCACAAG CATTGCGCAA GCTGTCAGGC TCTATCAACA 350
 AAACAAAGAC TATCGCCGTC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1870

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870

TGAAAGTTCA GGTAAAACAA CAGTTGCACT ACACGCTATT GCAGAAGTAC 50
 AAAAAAATGG CGGAACGGCC GCTTTCATTG ATGCTGAGCA TCGGTTAGAT 100
 CCGCAATATG CACAAAAATT AGGTGTGAAT ATCGATGAAC TACTTCTTTC 150
 30 ACAGCCTGAC ACAGGAGAAC AAGGTCTAGA GATCGCTGAT GCTTTAGTAT 200
 CAAGTGGGGC TGTAGATATC GTAGTAGTCG ATTCAGTTGC TGCTTTAGTT 250
 CCACGAGCAG AAATCGACGG CGAAATGGGT GACTCACATG TCGGGTTACA 300
 AGCACGTTTG ATGTCTCAAG CATTGCGTAA ACTCTCTGGT TCGATCAACA 350
 AAACAAAAC AATCGCTATT TTCATCAACC AAATCCGT 388
 35

2) INFORMATION FOR SEQ ID NO: 1871

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria monocytogenes*
 50 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871

AGAGAGTTCC GGTAACAACT CTGTTGCGCT TCATGCAATT GCGGAAGTAC 50
 AAGCACAAGG CGGAACAGCA GCATTTATCG ATGCTGAGCA TGC GTTGGAT 100
 CCGGCTTATG CTAAAAACCT AGGTGTAAAT ATTGATGAAT TATTACTATC 150
 TCAACCAGAT ACAGGAGAAC AAGCTTTAGA GATTGCTGAA GCTTTAGTTA 200
 5 GAAGTGGTGC AGTTGATATG TTAGTAATTG ACTCCGTTGC AGCACTTGTA 250
 CCACGTGCTG AAATCGAAGG CGAGATGGGC GATGCTCATG TTGGATTACA 300
 AGCACGTTTA ATGTCCCAAG CATTGCGTAA ACTTTCTGGT GTTATTAATA 350
 AATCAAAAAC CATTGCTATT TTCATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1872

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872

AGAGTCATCT GGTAAGACAA CGGTTGCCCT TCATGCAGTT GCGCAAGCAC 50
 AAAAAGAAGG TGGTATTGCT GCCTTTATCG ATGCGGAACA TGCCCTTGAT 100
 30 CCAGCTTATG CTGCGGCCCT TGGTGTCAAC ATTGACGAAT TGCTCTTGTC 150
 ACAACCAGAC TCAGGAGAGC AAGGTCTTGA GATTGCAGGA AAATTGATTG 200
 ACTCAGGAGC CGTGGATCTT GTCGTAGTCG ACTCAGTTGC GGCCCTTGTC 250
 CCTCGTGCGG AAATTGATGG AGATATCGGT GATAGCCACG TTGGTTTGCA 300
 GGCTCGTATG ATGAGCCAGG CTATGCGTAA ACTTGGTGCT TCTATCAATA 350
 35 AAACCAAAAC AATTGCCATC TTTATCAACC AATTGCGT 388

40

2) INFORMATION FOR SEQ ID NO: 1873

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873

	GAACATGACG	CCGACTTTTT	CACGCAATTG	GTTGATAAAG	ATGGCAATTG	50
	TTTTGGTTTT	ATTGATAGAA	GCTCCGAGTT	TACGCATGGC	CTGGCTCATC	100
	ATTCGAGCCT	GCAAACCAAC	GTGACTGTCT	CCAATATCCC	CATCAATTTC	150
5	CGCACGAGGT	ACAAGGGCCG	CAACTGAGTC	GATAACGACA	AGGTCAACTG	200
	CACCTGAGTC	AATCAATTTT	CCAGCAATTT	CAAGACCTTG	TTCACCTGAG	250
	TCTGGTTGTG	ACAAGAGCAA	TTCGTCAATA	TTCACACCAA	GGGCTGCAGC	300
	ATAGGCTGGG	TCAAGAGCAT	GTTCCGCATC	GATAAAGGCT	GCAATACCAC	350
	CTTCTTTCTG	TGCTTGCGCA	ACAGCGTGAA	GGGCAACCGT	TGTCTTACCA	400
10	GATGATTCTG	GCGCRTACAY	TTCGATGATA			430

2) INFORMATION FOR SEQ ID NO: 1874

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874

30	TTGTCGTTGT	TGCTGCCTCC	GACGGTCAGA	TGTAGGTGGA	ACATCTTGGG	50
	AAATACGTCG	TAAAACACGT	CGCTTACGTT	TTCGCGAATA	GGCCCCAGAC	100
	TCGTGAGCAT	TTGCTGCTCG	CCCGCCAGGT	TGGTGTCCAG	AAGATCGTTG	150
	TCTTCGTCAA	CAAAATCGAT	GCTATTGATG	ATCCGGAGAT	GCTGGAAGT	200
	GTCGAAGTCC	AGATGCGTGA	GCTGCTGAAC	AGCTACGGTT	TCGAGGGTGA	250
35	AGAGACTCCG	ATCATTTTTCG	GTTCCGCTCT	CTGTGCTCTC	GAAGGACGCC	300
	GTGACGACAT	CGGTAAAGAC	AGAATTGAGC	AGCTTATGAA	CGCTGTGCGAC	350
	ACCTGGATCC	CCACTCCTCA	GCGTGACCTC	GACAAACCTT	TCTTGATGTC	400
	TGTCGAGGAA	GTGTTCTCTA	TCGCCGGCCG	TGGTACCGTG	GCTTCTGGTC	450
	GTGTCGAGCG	TGGTATCTTG	AAGAAGGACT	CTGAGGTTGA	GATTGTTGGA	500
40	GGCTCCTTCG	AACCCAAGAA	GACCAAAGTC	ACCGACATTG	AAACCTTCAA	550
	GAAGAGCTGT	GATGAATCGC	GTGCTGGTGA	CAACTCTGGT	CTCCTCCTGC	600
	GTGGTATCCG	ACGTGAAGAC	GTCAAGCGTG	GTATGGTCAT	TGCTGTTCCC	650
	GGCAGCACCA	AGGCTCACGA	CAAGTTCCTC	GTCTCCATGT	ACGTCCTGAC	700
	CGAGGCGGAG	GGTGGTCGTC	GTACTGGCTT	CGGTGCCAAC	TACCGTCCCC	750
45	AAGTCTTCAT	CCGTACTGCA	GGTAAGTTCC	CGCACACCGT	GTCCAGATCT	800
	TCCGAGAGAT	TAGCGATATA	TGCTAATGAT	TCATCAGACG	AGGCTGCTGA	850
	CCTCAGCTTC	CCTGACGGCG	ACCAATCTCG	CAGAGTTATG	CCTGGTGACA	900
	ACGTCGAGAT	GATCCTGAAG	ACCCACCACC	CTGTTGCTGC	TGAGGCT	947

50

2) INFORMATION FOR SEQ ID NO: 1875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Aspergillus versicolor*
 (B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875

15	GCTGCTTCCG ATGGTCAAAT GTACGTCAAC CTTATATACA CCCTCTGATA	50
	TGACAGAATG TCGCCTAACA GCACGCGTGA ACTAGGCCCC AAACCCGTGA	100
	GCACTTGCTG CTTGCCCCGCC AGGTCGGTGT CCAGAAGATT GTTGTGTTCTG	150
	TCAACAAGGT TGATGCCGTC GATGACCCTG AGATGTTGGA ACTTGTTGAG	200
	CTGGAAATGC GTGAGCTTCT CAGCACTTAC GGCTTCGAAG GCGAGGAGAC	250
20	CCCTATCATC TTCGGTTCCG CCCTATGCGC CCTCGAGGGT CGCCGCCCCG	300
	ATATCGGTAC TGAGCGAATT GACAGCCTTC TTGAGGCCGT TGACACCTGG	350
	ATCCCTACCC CTCAGCGTGA CCTGGACAAG CCTTTCCTGA TGTCTGTCGA	400
	GGAGGTCTTC TCCATTGCCG GTCGTGGTAC CGTTGCCTCT GGCCGTGTTG	450
	AGCGTGGTCT CCTTAAGAAG GACAGCGAGG TCGAGATTCT CGGAGGTGGT	500
25	CAGGTCATGA AGACCAAGGT CACTGACATT GAGACATTCA AGAAGCACTG	550
	TGACGAATCC CGTGCTGGTG ACAACTCCGG TCTTCTTCTC CGTGGTATCC	600
	GCCGTGAGGA TGTCAAGCGC GGTATGGTTA TTGCTGCTCC CGCCTCTATC	650
	AAGGCCCAACA AGAAGTTCAT GGTCTCCATG TACGTCCTCA CTGAGGCAGA	700
	AGGTGGCCGT CGCAGTGGCT TCGGTGTCAA CTATCGTCCC CAGGCTTACA	750
30	TTCGCACTGC TGGTAAGTTT TCAAAACATT CGACCTCTCG CCTTAGAAGA	800
	AGAATACCTC TAACTTGTAT TTAGACGAGG CTTGCGACCT TTCTTTCCCC	850
	GATGGCGACA TGAGCCGCCG TGTCATGCCT GGTGACAACG TGGAAATGAT	900
	CCTCAACCTC AACAACCCTG TCG	923

35

2) INFORMATION FOR SEQ ID NO: 1876

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Basidiobolus ranarum*
 (B) STRAIN: ATCC 24670

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876

CATCATTTGTT GTGTCCGCCA CTGATGGTCA AATGCCTCAA ACTCGTGAGC	50
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	ATTTGTTGTT	GGCTCGCCAA	GTTGGTGTCC	AACACTTGGT	TGTCTTCATC	100
	AACAAGGTTG	ATGCCGTTGA	TGATCCTGAA	ATGTTGGAGT	TGGTCGAGAT	150
	GGAAATGCGT	GATTTGCTTT	CCCAATACGG	TTCCCCGGA	GACAACGTCC	200
	CCATTATCCA	GGGTTCCGCT	CTCTGCGCTC	TTGAGGACCG	CAACCCCGAG	250
5	ATCGGCCCGTA	ACGCCATCAT	GAAGTTGATG	GAGGCTGTTG	ATAGCAGCAT	300
	CCCCACCCCT	GCCCGTGATT	TGGACAAACC	TTTCCTCATG	CCCGTTGAAG	350
	ATGTGTTCTC	CATCTCTGGC	CGTGGTACTG	TTGCCACTGG	ACGTGTTGAG	400
	CGTGGTATGG	TCACCAAGGG	TACTGAAGTT	GAAATCGTCG	GTATGGGCGA	450
	GCACTTCAAG	ACCACCTTGA	CCGGTATTGA	AATGTTCCAC	AAGGAATTGG	500
10	ACAAGGGTAT	GGCTGGTGAC	AACATGGGTT	GCTTGCTTCG	TGGTGTCAAG	550
	CGTGAGCAAG	TCCGTCGTGG	TATGGTTATC	TGTGCCCCCG	GATCCGTCAA	600
	GCCACATAAG	AAGTTCATGG	CTCAGCTCTA	CATTCTCACC	AAGGATGAGG	650
	GAGGCCGCCA	CACTCCCTTC	GTCAACAAC	ACCGCCCACA	AATGTTCTTC	700
	AGAACTGTTG	ATGTTACCGC	CATCCTTAAG	CACCCCCCTG	GTACCCCCGA	750
15	TGCTGATGAG	AAGATGGTCA	TGCCCCGAGA	CAACGTTCAA	CTCGAGTGCG	800
	AGCTCTT					807

20 2) INFORMATION FOR SEQ ID NO: 1877

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter gracilis*
 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877

35	AGTTGTTTCT	GCTGCGGATG	GTCCTATGCC	TCAAACTCGC	GAGCATATCT	50
	TGCTTTCTCG	TCAAGTAGGC	GTTCCATACA	TCGTAGTTTT	CCTAAACAAA	100
	ACCGATATGG	TCGATGATCC	GGATCTTTTA	GAGTTAGTTG	AAGAGGAAGT	150
	TAGAGATCTT	TTAAAAGAGT	ATAAATTCCC	TGGCGACGAA	ACCCCAATCA	200
40	TTAAGGGTTC	TGCTCTTAAG	GCTCTTGAGG	AAGCTAAGGC	CGGACAAGAC	250
	GGCGAATGGT	CTGCAAAGAT	TATGGAGCTT	ATGGACGCGG	TTGATAGCTA	300
	TATTCCAAC	CCTGTTCGCG	ATACTGATAA	AGATTTCTCT	CTTCCGATCG	350
	AAGATATTTT	CTCGATTTC	GGTCGCGGTA	CCGTTGTAAC	CGGTAGAATC	400
	GAAAAAGGTA	TCGTTAAAGT	TGGTGATACT	ATCGAGATCG	TAGGTATTAA	450
45	ACCTACTCAG	ACTACTACCG	TCACTGGCGT	TGAGATGTTT	AGAAAAGAGA	500
	TGGATCAAGG	TGAAGCCGCG	GATAATGTAG	GTGTTTTATT	GCGCGGTACT	550
	AAGAAAGAGG	AAGTAGAGCG	CGGTATGGTT	TTATGCAAAC	CAAAATCGAT	600
	CACTCCTCAT	ACTAAATTTG	AGGGCGAGGT	TTATATCCTA	ACTAAAGAAG	650
	AAGGCGGACG	CCATACTCCA	TTCTTTAATA	ATTATAGACC	GCAGTTTTAC	700
50	GTTCGTACGA	CAGATGTTAC	CGGTTCGATT	ACTCTTCCTG	AAGGAACCGA	750
	GATGGTTATG	CCGGGCGACA	ACGTTAAAAT	CACCGTTGAG	CTAATCGCTC	800
	CGATCG					806

2) INFORMATION FOR SEQ ID NO: 1878

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33292

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878

GCTGCAGATG GCCCTATGCC ACAAACTAGA GAGCACATTC TTCTTTCTCG 50
 TCAAGTAGGC GTTCCATATA TTGTTGTTTT TATGAATAAA GCAGATATGG 100
 TTGATGATGC TGAACCTTTA GAGTTAGTTG AAATGGAAAT TAGAGAATTA 150
 20 TTAAGCTCTT ATGATTTCCT AGGCGATGAT ACACCTATTA TTTCTGGTTC 200
 TGCTTTAAAA GCTCTTGAAG AAGCTAAAGC TGGACAAGAT GGTGAATGGT 250
 CAGCAAAAAT TATGGATCTT ATGGCTGCAG TTGATAGCTA TATTCCAAC 300
 CCAACTCGTG ATACTGAAAA AGACTTCTTG ATGCCAATTG AAGATGTTTT 350
 CTCAATTTCA GGTCGTGGTA CTGTTGTTAC AGGTAGAATT GAAAAAGGTG 400
 25 TTGTAAAAGT AGGTGATACT ATCGAAATCG TTGGTATTAA AGATACTCAA 450
 ACAACAAC 500
 CGAAGCAGGA GATAACGTAG GTGTTCTTCT TCGTGGTACT AAAAAAGAAG 550
 AAGTTATCCG TGGTATGGTT CTTGCTAAAC CAAAATCAAT TACTCCACAC 600
 ACTGACTTCG AAGCTGAAGT TTATATCTTA AATAAAGATG AAGGTGGTAG 650
 30 ACATACTCCA TTCTTTAACA ACTATAGACC ACAGTTTTAT GTAAGAACAA 700
 CTGATGTTAC AGGTTCGATT AAATTAGCTG ATGGTGTTGA AATGGTTATG 750
 CCAGGTGAAA ATGTGAGAAT TACTGTAAGC TTGATCGCTC CAGTAGCACT 800
 TGAAGA 806

35

2) INFORMATION FOR SEQ ID NO: 1879

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879

ATGTATGCAA CCGAGAGCAC TCCCGGATCT TGGTTTAAAT GGCAC TAATA 50

	TAAGACAGGC	CTCAAAC TCG	AGAGCATTTA	CTTCTCGCCC	GTCAGATCGG	100
	TATCCAAAAA	ATCGTCGTCT	TCGTGAACAA	GGTTGATGCC	ATCGAGGACA	150
	AAGAGATGTT	GGAGCTTGTT	GAATTGGAGA	TGCGTGAAC T	CCTAACCAGC	200
	TACGGTTTCS	AGGGTGAAGA	AACTCCCATC	ATTTT TGGCT	CTGCTCTCTG	250
5	TGCCCTCSAA	GGAAGACAAC	CCGAGATCGG	TGTTACCAAG	ATTGATGAGC	300
	TCTTGCAGGC	CGTCGACACC	TGGATTCCCA	CTCCTCAGCG	TGAGACTGAC	350
	AAGCCCTTCT	TGATGTCCAT	TGAGGAAGTG	TTCTCTATTT	CCGGACGAGG	400
	AACCGTTGTC	TCCGGCCGTG	TGGAGCGTGG	TATCCTCAAG	AAGGACTCCG	450
	AAGTTGAAAT	TGTCGGCGGT	TCGCCCCGAGC	CAATCAAAAC	CAAGGTTACC	500
10	GATATCGAAA	CCTTTAAGAA	GTCTTGCGAC	GAGTCTCGCG	CTGGTGATAA	550
	CTCCGGCTTG	CTCCTACGAG	GCGTTAAGCG	TGAAGATATT	AGCCGTGGCA	600
	TGGTCGTCGC	TGTACCAGGA	AGTGTC AAGG	CCCATACTGA	ATTCTTAGTT	650
	TCGCTTTACG	TCCTCACC GA	AGCTGAGGGT	GGGCGCAAAT	CTGGATTCAG	700
	CAGCAAGTAC	CGCCCACAGA	TGTTCAATTCG	CACTGCCGGT	ATGTAATACT	750
15	GTGATAATTT	CGTTGACATG	GTACTGATTG	AATTCTATAG	ACGAAGCGGC	800
	TCAGCTCAGC	TGGCCCCGAG	AAGATCAAGA	CAAGATGGCT	ATGCCAGGAG	850
	ACAATATCGA	AATGATTTGC	ACCACCTTGC	ACCCAGTTGC	CGCCGA	896

20

2) INFORMATION FOR SEQ ID NO: 1880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880

	CTGGTAGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACYC	GTGAGCACAT	50
	CCTGCTGGGT	CGCCAGGTTG	GCGTGCCATA	CATCATCGTG	TTCCTGAACA	100
	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAGCTGGT	TGAAATGGAA	150
10	GTMCGTGACC	TGCTGTCACA	GTACGACTTC	CCAGGCGACG	ACACGCCAAT	200
	CGTGCRYGGT	TCTGCGCTGA	AAGCGCTGGA	RGGCGAAGCA	GAGTGGGAAG	250
	CGAAGATCAT	CGAACTGGCT	GGCCATCTGG	ATAACTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAACC	GTTCCTGCTG	CCAATTGAAG	ACGTGTTCTC	350
	CATCTCTGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	CGCGGTRTSG	400
15	TTAAAGTGGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	TACCGTGAAA	450
	TCAACCTGTA	CCGGCGTTGA	GATGTTCCGT	AAGCTGCTGG	ACGAAGGCCG	500
	TGCGGGTGAG	AACTGTGGTA	TCCTGCTGCG	CGGTATCAAG	CGCGAAGATA	550
	TCCAGCGTGG	TCAGGTTCTG	GCGAAGCCAG	GCACCATCAA	GCCACACACC	600
	AAGTTCGAGT	CAGAAGTTTA	TATTCTGTCT	AAAGACGAAG	GCGGCCGTCA	650
30	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACCGG	GACTATCGAA	CTGCCAGAAG	GCGTTGAGAT	GGTGATGCCA	750
	GGCGACAACA	TTCAGATGGT	TGTGACCCTG	ATCCACCCGA	TCGCCATG	798

2) INFORMATION FOR SEQ ID NO: 1881

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881

15
 20 ATCCTGGTTG TTGCTGCGAC TGACGGYCCG ATGCCGCAGA CCCGTGAGCA 50
 CATCCTGCTG GGTCGTCAGG TAGGCGTTCC GTACATCATC GTGTTCTCTGA 100
 ACAAATGCGA CATGGTTGAT GACGAAGAGC TGCTGGAAC TGGTTGAAATG 150
 GAAGTTCGYG AACTGCTGTC TCAGTACGAC TTCCCGGGCG ACGACACTCC 200
 GATCGTTCGT GGTTCTGCTC TGAAAGCGCT GGAAGGCGAC GCAGAGTGGG 250
 AAGCGAAAAT CATCGAACTG GCTGGCTTCC TGGATTCTTA CATYCCGGAA 300
 CCAGAGCGTG CGATTGACAA GCCGTTCTCTG CTGCCGATCG AAGACGTATT 350
 25 CTCCATCTCC GGTCGTGGTA CCGTTGTTAC CGGTCGTGTA GARGCGGGTA 400
 TCATCAAAGT GGGCGAAGAA GTTGAAATCG TTGGTATCAA AGAGACTCAG 450
 AAGTCTACCT GTACTGGCGT TGAAATGTTC CGCAAAC TGGACGAAGG 500
 CCGTGCCGGT GAGAACGTAG GTGTTCTGCT GCGTGGTATC AAACGTGAAG 550
 AAATCGAACG TGGTCAGGTA CTGGCTAAGC CGGGCACCAT CAAGCCGCAC 600
 30 ACCAAGTTCG AATCTGAAGT GTACATTCTG TCCAAAGATG AAGGCGGCCG 650
 TCATACTCCG TTCTTCAAAG GCTACCGTCC GCAGTTCTAC TTCCGTACTA 700
 CTGACGTGAC TGGCACCATC GAACTGCCGG AAGGCGTAGA GATGGTAATG 750
 CCGGGCGACA ACATCAAAAT GGTGTTACC CTGATCCACC CGATCGCGAT 800
 GGACGACGGT 810
 35

2) INFORMATION FOR SEQ ID NO: 1882

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Staphylococcus cohnii*
 50 (B) STRAIN: BM10711
 (C) ACCESSION NUMBER : AF015628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882

	ATGAATTTTT	ATTTAGAGGA	GTTTAACTTG	TCTATTCCCG	ATTCAGGTCC	50
	ATACGGTATA	ACTTCATCAG	AAGACGGAAA	GGTATGGTTC	ACACAACATA	100
	AGGCAAACAA	AATCAGCAGT	CTAGATCAGA	GTGGTAGGAT	AAAAGAATTC	150
5	GAAGTTCCTA	CCCCTGATGC	TAAAGTGATG	TGTTTAATTG	TATCTTCACT	200
	TGGAGACATA	TGGTTTACAG	AGAATGGTGC	AAATAAAATC	GGAAAGCTCT	250
	CAAAAAAAGG	TGGCTTTACA	GAATATCCAT	TGCCACAGCC	GGATTCTGGT	300
	CCTTACGGAA	TAACGGAAGG	TCTAAATGGC	GATATATGGT	TTACCCAATT	350
	GAATGGAGAT	CGTATAGGAA	AGTTGACAGC	TGATGGGACT	ATTTATGAAT	400
10	ATGATTTGCC	AAATAAGGGA	TCTTATCCTG	CTTTTATTAC	TTTAGGTTCG	450
	GATAACGCAC	TTTGGTTCAC	GGAGAACCAA	AATAATTCTA	TTGGAAGGAT	500
	TACAAATACA	GGGAAATTAG	AAGAATATCC	TCTACCAACA	AATGCAGCGG	550
	CTCCAGTGGG	TATCACTAGT	GGTAACGATG	GTGCACTCTG	GTTTGTCGAA	600
	ATTATGGGCA	ACAAAATAGG	TCGAATCACT	ACAAC TGGTG	AGATTAGCGA	650
15	ATATGATATT	CCAAC TCCAA	ACGCACGTCC	ACACGCTATA	ACCGCGGGGA	700
	AAAATAGCGA	AATATGGTTT	ACTGAATGGG	GGGCAAATCA	AATCGGCAGA	750
	ATTACAAACG	ACAAAACAAT	TCAAGAATAT	CAACTTCAA	CAGAAAATGC	800
	GGAACCTCAT	GGTATTACCT	TTGGAAAAGA	TGGATCCGTA	TGGTTTGCAT	850
	TAAAATGTAA	AATTGGGAAG	CTGAATTTGA	ACGAATGA		888

20

2) INFORMATION FOR SEQ ID NO: 1883

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883

35 AGCCGCTTGA GCAAATTAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1884

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884

50

GTATCCCGCA GATAATCAC CAC

23

2) INFORMATION FOR SEQ ID NO: 1885

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885

AGCGAAAAAC ACCTTGCCGA C 21

15

2) INFORMATION FOR SEQ ID NO: 1886

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886

30 GACGCCCCGCG CCACCACT 18

2) INFORMATION FOR SEQ ID NO: 1887

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887

45 GACGCCCCGCG ACACCACTA 19

2) INFORMATION FOR SEQ ID NO: 1888

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888

GACGCCCGCA ACACCACTA

19

10

2) INFORMATION FOR SEQ ID NO: 1889

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889

GTTCGCAACT GCAGCTGCTG

20

25

2) INFORMATION FOR SEQ ID NO: 1890

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890

40

TTCGCAACGG CAGCTGCTG

19

2) INFORMATION FOR SEQ ID NO: 1891

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891

CCGGAGCTGC CGAICGGG

18

5

2) INFORMATION FOR SEQ ID NO: 1892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892

CGGAGCTGCC AARCGGGG

18

20

2) INFORMATION FOR SEQ ID NO: 1893

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893

35 GGAGCTGGCG ARCGGGGT

18

2) INFORMATION FOR SEQ ID NO: 1894

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894

50

GACCGGAGCT AGCGARCG

18

2) INFORMATION FOR SEQ ID NO: 1895

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895

15 CGGAGCTAGC AARCGGGGT 19

2) INFORMATION FOR SEQ ID NO: 1896

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896

30 GAAACGGAAC TGAATGAGGC G 21

2) INFORMATION FOR SEQ ID NO: 1897

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897

45 CATTACCATG GGCGATAACA G 21

50 2) INFORMATION FOR SEQ ID NO: 1898

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898

CCATTACCAT GAGCGATAAC AG

22

10

2) INFORMATION FOR SEQ ID NO: 1899

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- 25 (B) STRAIN: 15571
- (C) ACCESSION NUMBER: AF124984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899

30	ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT	50
	GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA	100
	GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC	150
	CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC	200
	CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG	250
35	ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC	300
	TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA	350
	ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC	400
	TACTGGCCAC CGTCGGCGGC CCCGCAGGAT TGA CTGCCTT TTTGCGCCAG	450
	ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA	500
40	GGCGCTTCCC GGCGACGCC GCGACACCAC TACCCCGGCC AGCATGGCCG	550
	CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA	600
	CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT	650
	CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG	700
	GCGAGCGGGG TGC GCGCGGG ATTGTCGCCC TGCTTGCCCC GAATAACAAA	750
45	GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACCCCGG CGAGCATGGC	800
	CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT	850
	GGCAACGCTA A	861

50

2) INFORMATION FOR SEQ ID NO: 1900

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: SLK-47
- (C) ACCESSION NUMBER: Y11069

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900

15	CTGTTAGCCA	CCCTGCCGCT	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	50
	GCAAATTAAA	CTAAGCGAAA	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	100
	AAATGGATCT	GGCCAGCGGC	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	150
	CGCTTTCCCA	TGATGAGCAC	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	200
	GGCGCGGGTG	GATGCCGGTG	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	250
20	GCCAGCAGGA	TCTGGTGGAC	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	300
	GACGGCATGA	CGGTCGGCGA	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	350
	TAACAGCGCC	GCCAATCTGC	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	400
	TGACTGCCTT	TTTGCGCCAG	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	450
	TGGGAAACGG	AACTGAATGA	GGCGCTTCCC	GGCGACGCCC	GCGCCACCAC	500
25	TACCCCGGCC	AGCATGGCCG	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	550
	GTCTGAGCGC	CCGTTGCGAA	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	600
	CGGGTCGCCG	GACCGTTGAT	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	650
	CGCCGATAAG	ACCGGAGCTG	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	700
	TGCTTGGCCC	GAATAACAAA	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	750
30	GATACCCCGG	CGAGCATGGC	CGAGCGAAAT			780

2) INFORMATION FOR SEQ ID NO: 1901

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: U92041

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901

50	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200

	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
5	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCCC	GCAACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTGCGAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
10	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
	GGCAACGCTA	A				861

15

2) INFORMATION FOR SEQ ID NO: 1902

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: 803
 (C) ACCESSION NUMBER: AF164577

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902

35	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CAAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
40	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TGCTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
45	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTGCGAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	CCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
50	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
	GGCAACGCTA	A				861

2) INFORMATION FOR SEQ ID NO: 1903

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 700603
 (C) ACCESSION NUMBER: AF132290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903

15
 20
 25
 30
 35

ATGCGTTATT	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
GCCAGCTGTC	GGGCAGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
ACTCTGTGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
TGCTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
CCAAACGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
GCAGAGCGGA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
GGCAACGCTA	ACCCGGCGGT	GGCCGCGCGC	GTTATCCGGC	TCGTAG	896

2) INFORMATION FOR SEQ ID NO: 1904

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: JC2926
 (C) ACCESSION NUMBER: AF148851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904

	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
5	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
10	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
15	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGGCC	GAATAACAAA	750
	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
20	GGCAACGCTA	A				861

2) INFORMATION FOR SEQ ID NO: 1905

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: AF096930

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905

40	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
45	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTAC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
50	GGCGCTTCCC	GGCGACGCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700

GCAAACGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
GGCAACGCTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1906

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906

20 CCTTATTCCC TTTTGTGCGG

20

2) INFORMATION FOR SEQ ID NO: 1907

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907

35

CACCTATCTC AGCGATCTGT CT

22

40 2) INFORMATION FOR SEQ ID NO: 1908

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908

AACAGCGGTA AGATCCTTGA GAG

23

2) INFORMATION FOR SEQ ID NO: 1909

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909

ATGACTTGGT TAAGTACTCA CC

22

15

2) INFORMATION FOR SEQ ID NO: 1910

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910

ATGACTTGGT TGAGTACTCA CC

22

30

2) INFORMATION FOR SEQ ID NO: 1911

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911

45 CCATAACCAT GGGTGATAAC AC

22

2) INFORMATION FOR SEQ ID NO: 1912

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid

1000

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912

CCATAACCAT GAGTGATAAC AC

22

10

2) INFORMATION FOR SEQ ID NO: 1913

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913

CGCCTTGATC ATTGGGAACC

20

25

2) INFORMATION FOR SEQ ID NO: 1914

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914

40

CGCCTTGATC GTTGGGAACC

20

2) INFORMATION FOR SEQ ID NO: 1915

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915

CGCCTTGATA GTTGGGAACC

20

5

2) INFORMATION FOR SEQ ID NO: 1916

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916

CGTGGGTCTT GCGGTATCAT

20

20

2) INFORMATION FOR SEQ ID NO: 1917

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917

35 CGTGGGTCTG GCGGTATCAT

20

2) INFORMATION FOR SEQ ID NO: 1918

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918

50

GTGGGTCTCA CGGTATCATT G

21

2) INFORMATION FOR SEQ ID NO: 1919

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919

CGTGGGTCTC TCGGTATCAT T

21

15

2) INFORMATION FOR SEQ ID NO: 1920

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920

CGTGGNTCTC GCGGTATCAT

20

30

2) INFORMATION FOR SEQ ID NO: 1921

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1921

45 CGTGGGTCTA GCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1922

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922

GTTTCCAAT GATTAGCACT TTTA

24

10

2) INFORMATION FOR SEQ ID NO: 1923

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923

GTTTCCAAT GATAAGCACT TTTA

24

25

2) INFORMATION FOR SEQ ID NO: 1924

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924

40

GTTTCCAAT GCTGAGCACT TTT

23

2) INFORMATION FOR SEQ ID NO: 1925

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925

CGTTTTCCAA TGATGAGCAC TTT

23

5

2) INFORMATION FOR SEQ ID NO: 1926

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926

GTTTTCCAAT GGTGAGCACT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1927

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: MC9690-129
(C) ACCESSION NUMBER: AF126482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1927

40	ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT	50
	TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT	200
	GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG	250
45	CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	350
	AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA	400
	ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG	450
	CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT	500
50	GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA	550
	TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT	600
	TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC	650
	ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG	700

GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1928

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 20 (B) STRAIN: HB251
 (C) ACCESSION NUMBER: X57972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928

25	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
30	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTAAAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCATTGGG	AACCGGAGCT	500
35	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAACTG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
40	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

45

2) INFORMATION FOR SEQ ID NO: 1929

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: 26W
(C) ACCESSION NUMBER: U09188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929

10	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAGCT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGTGC	GGTATTATCC	CGTGTTGACG	250
15	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACCCGCCTT	GATAGTTGGG	AACCGGAGCT	500
20	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAACTG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTAA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
25	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATG					808

30 2) INFORMATION FOR SEQ ID NO: 1930

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: AF190692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930

45	ATGAGTATTC	AACATTTTCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
50	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCTGCCA	400

	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
5	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	GGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
10	AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 1931

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: BM2728
- (C) ACCESSION NUMBER: AF104442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1931

30

	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
35	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
40	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
45	GAGCCGGTGA	GCGTGGGTCT	CTCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

50

2) INFORMATION FOR SEQ ID NO: 1932

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932

15	ATGAGTATTC	AACATTTTCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGCT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGTGC	GGTATTATCC	CGTGTGACG	250
20	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCTGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
25	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	AGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
30	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

35

2) INFORMATION FOR SEQ ID NO: 1933

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190693

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933

	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100

CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC 150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGGT 200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG 250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG 300
5 GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA 400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG 450
CACAACATGG GGGATCATGT AACCCGCCTT GATCGTCGGG AACCGGAGCT 500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 550
10 TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT 600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 700
GAGCCGGTGA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT 750
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC 800
15 TATGGATGAA CGAGATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA 850
AGCATTGGTA A 861

20 2) INFORMATION FOR SEQ ID NO: 1934

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
25 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934

GAACGCCAGC GCGAAATTCA AAAAG

25

35

2) INFORMATION FOR SEQ ID NO: 1935

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935

AGCTCGGCAT ACTTCGACAG G

21

50

2) INFORMATION FOR SEQ ID NO: 1936

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936
10 TACCACCCGC ACGGC 15

15 2) INFORMATION FOR SEQ ID NO: 1937

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937
 CGGAGTCGCC GTCGATG 17

30 2) INFORMATION FOR SEQ ID NO: 1938

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938
 CCGCGCACCA TTGCTTCGTA CACTGAGGAG TCTCCGCGCG G 41

45 2) INFORMATION FOR SEQ ID NO: 1939

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 46 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939

5

CGACCCGGAT GGTAGTATCG ATAATGATCC GCCAGCGGCC GGGTCG

46

10 2) INFORMATION FOR SEQ ID NO: 1940

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940

GTATCGTTGG TGACGTAAT

19

25

2) INFORMATION FOR SEQ ID NO: 1941

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941

GCAATGGTCC GTTTAAGT

18

40

2) INFORMATION FOR SEQ ID NO: 1942

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942

GACTGGAACA AAGCCTATAA AAAATCA

27

5 2) INFORMATION FOR SEQ ID NO: 1943

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 16 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943

GCTGGTGGAC GGCCAG

16

20

2) INFORMATION FOR SEQ ID NO: 1944

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944

TTTCGCCGCC ATGCGTTAC

19

35

2) INFORMATION FOR SEQ ID NO: 1945

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945

CGGCGACTAC GCGGTAT

17

50

2) INFORMATION FOR SEQ ID NO: 1946

1013

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946

CGGCGACTTC GCGGTAT

17

15

2) INFORMATION FOR SEQ ID NO: 1947

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947

CGGTATACGG CACCATCGT

19

30

2) INFORMATION FOR SEQ ID NO: 1948

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948

GCGGTATACA ACACCATCG

19

45

2) INFORMATION FOR SEQ ID NO: 1949

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949

CGGTATACGC CACCATCGT

19

10

2) INFORMATION FOR SEQ ID NO: 1950

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 15 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950

GGCGACATCG CCTGC

15

25

2) INFORMATION FOR SEQ ID NO: 1951

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 17 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951

GGCGACAGAG CCTGCTA

17

40

2) INFORMATION FOR SEQ ID NO: 1952

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952

1015

CCTGCTATGG AGCGATGGT

19

5

2) INFORMATION FOR SEQ ID NO: 1953

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953

CGCCTGCTAT AAAGCGATGG T

21

20

2) INFORMATION FOR SEQ ID NO: 1954

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 589 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
(B) STRAIN: ATCC 13883
35 (C) ACCESSION NUMBER: AF052258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954

	ACACCGGTCA	ACATTGAGGA	AGAGCTTAAG	AACTCTTATC	TGGATTATGC	50
10	GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	GGATGTCCGA	GATGGCCTGA	100
	AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	TGAACGTATT	GGGCAATGAC	150
	TGGAACAAAG	CCTATAAAAA	ATCAGCCCGT	GTCGTTGGTG	ACGTAATCGG	200
	TAAATACCAC	CCGCACGGCG	ACTCCGCGGT	ATACGACACC	ATCGTGCGTA	250
	TGGCGCAGCC	GTTCTCGCTG	CGTTACATGC	TGGTGGACGG	CCAGGGTAAC	300
15	TTTGGTTCCA	TCGACGGCGA	CTCCGCCGCG	GCGATGCGTT	ATACCGAAAT	350
	TCGTCTGGCG	AAAATCGCTC	ATGAGCTGAT	GGCCGATCTT	GAAAAAGAGA	400
	CGGTCGATTT	CGTCGACAAC	TATGACGGTA	CGGAGCGTAT	TCCGGACGTC	450
	ATGCCGACCA	AAATTCCTAA	CCTGCTGGTG	AACGGCGCCT	CCGGGATCGC	500
	CGTAGGGATG	GCCACCAACA	TACCGCCACA	TAACCTGACG	GAAGTGATTA	550
30	ACGGCTGTCT	GGCGTATGTT	GACGATGAAG	ACATCAGCA		589

2) INFORMATION FOR SEQ ID NO: 1955

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 38 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955

CGCGCAACCA TTGCTTCGTA CACTGAGGAG TCTGCGCG

38

15

2) INFORMATION FOR SEQ ID NO: 1956

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 989 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956

	CGGTAAAACC	ACTTTAACTG	CTGCAATCAC	CAAAGTTT	TCTGAAGAAG	50
	GTGGTGCAGA	TTTCTTAGAT	TATTCATCTA	TTGATAAAGC	ACCAGAAGAG	100
35	AGAGCTAGAG	GTATTACCAT	TTCTACTGCT	CATGTTGAAT	ATGAAACTCC	150
	AAACAGACAT	TATTCACATG	TTGATTGTCC	AGGTCATCAA	GATTATATTA	200
	AGAACATGAT	TACTGGTGCA	GCTCAAATGG	ATGGTGCTAT	TATTGTTGTT	250
	GCAGCTACTG	ATGGTCAAAT	GCCACAAACT	AAGGAACATT	TATTATTAGC	300
	TAGACAAGTT	GGTGTTCAAC	ATTTAGTTGT	TTTTGTTAAC	AAGTGTGATA	350
40	CCGTTGATGA	TCCAGAAATG	TTRGAATTAG	TTGAAATGGA	AATGAGAGAA	400
	TTATTGACCG	AATATGGATT	YGATGGTGAT	AACACACCAG	TTATTATGGG	450
	TTCTGCATTA	ATGGCATTAG	AAGGTAAGAG	ACCAGAAGTT	GGTAAAGAAT	500
	CTATTGTTAA	GTTAATGGAA	GCTGTTGATA	CTTGGATTCC	AACTCCACAA	550
	AGAGACTTAG	AAAAACCATT	CTTATTACCA	ATTGATGAAG	TTTTCTCTAT	600
45	TTCTGGTAGA	GGTACTGTTG	TTTCTGGTAC	TGTTGATAGA	GGTACATTAA	650
	AGAAGGGTGA	AGAAGTTGAA	ATTGTTGGTG	GTAAAGAAGG	TGTTATTAAG	700
	ACTACTGTTA	CCGGTATTGA	AATGTATCAC	AAGGAATTAG	ATCAAGCACA	750
	AGCTGGTGAT	ACTCCAGGTA	TTTTGTTAAG	AGGTGTTAAG	AGAGATCAAA	800
	TTGCAAGAGG	TCAAATTCTT	GCAAAGCCAG	GWTCTGTTAA	GGCATACAAG	850
50	AAGTTCTTAT	CATCATTATA	CATTTTAACA	AAGGAAGAAG	GTGGTAGACA	900
	TACTCCATTT	TCTGAAAATT	ACAGACCTCA	AATGTACATT	AGAACTTCCA	950
	ATGTTAATGT	TACTTTGAAG	TTCCCAGAAA	CTGAAGAAG		989

2) INFORMATION FOR SEQ ID NO: 1957

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 991 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida utilis*
- (B) STRAIN: ATCC 22023
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957

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GGTAAGACCA CCCTTACTGC CGCCATCACC AAGTGCCTTG CTGAGAAGGG      50
AGGTGCCTCG TTCTTGGACT ACAGTGCCAT CGACAAGGCG CCAGAGGAGA      100
GAGCAAGAGG TATCACCATC TCCACTGCGC ACGTTGAGTA TGAAACTGCC      150
AACAGACACT ACTCGCACGT TGACTGTCCA GGTCACGCTG ATTACATCAA      200
GAACATGATT ACCGGTGCTG CGCAGATGGA CGGTGCTATC ATTGTCGTTG      250
CAGCCACTGA CGGTCAGATG CCACAGACCA GAGAACACTT GTTGCTTGCC      300
AGACAAGTTG GTGTCCAGCA CATTGTTGTC TTCGTCAACA AGGTTGACAC      350
CATCGACGAC CCTGAGATGC TTGAGCTTGT TGAAATGGAG ATGAGAGAGT      400
TGCTTACTTC GTATGGATTT GACGGTGATA ACACCCCACT TATCATGGGT      450
TCTGCTTTGT GTGCTTTGGA AGGCCGTGAG CCAGAGATTG GTGCTAAGGC      500
CATTGACAAG TTGATGGAGG CCATTGATGA GTACATCCCA ACTCCTCAGA      550
GAGACCTGGA AAAGCCATTC YTGATGGGTG TTGAAGACGT GTTCTCGATC      600
TCTGGTAGAG GTACCGTTGT CACRGGCCGT GTTGAGCGTG GTAACCTGAA      650
GAAAGGTGAT GAAATTGAAC TTGTTGGCTA CAACAAGAAC CCAATCAAGA      700
CCACCGTCAC CGGTATCGAA ATGTTCAAGA AGGAGTTGGA ATCTGCCATG      750
GCTGGTGACA ACTGTGGTAT CTTGTTGCGT GGTATCAAGA GAGATGACGT      800
CAAGAGAGGT ATGGTTGCTG CTAAGCCAGG CTCCGTCTCT GCACACACCA      850
AGTTCCTCGC TTCCTTGTAC ATCCTGACRA AGGAGGAAGG TGGTCGTCAC      900
AGTGCCTTTG CTGAGAACTA CAGACCACAG ATGTTCATCA GAACCGGAGA      950
TGTCACCACC ATCTTGACAT GGCCAGAGGA GCACGCTGAC C              991

```

2) INFORMATION FOR SEQ ID NO: 1958

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 985 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida zeylanoides*
- (B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958

	CGGTAAGACC	ACTTTGACCG	CCGCCATCAC	CAAGGTGTTG	AGCGCCAAAG	50
	GTGGTGCTTC	CTTCTTGGAC	TACGGGTCCA	TCGACAGAGC	CCCTGAGGAG	100
5	AGAGCCAGAG	GTATTACTAT	CTCGACTGCC	CACGTTGAGT	ACGAGACCGA	150
	TAAGAGACAC	TACGCCCACG	TTGATTGCC	TGGTCACGCT	GATTACATCA	200
	AGAACATGAT	CACTGGTGCC	GCCCAAATGG	ACGGTGCCAT	TATTGTCGTT	250
	GCTGCTTCTG	ATGGCCAAAT	GCCGCAGACC	AGAGAGCACT	TGTTGCTTGC	300
	CAGACAGGTT	GGTGTGCAGA	ACTTGGTTGT	GTTTGTTAAC	AAGGTGGACA	350
10	CCATCGACGA	CCCCGAAATG	TTGGAGTTGG	TGGAGATGGA	AATGAGAGAA	400
	TTGTTGACCC	ACTACGGCTT	TGACGGTGAC	AACACCCCTG	TCATCATGGG	450
	TTCGGCGTTG	TGTGCCTTGG	AAGACAGGCA	GCCTGAGATT	GGCGAGCAAG	500
	CCATCATGAA	GTTGTTGGAC	GCTGTGACG	AGTACATTCC	CACTCCTCAG	550
	AGAGACTTGG	AGCAACCATT	TTTGATGCCC	GTTGAGGATG	TTTTCTCCAT	600
15	CTCTGGCAGA	GGTACTGTTG	TCACCGGTCG	TGTTGAGAGA	GGCTCATTGA	650
	AGAAGGGTGA	GGAGATTGAG	ATTGTTGGCG	ACTTCCCCAA	GCCCTTCAAG	700
	ACTACCGTCA	CCGGCATTGA	GATGTTCAAG	AAGGAGTTGG	ATGCCGCGAT	750
	GGCGGGCGAC	AACGCCGGGA	TCTTGTTGAG	AGGTGTCAAG	AGAGACGAGG	800
	TCTCGAGAGG	TATGGTTTTG	GCCAAGCCCG	GTACTGTCAC	TTCGCACACC	850
20	AAGGTGTTGG	CGTCGCTTTA	CATCTTGACC	AAAGAGGAAG	GTGGCCGCCA	900
	CTCGCCCTTT	GGTGAGAACT	ACAAGCCACA	GTTATTCATC	AGAACCTCCG	950
	ATGTCACTGG	TACTTTGAGG	TTCCCCGCCG	GTGAG		985

25

2) INFORMATION FOR SEQ ID NO: 1959

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 973 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
 (B) STRAIN: ATCC 10565
 (C) ACCESSION NUMBER:

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959

	CGGTAAGACC	ACCTTGACTG	CCGCCATCAC	CAAGGTTCTC	TCCGAGAAGG	50
	GTGGTGCCGA	CTTCTTGGAC	TACGGTGCCA	TTGACAGAGC	CCCCGAGGAG	100
15	CGTGCCCGTG	GTATCACCAT	CTCCACTGCC	CACGTTGAGT	ACGAGACTGA	150
	CAACCGTCAC	TACGCCCACA	TTGACTGTCC	CGGTCACGCT	GATTACATCA	200
	AGAACATGAT	TACCGGTGCC	GCCCAGATGG	ACGGTGCCAT	TATTGTCCTT	250
	GCTGCTACTG	ACGGTGCCAT	GCCCCAGACC	CGCGAGCACT	TGCTTCTCGC	300
	CCGTCAGGTT	GGTATCCAGG	AATTGGTTGT	GTTTGTTAAC	AAGGTTGACA	350
50	CCATCGACGA	CCCCGAGATG	TTGGAGCTCG	TTGAGATGGA	GATCCGCGAG	400
	TTGTTGTCTG	AGTTCGGTTT	TGACGGTGAC	AACACCCCCG	TCATCATGGG	450
	TTCCGCTTTG	TGCGCTTTGG	AGGGCAAGCA	GCCCGAGATT	GGTGAGCAGG	500
	CTATCACCAA	GTTGATGGCC	GCCGTTGACG	AGCACATCCC	CACCCCCCAG	550

CGTGA CTTGG AGCAGCCTTT CTTGATGCCT GTTGAGGGTG TTTTCTCTAT 600
 CTCTGGCCGT GGTACCGTGG TGACTGGTAA GGTTGCCCGT GGTGTCCTCA 650
 AGAAGGGTGA GGAGATTGAG ATTGTTGGCA ACTTTGACAA GCCCTACAAG 700
 GTGACTGTTA CTGGTATTGA GATGTTCAAG AAGGAGTTGG ACCAGGCCAT 750
 5 GGCTGGTGAC AACGCCGGTA TCTTGTTGCG TGGTGTCAAG CGTGACGAGG 800
 TGTCTCGTGG TATGGTTTTG GCCAAGCCCG GCACTGTTGT CTCGCACAAG 850
 AAGGTTTTTG CTTGCTTTA CATCTTGACC CAGGAGGAGG GTGGCCGTAA 900
 GACCGGCTTC GGCTCCAACT ACAAGCCCCA GTTGTCTTGT CGCACTACCG 950
 ACGTCACTGG TACCCTCACC TTC 973

10

2) INFORMATION FOR SEQ ID NO: 1960

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*
 25 (B) STRAIN: ATCC 28870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960

AAGACTACCT TGA CTGCTGC AATCACCAAG GTCTTAGCTG ATCAAGGTGG 50
 30 TGCTGATTTC TTAGATTATG CATCTATTGA CAAGGCTCCT GAAGAAAGAG 100
 CAAGAGGTAT TACTATCTCT ACTGCTCACG TTGAGTATGA AACC CCAAAC 150
 AGACATTATT CTCATGTCGA TTGTCCTGGC CATCAAGATT ATATTAAGAA 200
 TATGATTACT GGTGCTGCAC AAATGGATGG TGCTATTATT GTTGTTGCTG 250
 CTACTGATGG TCAAATGCCA CAACTAAGG AACATTTATT ATTAGCAAGA 300
 35 CAAGTTGGTG TTCAACATTT AGTTGTCTTT GTTAATAAAT GTGACACCAT 350
 TGATGACCCA GAAATGTTGG AATTAGTTGA AATGGAAATG AGAGAACTAT 400
 TGTCTGAATA TGGTTTTGAT GGTGATAACA CTCCAGTTAT TATGGGTTCT 450
 GCATTGATGG CTTTAGAAGA CAAGAGACCT GAAGTTGGTA AGGAATCTAT 500
 TTAAAGTTA ATGGAAGCYG TTGACACATG GATTCCAACC CCAGAGAGAG 550
 40 ATTTAGAAAA ACCATTTTTG TTACCTATTG ATGAAGTTTT CTCAATCTCT 600
 GGTAGAGGTA CTGTCGTTTC TGGTACTGTC GAAAGAGGTA CTTTGAAGAA 650
 GGGTGAAGAA GTTGAAATTG TTGGTGGTAA GGATGGTTCT ATTAAAATA 700
 CTGTCACAGG TATTGAAATG TATCACAAGG AATTAGACCA AGCGCAAGCA 750
 GGTGATACTC CAGGTATTTT ATTAAGAGGT GTCAAGAGAG ACCAAATCAA 800
 45 GAGAGGTCAA ATTTTAGCAA AGCCAGATTC CGTTAAGGCA TACAAGAAGT 850
 TCTTGGCTTC CCTTTATATC TTAACCAAGG AAGAAGGTGG TAGACATACA 900
 CCATTCTCTG AAAACTACAG ACCACAAATG TACATCAGAA CTACCAATGT 950
 TAACGTTACT TTGAAGTTCC CAGACACTGA AGAAG 985

50

2) INFORMATION FOR SEQ ID NO: 1961

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961
10 GCTCAAGGCA GATGGCATTC CC 22

15 2) INFORMATION FOR SEQ ID NO: 1962

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962
GGACAAGGCG GTTGC GTTTG AT 22

30 2) INFORMATION FOR SEQ ID NO: 1963

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963
CATTCCCGTC TCGCTCGACA GT 22

45 2) INFORMATION FOR SEQ ID NO: 1964

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964

5

ATCTGCCTGC CCGTCTTGC

19

10 2) INFORMATION FOR SEQ ID NO: 1965

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmid pGS05
(C) ACCESSION NUMBER: M36657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965

25

ATGAATAAAT	CGCTCATCAT	TTTCGGCATC	GTCAACATAA	CCTCGGACAG	50
TTTCTCCGAT	GGAGGCCGGT	ATCTGGCGCC	AGACGCAGCC	ATTGCGCAGG	100
CGCGTAAGCT	GATGGCCGAG	GGGGCAGATG	TGATCGACCT	CGGTCCGGCA	150
TCCAGCAATC	CCGACGCCGC	GCCTGTTTCG	TCCGACACAG	AAATCGCGCG	200
30 TATCGCGCCG	GTGCTGGACG	CGCTCAAGGC	AGATGGCATT	CCCGTCTCGC	250
TCGACAGTTA	TCAACCCGCG	ACGCAAGCCT	ATGCCTTGTC	GCGTGGTGTG	300
GCCTATCTCA	ATGATATTCG	CGGTTTTCCA	GACGCTGCGT	TCTATCCGCA	350
ATTGGCGAAA	TCATCTGCCA	AACTCGTCGT	TATGCATTCT	GTGCAAGACG	400
GGCAGGCAGA	TCGGCGCGAG	GCACCCGCTG	GCGACATCAT	GGATCACATT	450
35 GCGGCGTTCT	TTGACGCGCG	CATCGCGGCG	CTGACGGGTG	CCGGTATCAA	500
ACGCAACCGC	CTTGTCCTTG	ATCCCGGCAT	GGGGTTTTTT	CTGGGGGCTG	550
CTCCCGAAAC	CTCGCTCTCG	GTGCTGGCGC	GGTTCGATGA	ATTGCGGCTG	600
CGCTTCGATT	TGCCGGTGCT	TCTGTCTGTT	TCGCGCAAAT	CCTTTCTGCG	650
CGCGCTCACA	GGCCGTGGTC	CGGGGGATGT	CGGGGCCGCG	ACACTCGCTG	700
40 CAGAGCTTGC	CGCCGCCGCA	GGTGGAGCTG	ACTTCATCCG	CACACACGAG	750
CCGCGCCCCT	TGCGCGACGG	GCTGGCGGTA	TTGGCGGCGC	TGAAAGAAAC	800
CGCAAGAATT	CGTTAA				816

15

2) INFORMATION FOR SEQ ID NO: 1966

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966

5 CATGCCAGTC TTGCCAACG

19

2) INFORMATION FOR SEQ ID NO: 1967

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967

20

CAGCAATAAG TAATCCAGCG ATG

23

25 2) INFORMATION FOR SEQ ID NO: 1968

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968

GGAGAGATTT CACCGCATAG

20

40

2) INFORMATION FOR SEQ ID NO: 1969

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969

AGCCAACCAT CATGCTATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1970

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1206 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Transposon Tn10
 (C) ACCESSION NUMBER: J01830

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970

	ATGAATAGTT	CGACAAAGAT	CGCATTGGTA	ATTACGTTAC	TCGATGCCAT	50
	GGGGATTGGC	CTTATCATGC	CAGTCTTGCC	AACGTTATTA	CGTGAATTTA	100
	TTGCTTCGGA	AGATATCGCT	AACCACTTTG	GCGTATTGCT	TGCACTTTAT	150
20	GCGTTAATGC	AGGTTATCTT	TGCTCCTTGG	CTTGGAAGAA	TGTCTGACCG	200
	ATTTGGTCGG	CGCCCAGTGC	TGTTGTTGTC	ATTAATAGGC	GCATCGCTGG	250
	ATTACTTATT	GCTGGCTTTT	TCAAGTGCGC	TTTGATGCT	GTATTTAGGC	300
	CGTTTGCTTT	CAGGGATCAC	AGGAGCTACT	GGGGCTGTCG	CGGCATCGGT	350
	CATTGCCGAT	ACCACCTCAG	CTTCTCAACG	CGTGAAGTGG	TTCGGTTGGT	400
25	TAGGGGCAAG	TTTTGGGCTT	GGTTTAATAG	CGGGGCCTAT	TATTGGTGGT	450
	TTTGCAGGAG	AGATTTCAAC	GCATAGTCCC	TTTTTTATCG	CTGCGTTGCT	500
	AAATATTGTC	ACTTTCCTTG	TGGTTATGTT	TTGGTTCCGT	GAAACCAAAA	550
	ATACACGTGA	TAATACAGAT	ACCGAAGTAG	GGGTTGAGAC	GCAATCGAAT	600
	TCGGTATACA	TCACTTTATT	TAAAACGATG	CCCATTTTGT	TGATTATTTA	650
30	TTTTTCAGCG	CAATTGATAG	GCCAAATTCC	CGCAACGGTG	TGGGTGCTAT	700
	TTACCGAAAA	TCGTTTTTGA	TGGAATAGCA	TGATGGTTGG	CTTTTCATTA	750
	GCGGGTCTTG	GTCTTTTACA	CTCAGTATTC	CAAGCCTTTG	TGGCAGGAAG	800
	AATAGCCACT	AAATGGGGCG	AAAAAACGGC	AGTACTGCTC	GAATTTATTG	850
	CAGATAGTAG	TGCATTTGCC	TTTTTAGCGT	TTATATCTGA	AGGTTGGTTA	900
35	GATTTCCTTG	TTTAAATTTT	ATTGGCTGGT	GGTGGGATCG	CTTTACCTGC	950
	ATTACAGGGA	GTGATGTCTA	TCCAAACAAA	GAGTCATGAG	CAAGGTGCTT	1000
	TACAGGGATT	ATTGGTGAGC	CTTACCAATG	CAACCGGTGT	TATTGGCCCA	1050
	TTACTGTTTA	CTGTTATTTA	TAATCATTTA	CTACCAATTT	GGGATGGCTG	1100
	GATTTGGATT	ATTGGTTTAG	CGTTTTACTG	TATTATTATC	CTGCTATCGA	1150
40	TGACCTTCAT	GTTAACCCCT	CAAGCTCAGG	GGAGTAAACA	GGAGACAAGT	1200
	GCTTAG					1206

15 2) INFORMATION FOR SEQ ID NO: 1971

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971

CYGACTGYGC CATCCTYATC A

21

5

2) INFORMATION FOR SEQ ID NO: 1972

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972

MGICAGCTCA TYITTGCWKS C

21

20

2) INFORMATION FOR SEQ ID NO: 1973

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973

35 RACACCRGIY TTGGWITCCT T

21

2) INFORMATION FOR SEQ ID NO: 1974

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

45

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974

50

ACAAGGGITG GRMSAAGGAG AC

22

2) INFORMATION FOR SEQ ID NO: 1975

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975

TGRCCRGGGT GGTTRAGGAC G

21

15

2) INFORMATION FOR SEQ ID NO: 1976

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976

GATGGAYTCY GTYAAITGGG A

21

30

2) INFORMATION FOR SEQ ID NO: 1977

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977

45 GATGGAYTCY GTYAARTGGG A

21

2) INFORMATION FOR SEQ ID NO: 1978

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978

CATCITGYAA TGGYAATCTY AAT

23

10

2) INFORMATION FOR SEQ ID NO: 1979

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979

CATCYTGYAA TGGYAASCTY AAT

23

25

2) INFORMATION FOR SEQ ID NO: 1980

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980

40

TCRATGGCIT CIAIRAGRGY YT

22

2) INFORMATION FOR SEQ ID NO: 1981

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981

TGGACACCIS CAAGIGGKCY G

21

5

2) INFORMATION FOR SEQ ID NO: 1982

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982

TGGACACYIS CAAGIGGKCY G

21

20

2) INFORMATION FOR SEQ ID NO: 1983

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983

35

CYGAYTGCGC YATICTCATC A

21

2) INFORMATION FOR SEQ ID NO: 1984

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

45

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984

50

CYGAYTGYGC YATYCTSATC A

21

2) INFORMATION FOR SEQ ID NO: 1985

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: M1-106
 (C) ACCESSION NUMBER: U81804

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
20	TCGACAAGCG	AACCATGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTCTT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCTA	250
	AGTACCAGGT	TACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATGTC	350
25	CACCGGTATC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCTGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGT	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
30	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCCGGTGTT	TCCAAGGGTA	AGACCCTTCT	CGAGGCCATC	GACGCCAGTA	700
	GGCCCCCTAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTGCGCCCC	ACCAACGTCA	850
35	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTCCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
40	TTGCAAGTTC	TCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTT	CCCAGAAGCC	TCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATTAA	GAGTGTGGAG	AAGTCCGATG	GGAAGAGCGG	CAAGGTTACC	1350
45	AAGGCCGCCG	AGAAGGCTGC	TAAGAAGAAG	TAA		1383

2) INFORMATION FOR SEQ ID NO: 1986

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
(B) STRAIN: B3501
(C) ACCESSION NUMBER: U81803

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
15	TCGACAAGCG	AACCAT TGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTTCTT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCCA	250
	GGTACCAGGT	CACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCAT TGC	350
20	CACCGGTATC	GGTGAGTTCG	AGGCCGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCCGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGT TGGC	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
25	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCTGGTGTT	TCCAGGGGTA	AGACCCTTCT	CGAGGCCATC	AGCGCCAGTA	700
	GGCCCCATAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTGCGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTGCGCCCC	ACCAACGTCA	850
30	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTTCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
35	CTGCAAGTTT	GCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTCTGTC AAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTG	CCCAGAAGCC	CCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCC	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATCAA	GAGCGTGGAC	AAGACCGAGA	AGGGTGGCAA	GGTCACCAAG	1350
40	GCTGCTGAGA	AGGCTGCCAA	GAAGAAGTAA			1380

2) INFORMATION FOR SEQ ID NO: 1987

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(C) ACCESSION NUMBER: X01638

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987

	ATGGGTAAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
10	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTC	GGTGAATTCG	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
15	GAGAACACGC	TTTGTTGGCT	TTCACCTTGG	GTGTTAGACA	ATTGATTGTT	450
	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCGTCCCA	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
20	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
	GTTTACAAGA	TCGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTCGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
25	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTC	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
30	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
	AAGTTCGTTC	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
	ACCATTAGGT	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

35

2) INFORMATION FOR SEQ ID NO: 1988

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

50

(C) ACCESSION NUMBER: M10992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988

	ATGGGTAAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
5	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTC	GGTGAATTCG	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTGGCT	TTCACCTTGG	GTGTTAGACA	ATTGATTGTT	450
10	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCGTCCCA	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
15	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
	GTTTACAAGA	TTGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
20	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTG	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
25	AAGTTCGTTT	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
	ACCATTAGGT	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

30

2) INFORMATION FOR SEQ ID NO: 1989

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Eremothecium gossypii*

(B) STRAIN: ATCC 10895

45 (C) ACCESSION NUMBER: X73978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989

	ATGGGTAAAG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTCACGTCGA	50
50	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250

	AGTACCACGT	CACTGTCATT	GACGCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
5	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550
	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
10	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
15	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCTTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
20	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
	ACCATTGGGT	AGATTGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCCAA	AGGCTGGTAA	GAAATAG			1377

25

2) INFORMATION FOR SEQ ID NO: 1990

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 1377 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*
- (C) ACCESSION NUMBER: A29820
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990

	ATGGGTAAGG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTCACGTCGA	50
	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTGGTA	100
45	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250
	AGTACCACGT	CACTGTCATT	GACCCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
50	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550

	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
5	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
10	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCTTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
15	ACCATTGGGT	AGATTGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCTG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCCAA	AGGCTGGTAA	GAAATAG			1377

20

2) INFORMATION FOR SEQ ID NO: 1991

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus oryzae*
 (B) STRAIN: KBN616
 (C) ACCESSION NUMBER: AB007770

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1991

	TGGGGTAAGT	TTATCAACCC	GTCGAGTTGT	GTTGCATCTC	AGATCATGGC	50
	TGACAAGTAC	TTTCCTCCTT	ACAGTAAGGA	AGACAAGCAG	CACATCAACA	100
40	TCGTCGTTAT	CGGCCACGTC	GATTCCGGCA	AGTCCACCAC	CACTGGTCAC	150
	TTGATCTACA	AGTGTGGTGG	TATCGACCAG	CGTACCATCG	AGAAGTTCGA	200
	GAAGGAAGCC	GCTGAGCTCG	GTAAGGGTTC	CTTCAAGTAC	GCCTGGGTTC	250
	TTGACAAGCT	CAAGTCCGAG	CGTGAGCGTG	GTATCACCAT	CGATATCGCC	300
	CTCTGGAAGT	TCCAGACCTC	CAAGTATGAG	GTCACCGTCA	TTGGTAAGCA	350
45	TTTGAGTTCC	AACCTACGTT	GCCCAACATT	TACAGTCATC	TAACAAAGTT	400
	CAATAGATGC	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	450
	ACTTCCCAGG	CTGACTGCGC	TATCCTCATC	ATTGCCTCCG	GTAAGTGGTGA	500
	ATTCGAGGCT	GGTATCTCCA	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	550
	TCGCTTTCAC	CCTCGGTGTC	CGTCAGCTCA	TCGTTGCCCT	CAACAAGATG	600
50	GACACCTGCA	AGTGGTCTCA	GGATCGTTAC	AACGAAATCG	TTAAGGAGAC	650
	TTCCAACCTC	ATCAAGAAGG	TCGGATACAA	CCCCAAGAGC	GTTCTTTTCG	700
	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCACCAAC	750
	TGCCCCTGGT	ACAAGGGCTG	GGAGAAGGAG	ACCAAGGCTG	GCAAGTCCAC	800

	CGGTAAGACC	CTTCTCGAGG	CCATCGATGC	CATCGAGCCC	CCCGTCCGTC	850
	CCACCGACAA	GCCTCTCCGT	CTTCCCCTCC	AGGATGTCTA	CAAGATCTCT	900
	GGTATCGGTA	CTGTGCCCCG	CGGTCGTGTC	GAGACTGGTG	TCATCAAGCC	950
	TGGTATGGTC	GTTACTTTCG	CTCCTGCCAA	CGTGACCACT	GAAGTCAAGT	1000
5	CCGTTGAAAT	GCACCACCAG	CAGCTCCAGG	CCGGTAACCC	CGGTGACAAC	1050
	GTTGGTTTCA	ACGTCAAGAA	CGTCTCCGTC	AAGGAAGTCC	GCCGTGGTAA	1100
	CGTTGCCGGT	GACTCCAAGA	ACGACCCCCC	TGCTGGCTGC	GATTCCTTCA	1150
	ACGCCCAGGT	CATCGTCCTT	AACCACCCCG	GTCAGGTCGG	CAACGGTTAC	1200
	GCTCCCCTCC	TGGACTGCCA	CACCGCTCAC	ATTGCTTGCA	AGTTCGCTGA	1250
10	GCTCCTTGAG	AAGATTGACC	GCCGTACCGG	TAAATCTGTT	GAGGACAAGC	1300
	CCAAGTTCAT	CAAGTCTGGT	GATGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1350
	AAGCCCATGT	GTGTGGAGTC	TTTCACTGAC	TTCCCCCCTC	TTGGTCGTTT	1400
	CGCTGTCCGT	GACGTAAGTT	TTTCCCTCTT	GACTATCTTC	ACAATTTTTC	1450
	ACATATTTTC	ACGCCTCGTC	CCACTCTTTT	TCCTCCCTTC	CTCTTTGGTT	1500
15	CCCCTTTTTG	CCTGCAAGTT	CTCTATAGCT	AACATGATGT	CTAGATGCGT	1550
	CAAACGTGTT	CCGTCGGAGT	TATCAAGTCG	GTTGAGAAGA	AACTGGCGG	1600
	TTCTGGCAAG	GTCACCAAGG	CCGCCCAGAA	GGCTGGCAAG	AAATAA	1646

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2) INFORMATION FOR SEQ ID NO: 1992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
 (B) STRAIN: R106
 (C) ACCESSION NUMBER: U19723

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992

	ATGGGTAAGG	AAAAGTCCCA	CATCAACGTC	GTCGTTATCG	GCCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
40	TCGACAAGCG	TACCATCGAG	AAGTTCGAGA	AGGAAGCCGC	CGAACTCGGC	150
	AAGGGTTCCT	TCAAGTACGC	CTGGGTCTCT	GACAAGCTGA	AGTCTGAGCG	200
	TGAGCGTGGT	ATCACTATCG	ATATCGCTCT	GTGGAAGTTC	GAGACCCCCA	250
	AGTACATGGT	CACCGTCATC	GATGCCCCCG	GTCACCGTGA	TTTCATCAAG	300
	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	TGCGCCATTC	TCATCATTCG	350
45	CGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGCCAGACTC	400
	GTGAGCACGC	CCTTCTCGCC	TACACCCTTG	GTGTCAAGCA	GCTCATCGTC	450
	GCTATCAACA	AGATGGACAC	CACCAAGTGG	TCTGAGGCCC	GTTACCAGGA	500
	GATCATCAAG	GAGACCTCCG	GTTTCATCAA	GAAGGTCGGC	TACAACCCCA	550
	AGCACGTTCC	CTTTGTCCCC	ATCTCGGGTT	TCAACGGTGA	CAACATGATT	600
50	GAGGTTTCTT	CCAAC TGCCC	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	650
	GGCCAAGGCC	ACTGGTAAGA	CTCTCCTCGA	GGCCATTGAC	GCCATCGACC	700
	CTCCTTCGCG	CCCCACCGAC	AAGCCCCTCC	GTCTTCCCCT	CCAGGATGTC	750
	TACAAGATCG	GTGGTATTGG	CACGGTGCCC	GTCGGCCGTG	TCGAGACCGG	800

	TACCATCAAG	GGTGGTATGG	TCGTCACCTT	CGCCCCCGCT	GGTGTACCA	850
	CTGAGGTCAA	GTCCGTCGAG	ATGCACCACG	AGCAGCTCTC	CGAGGGTCTC	900
	CCCGGTGACA	ACGTCGGCTT	CAACGTCAAG	AACGTCTCCG	TCAAGGAGAT	950
	CCGTCGTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTT	1000
5	GCGACTCCTT	CAACGCCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	1050
	GGTGCTGGTT	ACGCACCCGT	CCTCGATTGC	CACACTGCCC	ACATCGCCTG	1100
	CAAGTTCTCC	GAGCTTGTTG	AGAAGATTGA	CCGCCGTACC	GGCAAGTCCG	1150
	TTGAGGCCGC	CCCCAAGTTC	ATCAAGTCTG	GTGACGCCGC	CATCGTCAAG	1200
	ATGGTTCCCT	CCAAGCCTAT	GTGTGTTGAG	GCCTTCACTG	ACTACCCTCC	1250
10	TCTCGGTCGT	TTCGCCGTCC	GTGACATGAG	ACAGACCGTC	GCTGTCGGTG	1300
	TCATCAAGTC	CGTCGCCAAG	TCCGACAAGC	AGGGTGCCGG	TAAGGTTACC	1350
	AAGGCCGCTG	TCAAGGCTGG	CAAGAAGTAA			1380

15

2) INFORMATION FOR SEQ ID NO: 1993

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: 186AS
 (C) ACCESSION NUMBER: U14100

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993

	ATGGGTAAGG	AAGACAAGAC	TCACATTAAC	CTCGTCGTCA	TCGGCCACGT	50
	CGATTCGGGC	AAATCTACCA	CCACTGGTCA	TTTGATCTAC	AAATGCGGTG	100
35	GTATTGACAG	CCGTACCATT	GAGAAGTTCG	AAAAGGAAGC	CGAAGAGTTG	150
	GGCAAGAAAT	CCTTCAAATA	TGCGTGGGTC	CTTGACAAAC	TGAAGTCTGA	200
	GCGTGAGCGT	GGTATCACCA	TCGATATTGC	CCTCTGGAAA	TTGAGACTC	250
	CGAAGTACAG	TGTCACTGTC	ATTGATGCTC	CCGGCCATCG	TGACTTCATC	300
	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	GACTGCGCTA	TCCTCATCAT	350
40	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	400
	CTCGTGAGCA	CGCTCTGCTT	GCTTTCACCC	TTGGTGTGAG	GCAACTCATC	450
	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTTCAA	500
	CGAAATCATC	AAGGAGGTTT	CCAACTTCAT	CAAGAAGGTC	GGATATAACC	550
	CCAAGGCTGT	TCCCTTCGTG	CCAATCTCTG	GTTTCGAGGG	TGACAACATG	600
45	ATTGAACCCT	CCCCCAACTG	CACATGGTAC	AAGGGCTGGA	ACAAGGAGAC	650
	TGCCTCTGGC	AAGTCTTCTG	GTAAAACCCT	TCTCGATGCC	ATTGACGCCA	700
	TTGAACCCCC	AACCCGTCCT	ACCGATAAGC	CCCTCCGTCT	TCCCCTCCAG	750
	GATGTGTACA	AAATCTCTGG	TATTGGCACT	GTTCCCGTCG	GACGTGTTGA	800
	GACTGGTGTC	ATCAAGCCCCG	GTATGGTCGT	GACTTTCGCT	CCCTCCAACG	850
50	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	ACCACCAACA	ACTCCAGGCT	900
	GGTTACCCTG	GCGACAACGT	CGGCTTCAAC	GTCAAGAACG	TTTCAGTCAA	950
	GGAAGTCCGC	CGTGGCAACG	TTGCTGGCGA	CTCCAAAAT	GATCCCCCTA	1000
	AGGGCTGCGA	ATCCTTCAAT	GCCCAGGTCA	TCGTCCTTAA	CCACCCCGGC	1050

	CAGGTTGGCG	CTGGTTATGC	CCCAGTCCTC	GACTGCCACA	CTGCCCACAT	1100
	TGCTTGCAAG	TTCTCTGAGC	TTATTGAGAA	GATCGACCGC	CGTACCGGAA	1150
	AGTCTGTTGA	GAACAACCCC	AAGTTCATCA	AGTCTGGTGA	TGCTGCTATC	1200
	GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTGGAGCCCT	TCACTGACTA	1250
5	TCCCCCTCTT	GGACGTTTCG	CTGTCCGTGA	CATGAGACAA	ACCGTCGCTG	1300
	TCGGTGTCAT	CAAGTCCGTC	ATCAAGTCTG	ACAAGACTGC	TGGCAAGGTC	1350
	ACCAAGGCCG	CGCAGAAGGC	CACCAAGAAA	TAA		1383

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2) INFORMATION FOR SEQ ID NO: 1994

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1383 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neurospora crassa*
- (C) ACCESSION NUMBER: D45837

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994

	ATGGGCAAGG	AGGACAAGAC	TCACATCAAC	GTCGTCGTTA	TCGGCCACGT	50
	CGATTCCGGC	AAGTCTACCA	CTACCGGTCA	CTTGATCTAC	AAGTGCGGTG	100
	GTATCGACAA	GCGTACCATC	GAGAAGTTCG	AGAAGGAAGC	CGCTGAGCTC	150
30	GGTAAGGGTT	CCTTCAAGTA	TGCCTGGGTT	CTTGACAAGC	TCAAGGCCGA	200
	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	TTCGAGACTC	250
	CCAAGTACTA	CGTCACCGTC	ATCGATGCCC	CCGGTCATCG	TGATTTTCATC	300
	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	GATTGCGCTA	TCCTCATCAT	350
	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	400
35	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GCAGCTCATT	450
	GTTGCCATCA	ACAAGATGGA	CACCACCCAG	TGGTCCCAGA	CTCGTTTCGA	500
	GGAGATCATC	AAGGAGACCA	AGAACTTCAT	CAAGAAGGTT	GGCTACAACC	550
	CCGCTGGTGT	CGCTTTCGTC	CCCATCTCCG	GCTTCAACGG	CGACAACATG	600
	CTTGAGCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	650
40	CAAGGCCGGC	AAGGCCACTG	GCAAGACCCT	CCTCGAGGCC	ATCGACGCCA	700
	TTGAGCCCCC	CAAGCGTCCT	ACCGACAAGC	CCCTCCGTCT	TCCCCTCCAG	750
	GATGTCTACA	AGATCGGTGG	TATCGGCACA	GTGCCCCTCG	GCCGTATCGA	800
	GACTGGTGTC	CTCAAGCCCG	GTATGGTCGT	TACCTTCGCT	CCTTCCAACG	850
	TCACCACTGA	AGTCAAGTCC	GTGAGATGC	ACCACGAGCA	GCTTGCTCAG	900
45	GGTGTCCCCG	GTGACAACGT	CGGCTTCAAC	GTGAAGAACG	TTTCCGTCAA	950
	GGATATCCGC	CGTGGTAACG	TTGCCGGTGA	CTCCAAGAAC	GACCCCCCTG	1000
	CTGGCGCCGC	CTCTTTCACC	GCCCAGGTCA	TCGTTCTCAA	CCACCCCGGT	1050
	CAGGTCGGTG	CCCGCTACGC	CCCCGTCCTC	GACTGCCACA	CTGCCCACAT	1100
	TGCCTGCAAG	TTGCGCGAGC	TCCTCGAGAA	GATCGACCGC	CGTACTGGTA	1150
50	AGGCTGTTGA	GGCCTCCCCC	AAGTTCATCA	AGTCTGGTGA	TGCTGCCATC	1200
	GTCAAGATGA	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACCGACTA	1250
	CCCTCCCCTC	GGCCGTTTCG	CCGTCCGTGA	CATGCGTCAG	ACCGTCGCCG	1300
	TCGGTGTCAT	CAAGGCCGTC	GACAAGTCCA	CCGCTGCCGC	TGGCAAGGTC	1350

ACCAAGTCCG CTGCCAAGGC CGCCAAGAAG TAA

1383

5 2) INFORMATION FOR SEQ ID NO: 1995

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospira anserina*
(C) ACCESSION NUMBER: X74799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995

20 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100
GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150
GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA 200
25 GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAG TTCGAGACCC 250
CCAAGTACTA TGTCACCGTC ATTGATGCCC CCGGCCATCG TGATTTTCATC 300
AAGAACATGA TTACTGGTAC TTCCCAGGCC GATTGCGCCA TTCTCATCAT 350
TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450
30 GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGG CCCGCTTCAA 500
CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550
CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG 600
CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGGT 650
CAAGGGTGGC AAGGCCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700
35 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
GATGTCTACA AGATCGGCGG TATCGGCACA GTCCCTGTCT GCCGTATCGA 800
GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
GGTGTTCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA 950
40 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000
TGGGCGCCGC CTCTTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC 1050
CAGGTCGGTG CTGGTTACGC CCCCCTCCTC GATTGCCACA CTGCCCACAT 1100
CGCCTGCAAG TTCTCTGAGC TCCTGCAGAA GATCGACCGC CGTACTGGTA 1150
AGGCCGTTGA GGAGAGCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
45 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250
CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300
TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTT 1350
ACCAAGTCCG CTGCCAAGGC TGGCAAGAAA TAA 1383

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2) INFORMATION FOR SEQ ID NO: 1996

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospora curvicolla*
 (B) STRAIN: VLV
 (C) ACCESSION NUMBER: X96614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996

15 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
 CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100
 GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150
 GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA 200
 20 GCGTGAGCGT GGTATCACCA TTGATATCGC CCTCTGGAAG TTCGAGACCC 250
 CCAAGTACTA TGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTTCATC 300
 AAGAACATGA TTACTGGTAC TTCCCAGGCC GATTGCGCCA TTCTCATCAT 350
 TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450
 25 GTCGCCATCA ACAAGATGGA CACCACCAA TGGTCCGAGG CCCGCTTCAA 500
 CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550
 CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTC AACGG CGACAACATG 600
 CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGGT 650
 CAAGGGTGGC AAGGCTACTG GCAAGACCCT CCTCGAGGCC ATCGACTCCA 700
 30 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTTCAG 750
 GACGTTTACA AGATCGGCGG TATCGGCACA GTCCCTGTCT GCCGTATCGA 800
 GACTGGTATC CTCAAGCCCC GTATGGTCGT TACCTTCGCC CCTTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCTCTGAG 900
 GGTGTCCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA 950
 35 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTC 1000
 TTGGCGCCGC TTCTTTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC 1050
 CAGGTCGGTG CTGGTTACGC CCCCCTCCTC GATTGCCACA CTGCCCACAT 1100
 CGCCTGCAAG TTCGCTGAGC TCCTGCAGAA GATCGATCGC CGTACTGGTA 1150
 AGGCTGTTGA GGAGAGCCCT AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
 40 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250
 CCCTCCCCTC GGTCGTTTCG CTGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300
 TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTC 1350
 ACCAAGTCCG CTGCCAAGGC TGGTGGCAAG AAATAA 1386

45

2) INFORMATION FOR SEQ ID NO: 1997

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Sordaria macrospora*
 (B) STRAIN: 000
 (C) ACCESSION NUMBER: X96615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997

10
 ATGGGTAAGG AAGACAAGGC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
 CGATTCCGGC AAGTCCACCA CTACCGGTCA CCTGATCTAC AAGTGCGGTG 100
 GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC 150
 GGCAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA 200
 15 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC 250
 CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTTCATC 300
 AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TTCTCATCAT 350
 TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CTCGTGAGCA CGCTCTTCTC GCCTACACCC TCGGTGTCAA GCAGCTCATC 450
 20 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGG CTCGTTTCGA 500
 GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTC GGCTACAACC 550
 CCGCCACCGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG 600
 CTTGAGGCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC 650
 CAAGGCCGGC AAGTCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA 700
 25 TTGAGCAGCC CAAGCGCCCG ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
 GATGTCTACA AGATCGGCGG TATCGGCACA GTGCCCCTCG GCCGTATCGA 800
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG 900
 GGTGTTCCCG GTGACAACGT CGGCTTCAAC GTGAAGAACG TTTCCGTCAA 950
 30 GGATATCCGT CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG 1000
 TCGGCGCTGC CTCTTTCACC GCCCAGGTCA TCGTCCTTAA CCACCCCGGT 1050
 CAGGTCGGTG CCGGCTACGC TCCCGTCCTC GATTGCCACA CTGCCCACAT 1100
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGATCGC CGTACTGGTA 1150
 AGGCTGTTGA GACTTCTCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
 35 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTCGAGGCTT TCACCGACTA 1250
 CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300
 TCGGTGTCAT CAAGGCCGTC GACAAGACCC AGGCTGTCGC TGGCAAGGTC 1350
 ACCAAGTCTG CTGCCAAGGC TGCCAAGAAG TAA 1383

10

2) INFORMATION FOR SEQ ID NO: 1998

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichoderma reesei*

(B) STRAIN: QM9414

(C) ACCESSION NUMBER: Z23012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998

5
ATGGGTAAGG AGGACAAGAC TCACATCAAC GTGGTCGTCA TCGGCCACGT 50
CGACTCCGGC AAGTCTACCA CCACTGGTCA CTTGATCTAC CAGTGCGGTG 100
GTATCGACAA GCGTACCATT GAGAAGTTCG AGAAGGAAGC CGCCGAATC 150
GGCAAGGGTT CCTTCAAGTA CGCGTGGGTT CTTGACAAGC TCAAGGCCGA 200
10 GCGTGAGCGT GGTATCACCA TCGACATTGC CCTCTGGAAG TTCGAGACTC 250
CCAAGTACTA TGTCACCGTC ATTGACGCTC CCGGCCACCG TGACTTCATC 300
AAGAACATGA TCACTGGTAC TTCCCAGGCC GACTGCGCTA TCCTCATCAT 350
CGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
CCCGTGAGCA CGCTCTGCTC GCCTACACCC TGGGTGTCAA GCAGCTCATC 450
15 GTCGCCATCA ACAAGATGGA CACTGCCAAC TGGGCCGAGG CTCGTTACCA 500
GGAAATCATC AAGGAGACTT CCAACTTCAT CAAGAAGGTC GGCTTCAACC 550
CCAAGGCCGT TGCTTTCGTC CCCATCTCCG GCTTCAACGG TGACAACATG 600
CTCACCCCT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGAC 650
CAAGGCTGGC AAGTTCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700
20 TCGAGCCCCC CAAGCGTCCC ACGGACAAGC CCCTGCGTCT TCCCCTCCAG 750
GACGTCTACA AGATCGGTGG TATCGGAACA GTTCCCGTCG GCCGTATCGA 800
GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCCTCCAACG 850
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
GGCCAGCCTG GTGACAACGT TGGTTTCAAC GTGAAGAACG TTTCCGTCAA 950
25 GGAAATCCGC CGTGGAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCA 1000
TGGGCGCCGC TTCTTTCACC GCCCAGGTCA TCGTCATGAA CCACCCCGGC 1050
CAGGTCGGTG CCGGCTACGC CCCCGTCCTC GACTGCCACA CTGCCACAT 1100
TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACCGGTA 1150
AGGCTACCGA GTCTGCCCCC AAGTTCATCA AGTCTGGTGA CTCGCGCATC 1200
30 GTCAAGATGA TCCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250
CCCTCCCCTG GGTCGTTTCG CCGTCCGTGA CATGCGCCAG ACCGTCGCTG 1300
TCGGTGTCAT CAAGGCCGTC GAGAAGTCCT CTGCCGCCGC CGCCAAGGTC 1350
ACCAAGTCCG CTGCCAAGGC CGCCAAGAAA TAA 1383

35

2) INFORMATION FOR SEQ ID NO: 1999

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999

50 CATGTCAAYA TTGGTACTAT TGGTCATGT 29

2) INFORMATION FOR SEQ ID NO: 2000

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000

CCACCYTCIC TCAMGTTGAA RCGTT 25

15 2) INFORMATION FOR SEQ ID NO: 2001

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001

ACYACITTRA CIGCYGCIYAT YAC 23

30 2) INFORMATION FOR SEQ ID NO: 2002

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002

CCIGARGARA GAGCIMGWGG T 21

45 2) INFORMATION FOR SEQ ID NO: 2003

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003

CATYTCRAIR TTGTCACCTG G

21

2) INFORMATION FOR SEQ ID NO: 2004

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: SC5314
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004

GCTGCCTTCG	ACCGTTCTAA	ACCTCATGTC	AACATTGGTA	CTATTGGTCA	50
TGTTGATCAT	GGTAAACTA	CATTGACTGC	TGCTATCACC	AAAGTTTTAG	100
CCGAACAAGG	TGGTGCCAAC	TTCTTGGATT	ATGGTTCTAT	TGATAGAGCT	150
CCAGAAGAAA	GAGCTAGAGG	TATCACTATT	TCCACTGCCC	ACGTTGAATA	200
CGAAACCAAG	AACAGACACT	ATGCCCACGT	TGATTGTCCA	GGACACGCTG	250
ATTATATCAA	AAATATGATT	ACTGGTGCCG	CTCAAATGGA	TGGTGCTATC	300
ATTGTTGTTG	CTGCCACTGA	TGGTCAAATG	CCTCAAACCA	GAGAACATTT	350
GTTATTGGCC	AGACAAGTTG	GTGTTCAAGA	CTTGGTTGTG	TTTGTCAACA	400
AAGTCGATAC	TATTGATGAC	CCTGAAATGT	TGGAATTAGT	CGAAATGGAA	450
ATGAGAGAAT	TGTTATCCAC	CTACGGTTTT	GATGGTGACA	ACACTCCAGT	500
TATTATGGGA	TCTGCTTTAA	TGGCTTTGGA	AGACAAGAAA	CCAGAAATTG	550
GTAAGGAAGC	TATCTTGAAA	TTGTTAGATG	CTGTGCGATG	ACACATTCCA	600
ACTCCATCAA	GAGACTTGGA	ACAACCATTT	TTGTTACCAG	TTGAAGACGT	650
GTTCTCCATC	TCCGGTAGAG	GAAGTGTGT	CACTGGTAGA	GTTGAAAGAG	700
GTGTTTTGAA	GAAGGGTGAA	GAAATCGAAA	TTGTTGGTGG	TTTTGACAAA	750
CCTTACAAGA	CTACTGTTAC	CGGTATTGAA	ATGTTCAAAA	AAGAATTAGA	800
CTCTGCTATG	GCTGGTGACA	ACTGTGGTGT	TTTGTTAAGA	GGTGTTAAAA	850
GAGATGAAAT	CAAGAGAGGT	ATGGTTTTGG	CCAAACCAGG	TACTGCTACT	900
TCTCACAAGA	AGTTCTTGGC	TTCCTTGTAT	ATTTTGACTT	CCGAAGAAGG	950
TGGTCGTTCC	ACTCCATTTG	GTGAAGGTTA	CAAGCCTCAA	TGCTTCTTCA	1000
GAAC TAACGA	TGTC ACTACC	ACATTTTCAT	TCCCAGAAGG	AGAAGGTGTT	1050
GATCATTCTC	AAATGATCAT	GCCAGGTGAC	AACATTGAAA	TGGTTGGTGA	1100
ATTGATCAAA	TCTTGTC CAT	TAGAAGTCAA	CCAACGTTTC	AACTTGAGAG	1150
AAGGTGGTAA	AACTGTTGGT	ACTGGTTTGA	TTACCAGAAT	CATCGAATAA	1200
ACAGAATGTG	CACTGTGAAT	AATAAAAAGA	AAAGAGGTAT	ATATAGGTGA	1250
CTTTGTATTT	TGTATTGAAC	AATAAAATTC	TGTAAATAGT	AAGGGCCTCA	1300
GAAGTTTTGA	TTTGATTTAT	GCCATGTGGA	CTTG TAGAGA	TATCCTTCTC	1350
AAACTTCTTG					1360

2) INFORMATION FOR SEQ ID NO: 2005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

1044

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005

AAGCCGCATG	TCAATATTGG	TACTATTGGT	CATGTTGACC	ACGGTAAAAC	50
GACGTTGACG	GCTGCTATTA	CTAAATGCCT	TTCTGATCTT	GGTCAAGCTA	100
GTTTTATGGA	TTATAGTCAA	ATTGACAAGG	CCCCCGAGGA	AAAGGCACGT	150
GGTATTACCA	TTTCATCTGC	CCATGTTGAA	TACGAAACTG	CTAATCGTCA	200
CTATGCCCCAT	GTGGATTGTC	CTGGTCACGC	CGATTACATT	AAGAATATGA	250
TTACTGGTGTC	TGCTACAATG	GATGGCGCTA	TCATTGTTGT	TTCTGCTACC	300
GATGGTCAAA	TGCCTCAAAC	TCGTGAACAT	TTGCTTCTGG	CTCGTCAAGT	350
CGGTGTAAAG	CAAATTGTTG	TATACATCAA	TAAAGTCGAT	ATGGTCGAGC	400
CTGATATGAT	CGAGCTTGTC	GAAATGGAAA	TGCGTGAGCT	ACTCTCCGAA	450
TACGGATTTG	ATGGTGACAA	TACTCCAATT	GTTAGCGGCA	GTGCTTTATG	500
TGCCTTAGAG	GGTCGTGAGC	CTGAGATTGG	TCTCAATAGT	ATTACTAAAT	550
TGATGGAAGC	TGTTGATAGT	TATATTACTC	TTCCTGAAAG	AAAAACGGAT	600
GTCCCTTTCT	TGATGGCCAT	CGAGGACGTT	TTTTCAATTT	CAGGTCGCGG	650
AACTGTAGTC	ACTGGCCGTG	TCGAGCGCGG	TACTTTAAAG	AAGGGTGCTG	700
AAATCGAAAT	CGTCGGTTAT	GGTAGCCATT	TAAAGACTAC	CGTTACTGGA	750
ATTGAAATGT	TCAAAAAGCA	GCTTGATGCC	GCCGTTGCCG	GTGACAATTG	800
TGGCCTTTTA	CTTCGTTCTA	TCAAGCGAGA	GCAATTAAAA	CGTGGAATGA	850
TTGTCGCTCA	ACCAGGAACC	GTTGCTCCTC	ATCAGAAATT	CAAGGCATCA	900
TTCTATATTT	TGACAAAAGA	GGAAGGAGGT	CGTCGTACCG	GTTTCGTTGA	950
CAAGTATCGT	CCCCAACTGT	ACAGTCGTAC	TTCCGACGTT	ACTGTCGAAC	1000
TTACCCACCC	TGATCCTAAC	GACTCAGACA	AAATGGTTAT	GCCTGGAGAC	1050
AATGTCGAGA	TGATCTGTAC	GCTTATTCAC	CCCATTGTCA	TCGAAAAAGG	1100
ACAACGCTTC	ACAGTTCGTG	AGGGTGGAAG	CACTGTAGGC	ACAGCTTTGG	1150
TTACTGAACT	TTTGGATTAG	TGCATTTATG	AACTTATTGG	CTTTAAAAAT	1200
TTTGCATGCT	GAATACCAAT	ATTATGTCCC	TTCTCAGAAAT	TCTATAACTA	1250
CAGTGTCATT	ATTGTAATAA	GACTTTTGCA	TCCATTGACA	ATGGTATTTG	1300
ATACTTTTAT	AGTTTCTACT	ATTGTTAGCC	AAAGTTATAA	AA	1342

2) INFORMATION FOR SEQ ID NO: 2006

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006

TGGAGCCGGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2007

1045

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007

TGGAGCCAGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2008

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008

TCTGGAGCCG ATGAGCGTG

19

2) INFORMATION FOR SEQ ID NO: 2009

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009

CTGGAGCCAG TAAGCGTGG

19

2) INFORMATION FOR SEQ ID NO: 2010

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: KMK107
 (C) ACCESSION NUMBER: AF027199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010

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ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTAAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
CACAAATGCG GGGATCATGT AACTCGCCTT GATCGTTGGG AACC GGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGACG CCTGCAGCAA      550
TGGCAACAAC GTTGC GCAAA CTATTA ACTG GCGAACTACT TACTCTAGCT      600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
GAGCCAGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
AGCATTGGTA A                                     861
  
```

2) INFORMATION FOR SEQ ID NO: 2011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: CLSis L-491
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCTTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
CACAAATGCG GGGATCATGT AACC CGCCTT GATCGTTGGG AACC GGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
TGGCAACAAC GTTGC GCAAA CTATTA ACTG GCGAACTACT TACTCTAGCT      600
  
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TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
GAGCCAGTAA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ATGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 2012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012

CCGCGGATTA TTAAACCGCC CTTCCGCGG-MR-HEG-ATGTCAGAGG GATAGATCCA 49

2) INFORMATION FOR SEQ ID NO: 2013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013

AGCTTAAGAA	CTCTTATCTG	GATTACGCGA	TGTCGGTCAT	TGTTGGCCGT	50
GCGCTGCCGG	ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	100
TTACGCCATG	AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	150
CAGCCCGTGT	CGTGGGTGAC	GTGATCGGTA	AATATCACCC	GCATGGTGAT	200
ACTGCCGTCT	ATGACACTAT	CGTCCGTATG	GCACAGCCAT	TCTCACTGCG	250
ATACATGCTG	GTAGATGGTC	AAGGTAACCT	CGGTTCTGTC	GATGGCGACT	300
CCGCCGCAGC	GATGCGTTAT	ACGGAAATCC	GTATGTCGAA	AATCGCCCAT	350
GAG					353

2) INFORMATION FOR SEQ ID NO: 2014

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 bases
- (B) TYPE: Nucleic acid

1048

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
- (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014

AGCTCCTATC	TGGATTATGC	GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	50
AGATGTCCGA	GATGGCCTGA	AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	100
TGAACGTACT	AGGCAATGAC	TGGAACAAAG	CCTATAAAAA	ATCTGCCCGT	150
GTCGTTGGTG	ACGTAATCGG	TAAATACCAT	CCCCATGGTG	ACTCGGCGGT	200
CTATGACACG	ATCGTCCGCA	TGGCGCAGCC	ATTCTCGCTG	CGTTATATGC	250
TGGTAGACGG	TCAGGGTAAC	TTCGGTTCTA	TCGACGGCGA	CTCTGCGGCG	300
GCAATGCGTT	ATACGGAAAT	CCGTCTGGCG	AAAATTGCCC	ATGAACTGAT	350
GGCCG					355

2) INFORMATION FOR SEQ ID NO: 2015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015

CCAAGAAGCT	CAAAAACATC	TG	22
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2) INFORMATION FOR SEQ ID NO: 2016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016

TADCCTGTCC	AWACAGCCAT	20
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2) INFORMATION FOR SEQ ID NO: 2017

(i) SEQUENCE CHARACTERISTICS:

1049

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017

ACTTTGAATA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018

ACACTAAACA AGGTTGGTTT AG

22

2) INFORMATION FOR SEQ ID NO: 2019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019

ACACTAAACA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020

WO 01/23604
GTAGCTCCAG ATGAAATGTT TG

PCT/CA00/01150

22

2) INFORMATION FOR SEQ ID NO: 2021

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021

GTAGCTCCAG ACGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2022

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022

GTAGCTCCAG ATGAAACGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2023

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023

GTAAGTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2024

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid

1051

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024

AGTGAAAAGA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025

AGTGAGAAAA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026

TCCAAGCATG CATTATGCAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027

TCGGTCTAGA TAGAGCTAAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2028

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028

TATGCTCTTC AACAAATCACG

20

2) INFORMATION FOR SEQ ID NO: 2029

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029

AGCCGTTGAG ACTTTGAATA AG

22

2) INFORMATION FOR SEQ ID NO: 2030

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030

CTTAATGGTC TTGGTATCG

19

2) INFORMATION FOR SEQ ID NO: 2031

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1053

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031

CGTGACTGGG GTTCTGCTAT GA

22

2) INFORMATION FOR SEQ ID NO:2032

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032

CGTGACTGGG GATCATCAAT GA

22

2) INFORMATION FOR SEQ ID NO: 2033

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033

CGTGACTGGG GTTCTGCCAT GA

22

2) INFORMATION FOR SEQ ID NO: 2034

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034

ATCAAGAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2035

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035

ATCAAGAACA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2036

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036

ATCAAGAACA CTGGTTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2037

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037

ATCAAAAATA CTGGTTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2038

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1055

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038

ATCAAGAATA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2039

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039

ATCAAAAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2040

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040

TGTGACCCCA GACAAACCC

19

2) INFORMATION FOR SEQ ID NO: 2041

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041

GTTGAGCGGC AGCACTATCT

20

2) INFORMATION FOR SEQ ID NO: 2042

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042

CACGGGGATT TCTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2043

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043

CACGGGGATT ACTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2044

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044

ACCGTAAGTC GGCCAAGTCA

20

2) INFORMATION FOR SEQ ID NO: 2045

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045

1057

GTTCTTTCTC CGTATCGTC

19

2) INFORMATION FOR SEQ ID NO: 2046

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046

ACGGGGATTT TTCTATCTAT

20

2) INFORMATION FOR SEQ ID NO: 2047

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- (C) ACCESSION NUMBER: Z49094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTATGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACCTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAATTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACA AAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900

1058

AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCAC	AACTTGGTGC	TCGTCATCAA	1050
GCAAGTAATG	TTTCATTCGG	TACCAACCAG	GCCGTAGAAA	CCAATCGTGA	1100
CTGGGGATCA	TCAATGAAAC	CAATCACTGA	CTATGCTCCC	GCTTTAGAAT	1150
ATGGAGTCTA	TGACTCTACT	GCTTCTATTG	TACATGATGT	CCCTTATAAC	1200
TATCCTGGCA	CTGATACTCC	ACTCTACAAC	TGGGATCATG	TCTACTTTGG	1250
AAACATTACA	ATCCAGTATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAACACAAC	GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTATCA	CAAACCAATG	1500
TATATCAATA	AAATCGTCTT	TAGTGATGGT	AGCGAAAAAG	AATTTTCTGA	1550
TGCTGGTACA	CGAGCTATGA	AAGAGACTAC	TGCCTATATG	ATGACTGAAA	1600
TGATGAAAAC	TGTTTTAACT	TACGGAACAG	GACGTGGAGC	CTACCTACCA	1650
TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	CTGACGAAGA	1700
AATTGAAAAG	TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GATGAAATGT	1750
TTGTAGGGTA	TACCCGTAAA	TATGCAATGG	CTGTTTGGAC	AGGATACTCA	1800
AATCGTCTAA	CTCCAATCAT	CGGAGATGGT	TTCCTTGTTG	CTGGTAAAGT	1850
CTATCGTTCA	ATGATAACTT	ACCTTTCTGA	AGATGACCAA	CCTGGAGATT	1900
GGACAATGCC	AGATGGCTTG	TATAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAACTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2048

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: M90527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAG	CTCTCACTCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	TTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAGC	AAGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGGAAC	TATGGAATGC	550

AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGC	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGGCTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	AGGCTATAAC	CTACTCACAA	CTGGGATGGA	TGTCTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATTT	ACAATACAGA	950
CGAATACGTT	GCCTATCCAG	ACGATGAATT	GCAAGTCGCT	TCTACCATTG	1000
TTGATGTTTC	TAACGGTAAA	GTCATTGCC	AGCTAGGAGC	ACGCCATCAG	1050
TCAAGTAATG	TTTCCTTCGG	AATTAACCAA	GCAGTAGAAA	CAAACCGCGA	1100
CTGGGGATCA	ACTATGAAAC	CGATCACAGA	CTATGCTCCT	GCCTTGAGT	1150
ACGGTGTCTA	CGAGTCAACT	GCCACTATCG	TTCACGATGA	GCCCTATAAC	1200
TACCCTGGGA	CAAATACCCC	TGTTTATAAC	TGGGATAGGG	GCTACTTTGG	1250
CAACATCACC	TTGCAATACG	CCCTGCAACA	ATCGCGAAAC	GTCCCAGCCG	1300
TGGAAACTCT	AAACAAGGTC	GGACTCAACC	GCGCCAAGAC	TTTCCTAAAT	1350
GGTCTCGGAA	TCGACTACCC	AAGTATTCAC	TACTCAAATG	CCATTTCAAG	1400
TAACACAACC	GAATCAGACA	AAAAATATGG	AGCAAGTAGT	GAAAAGATGG	1450
CTGCTGCTTA	CGCTGCCTTT	GCAAATGGTG	GAACCTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	TAGTGATGGG	AGTGAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AAGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGAGT	TATGGAACTG	GACGAAATGC	CTATCTTGCT	1650
TGGCTCCCTC	AGGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGACGAGGA	1700
AATTGAAAAC	CACATCAAGA	CCTCTCAATT	TGTAGCACCT	GATGAACTAT	1750
TTGCTGGCTA	TACGCGTAAA	TATTCAATGG	CTGTATGGAC	AGGCTATTCT	1800
AACCGTCTGA	CACCACTTGT	AGGCAATGGC	CTTACGGTCG	CTGCCAAAGT	1850
TTACCGCTCT	ATGATGACCT	ACCTGTCTGA	AGGAAGCAAT	CCAGAGGATT	1900
GGAATATACC	AGAGGGGCTC	TACAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2049

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: URU-E159
- (C) ACCESSION NUMBER: AF139890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200

TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTTCAGTT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
TGTCGGAACT	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGACT	TATGGAACTG	GGCGTGGAGC	CTATCTTCCT	1650
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAATG	GAGAATTTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAA	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2050

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 8303; 35193
- (C) ACCESSION NUMBER: AF046230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050

CTGTGGGATA	TCTACAACTC	CGATCAATAC	GTCTCTTACC	CTGACGATGA	50
TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	TTCAAATGGT	AAAGTCATCG	100
CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	ACGTTTCATT	TGGTACCAAC	150
CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	TCTGCTATGA	AACCAATCAC	200
CGATTATGCA	CCTGCCATAG	AATACGGTGT	TTATGATTCC	ACTGCAACTA	250
TGGTTAATGA	TATTCCTTAT	AACTATCCGG	GAACAAGCAC	ACCTGTCTAC	300
AACTGGGATA	GAGCATATTT	CGGTAATATT	ACTCTGCAAT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AAGTAATACA	ACAGAATCTA	ATAAACAATA	500
CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	TTATGCTGCC	TTTGCAAATG	550
GTGGCACTTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTCAGTGAT	600
GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	700
CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	CTCAAGCTGG	TAAAACAGGA	750
ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	AACCACATCA	AGAACACTGG	800
CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	TAACTCCTAT	CGTTGGAGAT	900
GTTTTCCTAG	TTGCAGCTAA	AGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 63509; M11
- (C) ACCESSION NUMBER: AF046238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGATGATGA	50
CATGCAAGTA	GCTTCGACTA	TTGTAGATGT	ATCTAATGGT	AACGTTATTG	100
CACAACTTGG	TGCTCGTCAT	CAAGCAAGTA	ATGTTTCATT	CGGCACCAAC	150
CAGGCTGTGG	AGACCAATCG	TGACTGGGGT	TCTTCTATGA	AACCAATCAC	200
TGACTATGCT	CCCGCTTTAG	AATATGGAGT	CTATGACTCT	ACTGCTTCTA	250
TTGTACATGA	TGTTCCCTTAT	AACTATCCTG	GCACTGATAC	TCCAGTCTAC	300
AACTGGGATC	ATGTCTACTT	TGGAAACATT	ACAATCCAGT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AAGTAACACA	ACTGAATCCA	ACAAACAGTA	500
CGGTGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTATGCCGCC	TTTTCTAATG	550
GTGGTATTTA	CCACAAACCA	ATGTATATCA	ATAAAATCGT	CTTCAGTGAT	600
GGTAGTGAAA	AAGAATTTTC	TGATGCTGGT	ACACGAGCTA	TGAAAGAAAC	650
TACTGCCTAT	ATGATGACCG	AAATGATGAA	AACTGTTTTA	GCTTACGGAA	700
CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	CACAAGCAGG	TAAGACAGGT	750

ACTTCTAACT	ATACTGACGA	CGAAATTGAA	AAGTATATCA	AGAACACTGG	800
CTACGTAGCT	CCAGATGAAA	TGTTTGTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	TAACTCCAAT	CGTAGGAGAT	900
GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: #22/HA5
- (C) ACCESSION NUMBER: AB006877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052

GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	50
TTCCAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	100
ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	150
TCAACAATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	200
ATATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	250
GAACAAGCAC	ACCTGTCTAC	AACTGGGATC	GAGCATATTT	TGGTAATATT	300
ACTCTGCAAT	ATGCCCTTCA	ACAATCACGT	AATGTTACAG	CAGTTGAAAC	350
ATTAAACAAG	GTTGGTTTAG	ATCGAGCCAA	AACTTTCCTA	AATGGCTTAG	400
GTATCGATTA	CCCAAGCATA	CACTATGCTA	ACGCCATTTT	AAGTAATACA	450
ACAGAATCTA	ACAAACATTA	CGGTGCAAGT	AGTGAAAAAA	TGGCTGCTGC	500
TTATGCCGCC	TTTGCTAATG	GTGGTATTTA	CCACAAACCA	ATGTATATCA	550
ATAAAATCGT	CTTTAGTGAT	GGTAGTGAGA	AAGAATTTTC	TGATGCTGGT	600
ACACGAGCTA	TGAAAGAAAC	TACTGCCTAT	ATGATGACCG	AAATGATGAA	650
AACTGTTTTA	GCTTACGGAA	CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	700
CACAAGCAGG	TAAGACAGGT	ACTTCTAACT	ATACTGATGA	CGAAATCGAA	750
AAACATATCA	AGAATACTGG	CTACGTAGCT	CCAGATGAAA	TGTTTGTAGG	800
CTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	850
TAACTCCAAT	TGTTGGAGAT	GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC	900
TCAATGATAT	CGTATCTATC	AGAAGATGAC	CAACCTGGAG	ATTGGACGAT	950
GCCAGACGGC	CTGTTCCGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1000
GTTCTACGTG	GAACTCACCT	GCTCCACAAC	AACCCCCATC	AACTGAAAGT	1050
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1100
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1150
CAAATACAAC	CCCTGATCAA	CAAATCAGA	ATCCTCAACC	AGCAC	1195

2) INFORMATION FOR SEQ ID NO: 2053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 17619

(C) ACCESSION NUMBER: AF046237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	50
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	100
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	150
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	200
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	250
TCGTTACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	300
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	350
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	400
ACCGCGCCAA	GACTTTCCTA	AATGGTCTCG	GAATCGACTA	CCCAAGTATT	450
CACTACTCAA	ATGCCATTTT	AAGTAACACA	ACCGAATCAG	ACAAAAATA	500
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	550
GTGGAACCTA	CTATAAACCA	ATGFATATCC	ATAAAGTCGT	CTTTAGTGAT	600
GGGAGTGAAA	AAGAGTTCTC	TAATGTCCGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	AAATGATGAA	AACAGTCTTG	AGTTATGGAA	700
CTGGACGAAA	TGCCTATCTT	GCTTGGCTTC	CTCAAGCTGG	TAAAACAGGT	750
ACCTCTAACT	ATACAGATGA	AGAAATTGAA	AAACACATCA	AAAACACTGG	800
CTATGTAGCT	CCAGATGAAA	CGTTTGTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAC	ACAAACCGTC	TCACACCAAT	TGTGGGGGAT	900
GGCTTCACAG	TTGCTGCCAA	AGTTTACCGC			930

2) INFORMATION FOR SEQ ID NO: 2054

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: R6

(C) ACCESSION NUMBER: Y07845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054

CGTCGCATTC	TCTACGGAAT	GAATGAATTG	GGTGTGACCC	CAGACAAACC	50
CCATAAAAAA	TCTGCTCGTA	TTACAGGGGA	TGTCATGGGT	AAATACCACC	100
CACACGGGGA	TTCCTCTATT	TATGAAGCCA	TGGTCCGTAT	GGCTCAATGG	150
TGGAGCTACC	GTTACATGCT	TGTAGATGGT	CATGGGAATT	TTGGTTCCAT	200
GGATGGAGAT	AGTGCTGCCG	CTCAACGTTA	TACCGAGGCA	CGTATGAGCA	250
AGATTGCTCT	GGAAATGCTT	CGTGATATCA	ACAAAATAC	AGTTGATTTC	300
GTTGAT					306

2) INFORMATION FOR SEQ ID NO: 2055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 7785
- (C) ACCESSION NUMBER: Z67739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055

ATGTCTAACA	TTCAAAACAT	GTCCCTGGAG	GACATCATGG	GAGAGCGCTT	50
TGGTCGCTAC	TCCAAGTACA	TTATTCAAGA	CCGGGCTTTG	CCAGATATTC	100
GTGATGGGTT	GAAGCCGGTT	CAGCGCCGTA	TTCTTTATTC	TATGAATAAG	150
GATAGCAATA	CTTTTGACAA	GAGCTACCGT	AAGTCGGCCA	AGTCAGTCGG	200
GAACATCATG	GGGAATTTCC	ACCCACACGG	GGATTCTTCT	ATCTATGATG	250
CCATGGTTCG	TATGTCACAG	AACTGGAAAA	ATCGTGAGAT	TCTAGTTGAA	300
ATGCACGGTA	ATAACGGTTC	TATGGACGGA	GATCCTCCTG	CGGCTATGCG	350
TTATACTGAG	GCACGTTTGT	CTGAAATTGC	AGGCTACCTT	CTTCAGGATA	400
TCGAGAAAAA	GACAGTTCCT	TTTGCATGGA	ACTTTGACGA	TACGGAGAAA	450
GAACCAACGG	TCTTGCCAGC	AGCCTTTCCA	AACCTCTTGG	TCAATGGTTC	500
GACTGGGATT	TCGGCTGGTT	ATGCCACAGA	CATTCCTCCC	CATAATTTAG	550
CTGAGGTCAT	AGATGCTGCA	GTTTACATGA	TTGACCACCC	AACTGCAAAG	600
ATTGATAAAC	TCATGGAATT	CTTACCTGGA	CCAGACTTCC	CTACAGGGGC	650
TATTATTCAG	GGTCGTGATG	AAATCAAGAA	AGCTTATGAG	ACTGGGAAAG	700
GGCGCGTGGT	TGTTCGTTCC	AAGACTGAAA	TTGAAAAGCT	AAAAGGTGGT	750
AAGGAACAAA	TCGTTATTAC	TGAGATTCTT	TATGAAATCA	ATAAGGCCAA	800
TCTAGTCAAG	AAAATCGATG	ATGTTCTGTG	TAATAACAAG	GTAGCTGGGA	850
TTGCTGAGGT	TCGTGATGAG	TCTGACCGTG	ATGGTCTTCG	TATCGCTATC	900
GAACCTAAGA	AAGACGCTAA	TACTGAGCTT	GTTCTCAACT	ACTTATTTAA	950
GTACACCGAC	CTACAAATCA	ACTACAACTT	TAATATGGTG	GCGATTGACA	1000
ATTTACACAC	TCGTCAGGTT	GGGATTGTTC	CAATCCTGTC	TAGCTACATC	1050
GCTCACCGTC	GAGAAGTGAT	TTTGGCGCGT	TCACGCTTTG	ACAAAGAAAA	1100
GGCTGAGAAA	CGTCTCCATA	TCGTCGAAGG	TTTGATTTCG	GTGATTTTCA	1150
TTTTGGATGA	AGTCATTGCT	CTTATCCGTG	CTTCTGAGAA	TAAGGCGGAC	1200
GCCAAGGAAA	ACCTCAAAGT	TAGCTATGAT	TTTACGGAAG	AACAGGCTGA	1250
GGCTATCGTA	ACTTTGCAAC	TGTACCGTTT	GACCAATACC	GATGTGGTTG	1300
TCTTGACAGG	AGAAGAAGCA	GAGCTTCGTG	AGAAGATTGC	TATGCTGGCG	1350
GCTATTATCG	GTGATGAAAG	GACTATGTAC	AATCTCATGA	AGAAAGAACT	1400
TCGTGAGGTC	AAGAAGAAAT	TTGCAACTCC	TCGTTTGAGT	TCTTTAGAAG	1450
ACACTGCGAA	AGCAATTGAG	ATTGATACAG	CTAGTCTTAT	CGCTGAGGAA	1500
GATACCTACG	TCAGCGTGAC	CAAGGCAGGT	TACATCAAGC	GTACCAGTCC	1550
ACGTTCTTTT	GCGGCTTCCA	CCTTGGAAGA	AATTGGCAAG	CGTGATGATG	1600
ACCGTTTGAT	TTTTGTTCAA	TCTGCCAAGA	CAACCCAGCA	CCTCTTGATG	1650
TTCACAAGTC	TTGGAAATGT	CATCTACAGA	CCAATCCATG	AGTTGGCAGA	1700
TATTCGTTGG	AAGGACATCG	GAGAGCATCT	GAGCCAAACC	ATCACAAACT	1750
TTGAAACGAA	TGAAGAAATC	CTTTATGTGG	AAGTACTGGA	TCAGTTTGAC	1800
GATGCGACAA	CCTACTTTGC	AGTGACTCGC	CTTGGTCAAA	TCAAACGGGT	1850

AGAGCGAAAA	GAATTCCTC	CATGGCGGAC	CTATAGATCT	AAGTCTGTCA	1900
AGTATGCTAA	GCTCAAAGAC	GATACAGATC	AGATTGTAGC	AGTGGCTCCG	1950
ATTAAACTAG	ATGATGTTGT	CTTGGTTAGT	CAAAATGGTT	ATGCCCTGCG	2000
TTTCAATATC	GAAGAGGTTC	CGGTTGTCCG	TGCTAAGGCA	GCAGGTGTCA	2050
AGGCTATGAA	TTTGAAAGAA	GATGATGTCC	TCCAATCTGG	CTTTATCTGT	2100
AATACTTCGT	CCTTCTACCT	CTTGACCCAG	CGTGGAAGCT	TGAAACGTGT	2150
TTCTATTGAG	GAAATTCTAG	CAACCAGCCG	TGCCAAACGA	GGATTACAAG	2200
TCTTGCGTGA	GTTGAAAAAC	AAACCGCATC	GTGTCTTCTT	GGCAGGAGCA	2250
GTTGCAGAGC	AAGGATTTGT	TGGCGATTTC	TTCAGTACGG	AAGTGGATGT	2300
GAACGACCAA	ACTCTGCTTG	TCCAATCCAA	TAAAGGAACA	ATCTATGAAA	2350
GCCGATTGCA	AGACTTGAAC	TTGTCAGAAC	GCACTAGCAA	TGGAAGCTTC	2400
ATTTCTGACA	CGATTTGAGA	TGAAGAAGTT	TTTGACGCTT	ATCTTCAGGA	2450
AGTAGTTACT	GAAGATAAAT	AA			2472

2) INFORMATION FOR SEQ ID NO: 2056

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTA	ATGTTTCAAA	100
TGGTAAAGTC	ATTGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
CATTTGGCAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCAACA	200
ATGAAACCAA	TCACAGACTA	TGCTCCTGCC	TTGGAATACG	GTGTCTACGA	250
TTCAACTGCT	ACTATCGTTC	ACGATGAGCC	CTATAACTAT	CCTGGGACAG	300
ATACCCCTGT	CTATAACTGG	GATAGGGGCT	ACTTTGGCAA	TATCACCTTG	350
CAATACGCCC	TGCAACAATC	GCGAAACGTC	CCAGCCGTGG	AAACACTAAA	400
CAAGGTCGGG	CTCAACCGCG	CCAAGACTTT	TCTAAATGGT	CTCGGAATCG	450
ACTACCCAAG	TATTCACTAC	TCAAATGCCA	TTTCAAGTAA	CACAACCGAG	500
TCAGACAAAA	AATATGGAGC	AAGTAGTGAA	AAGATGGCTG	CTGCTTACGC	550
TGCCTTTGCA	AATGGTGGAA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
TCGTCTTTAG	TGATGGAAGT	GAAAAAGAGT	TCTCTAATGT	CGGAACTCGC	650
GCCATGAAAG	AAACGACTGC	TTACATGATG	ACAGAAATGA	TGAAAACAGT	700
CTTGACGTAC	GGAATTGGTC	GTGGTGCCTA	CCTGCCTTGG	CTTCCTCAAG	750
CTGGTAAAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AACTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TATGGACAGG	CTATTCTAAC	CGTCTGACAC	900
CACTTGTAGG	CGATGGCCTT	ACGGTCGCTG	CCAAGGTTTA	CCGCTCTATG	950
ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TC				1212

2) INFORMATION FOR SEQ ID NO: 2057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057

ATGTAGACCA	AGAAGCTCAA	AAACATCTGT	GGGATATTTA	CAATACAGAC	50
GAATACGTTG	CCTATCCAGA	CGATGAATTG	CAAGTCGCTT	CTACCATTTGT	100
TGATGTTTCT	AACGGGAAAG	TTATTGCTCA	GTTAGGTTCT	CGTCACCAAT	150
CAAGCAATGT	TTCTTCGGA	ATCAACCAAG	CTGTTGAAAC	CAACCGTGAC	200
TGGGGTTCTG	CCATGAAGCC	AATCACAGAC	TATGCTCCTG	CCTTAGAGTA	250
TGACATCTAC	GACTCAACTG	CTTCGATTGT	ACATGATGTT	CCTTATAACT	300
ATCCAGGTAC	TGATACTCCC	CTCTACAAC	GGGATAAAGT	CTACTTTGGA	350
AATATTACAA	TCCAGTATGC	ACTTCAACAG	TCACGTAATG	TCACAGCCGT	400
TGAGACTTTG	AATAAGGTCG	GTCTAGATAG	AGCTAAAACC	TTTCTTAATG	450
GTCTTGGTAT	CGACTATCCA	AGCATGCATT	ATGCAAACGC	CATTTCAAGT	500
AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	AGAAAATGGC	550
TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	AAACCAATGT	600
ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	ATACGCTGAT	650
CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	TGACAGAAAT	700
GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	TATCTCCCTT	750
GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATATAC	AGATGATGAA	800
ATTGAAACT	ACATCAAAAA	TACTGGTTAT	GTAGCTCCAG	ACGAAATGTT	850
TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	GGTATGGACA	GGTTACTCAA	900
ACCGCCTGAC	TCCTATCGTT	GGTGATGGCT	TCTATGTTGC	AGCTAAGGTT	950
TACCGTTCAA	TGATGACTTA	TCTGTCTGAG	GATAACAACC	CTGGCGACTG	1000
GACTATGCCA	GAAGGTCTCT	ATCGAAGTGG	TGAGTTCGTC	TTTAAAAAAG	1050
GTGCTCGTTC	TGCATGGACT	GCTCCTGCTC	CGCAACAGGC	CCCAACACCA	1100
GAAAGTTCGA	GCTCGACATC	AGAAAGTTCA	ACTTCACAGT	CAAGCTCAAC	1150
TACTCCAAGC	ACGAATAATA	GTGCAAACAA	TAATACCAAT	AACCAGCAAC	1200
CAAATACAAC	GCCTGGTCAA	CAAAACCAGA	ACCAAAATCA	GA	1242

2) INFORMATION FOR SEQ ID NO: 2058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058

GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	AATACGTTGC	50
CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	GATGTTTCTA	100
ACGGGAAAGT	TATTGCTCAG	TTAGGTTCTC	GTCACCAATC	AAGCAATGTT	150
TCCTTCGGAA	TCAACCAAGC	TGTTGAAACC	AACCGTGACT	GGGGTTCTGC	200
CATGAAGCCA	ATCACAGACT	ATGCTCCTGC	CTTAGAGTAT	GACATCTACG	250
ACTCAACTGC	TTCGATTGTA	CATGATGTTC	CTTATAACTA	TCCAGGTACT	300
GATACTCCCC	TCTACAACTG	GGATAAAGTC	TACTTTGGAA	ATATTACAAT	350
CCAGTATGCA	CTTCAACAGT	CACGTAATGT	CACAGCCGTT	GAGACTTTGA	400
ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TTCTTAATGG	TCTTGGTATC	450
GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	ATACGACTGA	500
GTCAAACAAA	AAGTACGGAG	CAAGTAGTGA	GAAAATGGCT	GCTGCTTACG	550
CTGCTTTTGC	TAACGGTGGT	ATCTACCATA	AACCAATGTA	TATCAACAAA	600
ATCGTCTTTA	GCGATGGTAG	CTCAAAAGAA	TACGCTGATC	CTGGTACTCG	650
TGCCATGAAA	GAGACGACCG	CCTATATGAT	GACAGAAATG	ATGAAGACTG	700
TCTTGGCATA	CGGAACGGGT	CGTGGTGCTT	ATCTCCCTTG	GCTACCTCAA	750
GCTGGTAAGA	CTGGTACATC	AAACTATACA	GATGATGAAA	TTGAAAATA	800
CATCAAAAAT	ACTGGTTATG	TAGCTCCAGA	CGAAATGTTT	GTTGGTTATA	850
CTCGCAAATA	TTCAATGGCG	GTATGGACAG	GTTACTCAAA	CCGCCTGACT	900
CCTATCGTTG	GTGATGGCTT	CTATGTTGCA	GCTAAGGTTT	ACCGTTCAAT	950
GATGACTTAT	CTGTCTGAGG	ATAACAACCC	TGGCGACTGG	ACTATGCCAG	1000
AAGGTCTCTA	TCGAAGTGGT	GAGTTCGTCT	TTAAAAAAGG	TGCTCGTTCT	1050
GCATGGACTG	CTCCTGCTCC	GCAACAGGCC	CCAACACCAG	AAAGTTCGAG	1100
CTCGACATCA	GAAAGTTCAA	CTTCACAGTC	AAGCTCAACT	ACTCCAAGCA	1150
CGAATAATAG	TGCAAACAAT	AATACCAATA	ACCAGCAACC	AAATACAACG	1200
CCTGGTCAAC	AAAACCAGAA	CCAAA			1225

2) INFORMATION FOR SEQ ID NO: 2059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059

TGGCTACTTT	GGAAACATTA	CAGTCCAGTA	TGCTCTTCAA	CAATCACGAA	50
ATGTCACAGC	CGTTGAGACT	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	100
ACCTTCCTCA	ATGGACTTGG	TATCGATTAT	CCAAGCATGC	TTTATGCAAA	150
CGCCATTTCA	AGTAACACAA	CTGAATCCAA	CAAAAAGTAC	GGAGCAAGTA	200
GTGAAAAAAT	GGCCGCTGCC	TACGCAGCTT	TTGCTAATGG	TGGTACTTAC	250
CACAAACCAA	TGTATATCAA	TAAAATCGTC	TTTAGTGATG	GTAGTGAAAA	300
AGAATTTTCT	GATGCCGGTA	CTCGGGCTAT	GAAAGAAACT	ACTGCCTATA	350

TGATGACCGA	AATGATGAAA	ACTGTCTTAT	TATACGGAAC	CGGACGTGGA	400
GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	450
TACTGACGAA	GAAATTGAAA	AGTATATCAA	GAATGCTGGT	TACGTAGCTC	500
CAGATGAAAT	GTTTGTGGT	TATACCCGCA	AATATGCAAT	GGCTGTTTGG	550
ACAG					554

2) INFORMATION FOR SEQ ID NO: 2060

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060

CAACTGGGAT	GGATGTCTAC	ACAAATGTAG	ACCAAGAAGC	TCAAAAACAT	50
CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	100
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	150
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	200
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	250
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	300
TCGTTACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	350
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	400
ACAATCGCGA	AACGTCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	450
ACCGCGCCAA	GACTTTCCTA	AATGGTCTAG	GAATCGACTA	CCCAAGTATT	500
CACTACTCAA	ATGCCATTTC	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	550
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	600
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	650
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	700
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	750
CTGGACGAAA	TGCCTATCTT	GCTTGGCTCC	CTCAGGCTGG	TAAACAGGA	800
ACCTCTAACT	ATACAGACGA	GGAAATTGAA	AACCACATCA	AGACCTCTCA	850
ATTTGTAGCA	CCTGATGAAC	TATTTGCTGG	CTATACGCGT	AAATATTCAA	900
TGGCTGTATG	GACAGGCTAT	TCTAACCGTC	TGACACCACT	TGTAGGCAAT	950
GGCCTTACGG	TCGCTGCCAA	AGTTTACCGC	TCTATGATGA	CCTACCTGTC	1000
TGAAGGAAGC	AATCCAGAAG	ATTGGAATAT	ACCAGAGGGG	CTCTACAGAA	1050
ATGGAGAATT	CGTATTTTAA	AATGGTGCTC	GTTCTACGTG	GAGCTCACCT	1100
GCTCCACAAC	AACCCCCATC	AACTGAAAGT	TCAAGCTCAT	CATCAGATAG	1150
TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	AAGCACAAAT	AATAGTACGA	1200
CTACCAATCC	TAACAATAAT	ACGCAACAAT	CAAATACAAC	CCCTGATCA	1249

2) INFORMATION FOR SEQ ID NO: 2061

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061

GAAGTTGAAC	AGACTGGTCA	CCAAGCTCCT	TCATATCCGC	CAACACTGCA	50
ATTTTCTTGC	CACCTTCATT	GGCTGGAATG	GCAGAGAAAG	TCTCTAAAAT	100
CAGTTTCATA	GCAGTTGGAT	TGGCATTATA	AACATCTGAC	AGGATATCTG	150
CTCCATTGGC	TGCTTTCTTC	CACTCGGTAC	GGTTACGCGT	CAATTCAAGA	200
TGTTGGAAGG	CCAAACGAAT	TTGCTCCTCT	GAAACTCCTT	CTTGCAAGGC	250
AACATAGGAT	GCAATCATAG	CATTTGTCGC	ATTGTACTTG	CCAGTTACTG	300
GCAAATCAAG	GGCTTGCTCT	AAGAAATTGA	CCTTGAAGGT	CAGACTATCT	350
TTGCGCTCAA	CCAAGTCGGT	AATTCCCAGC	TCTGCTCCTT	GACCAAAACG	400
AACCACCTTT	TTATCAGTTG	GCAAATAGTC	CTCTACGATA	GGGTCAGCCG	450
GCGCTAAAAG	CAAGGAACCT	GAAGCCATTC	CGTCTGCAAT	TTGCATTTT	500
CCTTTAGCAA	TCTCAGAACG	GTCTTTGAAA	AAGGCCAAAT	GAGCTTCTCC	550
AACCAAGGTC	ACGATGGCTG	TATGGACAG			579

2) INFORMATION FOR SEQ ID NO: 2062

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCACAAC	TTGGTGCTCG	TCATCAAGCA	AGTAATGTTT	150
CATTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	GGGATCATCA	200
ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	GAGTCTATGA	250
CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	CCTGGCACTG	300
ATACTCCACT	CTACAACCTG	GATCATGTCT	ACTTTGGAAA	CATTACAATC	350
CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	CACAACTGAA	500
TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	CTGCCTACGC	550
TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	ATCAATAAAA	600
TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	TGGTACACGA	650
GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	TGAAAACCTGT	700
TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	CTTCCACAAG	750

CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AGCTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TTTGGACAGG	ATACTCAAAT	CGTCTAACTC	900
CAATCATCGG	AGATGGTTTC	CTTGTGCTG	GTAAAGTCTA	TCGTTCAATG	950
ATAACTTACC	TTTCTGAAGA	TGACCAACCT	GGAGATTGGA	CAATGCCAGA	1000
TGGCTTGTAT	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TCAACA				1216

2) INFORMATION FOR SEQ ID NO: 2063

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063

AATACGTCTC	TTACCCTGAC	GATGATTTC	AAGTCGCATC	CACGGTCGTA	50
GATGTTTCAA	ATGGTAAAGT	CATCGCCCAA	CTTGGAGCTC	GTCACCAAGC	100
AAGTAACGTT	TCATTTGGTA	CCAACCAAGC	TGTGGAAACC	AATCGTGACT	150
GGGGTTCAAC	AATGAAACCC	ATCACCGATT	ATGCACCTGC	CATAGAATAC	200
GGTGTATATG	ATTCCACTGC	AACTATGGTT	AATGATATTC	CTTATAACTA	250
TCCGGGAACA	AGCACACCTG	TCTACAACCTG	GGATCGAGCA	TATTTTGGTA	300
ATATTACTCT	GCAATATGCC	CTTCAACAAT	CTCGTAACGT	ACCCGCCGTT	350
GAGACACTAA	ACAAGGTTGG	TTTAGATAGA	GCTAAAAGTT	TCCTAAATGG	400
TTTAGGAATC	GACTATCCTG	TAATGCACTA	TTCAAATGCT	ATTTCAAGTA	450
ATACTACCGA	ATCTAGTAAA	CAGTACGGGG	CAAGTAGTGA	AAAAATGGCC	500
ACTGCCTATG	CCGCATTTCG	AAACGGCGGT	ATTTACCACA	AACCAATGTA	550
CATCAATAAG	GTTGTCTTTA	GCGATGGTAG	CGAAAAAGAA	TTTTCTGACC	600
CTGGCACAAG	AGCCATGAAA	GAAACGACTG	CTTACATGAT	GACAGAGATG	650
ATGAAAACAG	TCTGGACTTA	CGGAACTGGT	CGCGGTGCCT	ACCTACCTTG	700
GCTTCCACAA	GCAGGTAAAA	CAGGTACTTC	TAAGTATACT	GACGAAGAAA	750
TTGAAAAGTA	TATCAAGAAC	ACTGGTTACG	TAGCTCCAGA	TGAAATGTTT	800
GTAGGGTATA					810

2) INFORMATION FOR SEQ ID NO: 2064

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: ATCC 700678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064

TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	TAGATGTTTC	50
AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	GCAAGTAACG	100
TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	CTGGGGATCA	150
ACTATGAAAC	CAATCACAGA	CTATGCTCCT	GCCTTGGAGT	ACGGTGTCTA	200
CGATTCAACT	GCTACTATCG	TTCACGATGA	GCCCTATAAC	TACCCTGGGA	250
CAGATATCCC	TCTCTATAAC	TGGGATCGAG	CATATTTTCG	TAATATTACT	300
CTGCAATATG	CCCTTCAACA	ATCTCGTAAC	GTACCTGCCG	TTGAAACACT	350
AAACAAGGTC	GGTCTAGATA	AGGCTAAAAC	CTTCCTTAAT	GGTCTTGGTA	400
TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	TAATACAAC	450
GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATAG	CTACCGCCTA	500
TGCCGCATTC	GCAAATGGTG	GTATTTACCA	CAAACCAATG	TACATCAATA	550
AAGTTGTCTT	TAGCGATGGT	AGCGAAAAAG	AATTTTCTGA	CCCTGGCACA	600
AGAGCCATGA	AAGAAACGAC	TGCTTACATG	ATGACAGAAA	TGATGAAAAC	650
AGTCTGGACG	TACGGAAC	GTCGTGGTGC	CTACCTGCCT	TGGCTTCCTC	700
AAGCTGGTAA	AACAGGTACC	TCTAACTATA	CTGACGAAGA	AATTGAAAAG	750
TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GA		782

2) INFORMATION FOR SEQ ID NO: 2065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2065

CCAGGACGTG GAGGCGATCA CA

22

2) INFORMATION FOR SEQ ID NO: 2066

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066

CACCGACAGC GAGCCGATCA GA

22

2) INFORMATION FOR SEQ ID NO: 2067

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067

AGCTGAGCCA ATTCATGG

18

2) INFORMATION FOR SEQ ID NO: 2068

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

ATTCATGGAC CAGAACAAC

19

2) INFORMATION FOR SEQ ID NO: 2069

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069

CGCTGTCGGG GTTGACCC

18

2) INFORMATION FOR SEQ ID NO: 2070

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1073

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070

GTGACCCAC AAGCGCCG

18

2) INFORMATION FOR SEQ ID NO: 2071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071

CGACTGTCGG CGCTGGGG

18

2) INFORMATION FOR SEQ ID NO: 2072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: Rv
- (C) ACCESSION NUMBER: L27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072

GTGCTGGAAG	GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCCGC	50
TAGTCCTAGT	CCGAGTCGCC	CGCAAAGTTC	CTCGAATAAC	TCCGTACCCG	100
GAGCGCCAAA	CCGGGTCTCC	TTGCTAAGC	TGCGCGAACC	ACTTGAGGTT	150
CCGGGACTCC	TTGACGTCCA	GACCGATTCC	TTGAGTGGC	TGATCGGTTC	200
GCCGCGCTGG	CGCGAATCCG	CCGCCGAGCG	GGGTGATGTC	AACCCAGTGG	250
GTGGCCTGGA	AGAGGTGCTC	TACGAGCTGT	CTCCGATCGA	GGACTTCTCC	300
GGGTCGATGT	CGTTGTCTGT	CTCTGACCCT	CGTTTCGACG	ATGTCAAGGC	350
ACCCGTCGAC	GAGTGCAAAG	ACAAGGACAT	GACGTACGCG	GCTCCACTGT	400
TCGTCACCGC	CGAGTTCATC	AACAACAACA	CCGGTGAGAT	CAAGAGTCAG	450
ACGGTGTTCA	TGGGTGACTT	CCCGATGATG	ACCGAGAAGG	GCACGTTCAT	500
CATCAACGGG	ACCGAGCGTG	TGGTGGTCAG	CCAGCTGGTG	CGGTCGCCCC	550
GGGTGTACTT	CGACGAGACC	ATTGACAAGT	CCACCGACAA	GACGCTGCAC	600
AGCGTCAAGG	TGATCCCGAG	CCGCGGCGCG	TGGCTCGAGT	TTGACGTCGA	650
CAAGCGCGAC	ACCGTCGGCG	TGCGCATCGA	CCGCAAACGC	CGGCAACCGG	700

1074

TCACCGTGCT	GCTCAAGGCG	CTGGGCTGGA	CCAGCGAGCA	GATTGTCGAG	750
CGGTTCGGGT	TCTCCGAGAT	CATGCGATCG	ACGCTGGAGA	AGGACAACAC	800
CGTCGGCACC	GACGAGGCGC	TGTTGGACAT	CTACCGCAAG	CTGCGTCCGG	850
GCGAGCCCCC	GACCAAAGAG	TCAGCGCAGA	CGCTGTTGGA	AAACTTGTTC	900
TTCAAGGAGA	AGCGCTACGA	CCTGGCCCCG	GTCGGTCGCT	ATAAGGTCAA	950
CAAGAAGCTC	GGGCTGCATG	TCGGCGAGCC	CATCACGTCC	TCGACGCTGA	1000
CCGAAGAAGA	CGTCGTGGCC	ACCATCGAAT	ATCTGGTCCG	CTTGACAGAG	1050
GGTCAGACCA	CGATGACCGT	TCCGGGCGGC	GTCGAGGTGC	CGGTGGAAAC	1100
CGACGACATC	GACCACTTCG	GCAACCGCCG	CCTGCGTACG	GTCGGCGAGC	1150
TGATCCAAAA	CCAGATCCGG	GTCGGCATGT	CGCGGATGGA	GCGGGTGGTC	1200
CGGGAGCGGA	TGACCACCCA	GGACGTGGAG	GCGATCACAC	CGCAGACGTT	1250
GATCAACATC	CGGCCGGTGG	TCGCCGCGAT	CAAGGAGTTC	TTCCGGCACCA	1300
GCCAGCTGAG	CCAATTCATG	GACCAGAACA	ACCCGCTGTC	GGGGTTGACC	1350
CACAAGCGCC	GACTGTCGGC	GCTGGGGCCC	GGCGGTCTGT	CACGTGAGCG	1400
TGCCGGGCTG	GAGGTCCGCG	ACGTGCACCC	GTCGCACTAC	GGCCGGATGT	1450
GCCCGATCGA	AACCCCTGAG	GGGCCCAACA	TCGGTCTGAT	CGGCTCGCTG	1500
TCGGTGTACG	CGCGGGTCAA	CCCGTTCGGG	TTCATCGAAA	CGCCGTACCG	1550
CAAGGTGGTC	GACGGCGTGG	TTAGCGACGA	GATCGTGTAC	CTGACCGCCG	1600
ACGAGGAGGA	CCGCCACGTG	GTGGCACAGG	CCAATTCGCC	GATCGATGCG	1650
GACGGTCGCT	TCGTGAGGCC	GCGCGTGCTG	GTCCGCCGCA	AGGCGGGCGA	1700
GGTGGAGTAC	GTGCCCTCGT	CTGAGGTGGA	CTACATGGAC	GTCTCGCCCC	1750
GCCAGATGGT	GTCGGTGGCC	ACCGCGATGA	TTCCTTCCT	GGAGCACGAC	1800
GACGCCAACC	GTGCCCTCAT	GGGGGCAAAC	ATGCAGCGCC	AGGCGGTGCC	1850
GCTGGTCCGT	AGCGAGGCC	CGCTGGTGGG	CACCGGGATG	GAGCTGCGCG	1900
CGGCGATCGA	CGCGGCGACG	TCGTGTCGCG	AAGAAAGCGG	CGTCATCGAG	1950
GAGGTGTCCG	CCGACTACAT	CACTGTGATG	CACGACAACG	GCACCCGGCG	2000
TACCTACCGG	ATGCGCAAGT	TTGCCCGGTC	CAACCACGGC	ACTTGCGCCA	2050
ACCAGTGCCC	CATCGTGGAC	GCGGGCGACC	GAGTCGAGGC	CGGTCAGGTG	2100
ATCGCCGACG	GTCCCTGTAC	TGACGACGGC	GAGATGGCGC	TGGGCAAGAA	2150
CCTGCTGGTG	GCCATCATGC	CGTGGGAGGG	CCACAACCTAC	GAGGACGCGA	2200
TCATCCTGTC	CAACCGCCTG	GTCGAAGAGG	ACGTGCTCAC	CTCGATCCAC	2250
ATCGAGGAGC	ATGAGATCGA	TGCTCGCGAC	ACCAAGCTGG	GTGCGGAGGA	2300
GATCACCCGC	GACATCCCGA	ACATCTCCGA	CGAGGTGCTC	GCCGACCTGG	2350
ATGAGCGGGG	CATCGTGCGC	ATCGGTGCCG	AGGTTGCGCA	CGGGGACATC	2400
CTGGTCGGCA	AGGTCACCCC	GAAGGGTGAG	ACCGAGCTGA	CGCCGGAGGA	2450
GCGGCTGCTG	CGTGCCATCT	TCGGTGAGAA	GGCCCGCGAG	GTGCGCGACA	2500
CTTCGCTGAA	GGTGCCGCAC	GGCGAATCCG	GCAAGGTGAT	CGGCATTCCG	2550
GTGTTTTCCC	GCGAGGACGA	GGACGAGTTG	CCGGCCGGTG	TCAACGAGCT	2600
GGTGCGTGTC	TATGTGGCTC	AGAAACGCAA	GATCTCCGAC	GGTGACAAGC	2650
TGGCCGGCCG	GCACGGCAAC	AAGGGCGTGA	TCGGCAAGAT	CCTGCCGGTT	2700
GAGGACATGC	CGTTCCTTGC	CGACGGCACC	CCGGTGGACA	TTATTTTGAA	2750
CACCCACGGC	GTGCCGCGAC	GGATGAACAT	CGGCCAGATT	TTGGAGACCC	2800
ACCTGGGTTG	GTGTGCCAC	AGCGGCTGGA	AGGTCGACGC	CGCCAAGGGG	2850
GTTCCGGACT	GGGCCGCCAG	GCTGCCCGAC	GAAGTCTCG	AGGCGCATGC	2900
GAACGCCATT	GTGTCGACGC	CGGTGTTCTGA	CGGCGCCAG	GAGGCCGAGC	2950
TGCAGGGCCT	GTTGTGCTGC	ACGCTGCCCA	ACCGCGACGG	TGACGTGCTG	3000
GTCGACGCCG	ACGGCAAGGC	CATGCTCTTC	GACGGGCGCA	GCGGCGAGCC	3050
GTTCCCGTAC	CCGGTCACGG	TTGGCTACAT	GTACATCATG	AAGCTGCACC	3100
ACCTGGTGGA	CGACAAGATC	CACGCCCCTG	CCACCGGGCC	GTACTCGATG	3150
ATCACCCAGC	AGCCGCTGGG	CGGTAAGGCG	CAGTTCGGTG	GCCAGCGGTT	3200
CGGGGAGATG	GAGTGCTGGG	CCATGCAGGC	CTACGGTGCT	GCCTACACCC	3250
TGCAGGAGCT	GTTGACCATC	AAGTCCGATG	ACACCGTCCG	CCGCGTCAAG	3300
GTGTACGAGG	CGATCGTCAA	GGGTGAGAAC	ATCCCGGAGC	CGGGCATCCC	3350
CGAGTCGTTC	AAGGTGCTGC	TCAAAGAACT	GCAGTCGCTG	TGCCTCAACG	3400
TCGAGGTGCT	ATCGAGTGAC	GGTGCGGCGA	TCGAACTGCG	CGAAGGTGAG	3450
GACGAGGACC	TGGAGCGGGC	CGCGGCCAAC	CTGGGAATCA	ATCTGTCCCG	3500
CAACGAATCC	GCAAGTTTCG	AGGATCTTGC	GTAA		3534

2) INFORMATION FOR SEQ ID NO: 2073

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073

CCGAGCAACA TGATTGAACC ATCCACCAAC TGGCTCGG 38

2) INFORMATION FOR SEQ ID NO: 2074

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074

CCGAGCAACA TGATTGAAGC TTCCACCAAC TGGCTCGG 38

2) INFORMATION FOR SEQ ID NO: 2075

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075

CCGAGCCAGG TTCTGAAGTC TCTGCATTAT TAGGTGCTCG G 41

2) INFORMATION FOR SEQ ID NO: 2076

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1076

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076

CCGAGCYGAY AACATTTTCA GATTCACCCA RCGCTCGG

39

2) INFORMATION FOR SEQ ID NO: 2077

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077

CCGAGCAACC GATCCAGCTC CAGCTACGCT CGG

33

2) INFORMATION FOR SEQ ID NO: 2078

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078

CCGAGCCTTG GTCTTCGGCC AAATGAACGC TCGG

34

2) INFORMATION FOR SEQ ID NO: 2079

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079

CCGAGCGTTC AGTTACTTCA GTCCAAGCCG GCTCGG

36

2) INFORMATION FOR SEQ ID NO: 2080

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080

CCGAGCCGAA GAGGGCCAAG ATGTCGCTCG G

31

2) INFORMATION FOR SEQ ID NO: 2081

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081

GRATYRTYAA AGTTGGTGAG GAAG

24

2) INFORMATION FOR SEQ ID NO: 2082

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082

CMACTTCATC YCGCTTCGTA CC

22

2) INFORMATION FOR SEQ ID NO: 2083

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1078

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083

CCGCCGATGT TCCGTAAATT ACTTGAIGAA GGTCGAGCCG GCGG

44

2) INFORMATION FOR SEQ ID NO: 2084

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084

CACGCGTCAA CACCCGTACA AGTCGTCTTT TGC GCGTG

38

2) INFORMATION FOR SEQ ID NO: 2085

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085

CAA ACTAAAG AACATATCTT GCTA

24

2) INFORMATION FOR SEQ ID NO: 2086

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086

ATATAATTTG CATCACCTTC AAG

23

2) INFORMATION FOR SEQ ID NO: 2087

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087

TCAGCTCGTG GGATTAGGAG AG

22

2) INFORMATION FOR SEQ ID NO: 2088

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088

AGGCTTCACG CTGTTAGGCT GA

22

2) INFORMATION FOR SEQ ID NO: 2089

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089

ATGCTGAACT TATTGACCTT

20

2) INFORMATION FOR SEQ ID NO: 2090

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1080

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090

CGTTACTGGA GTCGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2091

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091

CGCGACTTGA GATGGAACTT AGTGAGCTTC TTGGTCGCG

39

2) INFORMATION FOR SEQ ID NO: 2092

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092

CGCGACGAAA GAACTTCCTG AAGGTCGTGC AGGTCCAG

38

2) INFORMATION FOR SEQ ID NO: 2093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093

TGTTGGCAAT CGAAGACACC

20

2) INFORMATION FOR SEQ ID NO: 2094

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094

TTCAATTTCT TGACCTACTT TCAA

24

2) INFORMATION FOR SEQ ID NO: 2095

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095

CGGTCGGGTT GAACGTGG

18

2) INFORMATION FOR SEQ ID NO: 2096

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096

CGCGACCGGT ACCACGGCCA GTAATCGTGT CGCG

34

2) INFORMATION FOR SEQ ID NO: 2097

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1185 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1082

- (A) ORGANISM: *Mycoplasma pneumoniae*
 (B) STRAIN: ATCC 29342
 (C) ACCESSION NUMBER: AE000019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097

ATGGCAAGAG	AGAAATTTGA	CCGATCTAAA	CCCCACGTTA	ATGTAGGTAC	50
TATTGGCCAC	ATTGACCACG	GTAACAACAAC	TTTAACAGCA	GCTATTTGTA	100
CTGTATTAGC	AAAAGAAGGT	AAATCAGCTG	CTACTCGTTA	CGACCAAATC	150
GATAAGGCTC	CGGAAGAAAA	AGCACGGGGA	ATTACGATTA	ACTCCGCTCA	200
CGTGGAGTAC	TCCTCTGACA	AGCGTCACTA	TGCTCACGTT	GACTGTCCAG	250
GACACGCTGA	CTACATTAAG	AACATGATTA	CTGGTGCTGC	ACAAATGGAT	300
GGTGCCATTC	TAGTAGTTTC	AGCAACTGAC	AGTGTTATGC	CCCAAACCCG	350
TGAACACATT	TTGTTGGCCC	GCCAAGTGGG	TGTGCCACGC	ATGGTAGTGT	400
TCCTAAACAA	GTGTGACATT	GCAACTGATG	AAGAAGTGCA	AGAGTTAGTA	450
GCAGAAGAGG	TACGTGACTT	ATTAACCTTCT	TACGGCTTTG	ATGGCAAGAA	500
CACCCCTATT	ATTTATGGTT	CTGCACTTAA	AGCGCTTGAA	GGTGATCCTA	550
AGTGGGAAGC	TAAGATCCAT	GATTTAATGA	ATGCAGTTGA	TGAATGGATT	600
CCAACCTCCTG	AACGTGAAGT	GGACAAACCC	TTCTTGTTGG	CAATCGAAGA	650
CACCATGACG	ATTACTGGCC	GTGGTACCGT	GGTTACCGGT	CGGGTTGAAC	700
GTGGTGAATT	GAAAGTAGGT	CAAGAAATTG	AAATCGTTGG	TTTACGTCCA	750
ATCCGTAAAG	CAGTTGTTAC	CGGAATCGAA	ATGTTCAAAA	AGGAACTTGA	800
TTCAGCAATG	GCTGGGGACA	ACGCTGGGGT	ATTACTCCGT	GGTGTGGACC	850
GTAAAGAAGT	GGAACGTGGT	CAAGTGTTAG	CTAAACCAGG	TTCGATTAAA	900
CCGCACAAGA	AATTTAAAGC	GGAAATCTAT	GCTTTAAAGA	AGGAAGAAGG	950
TGGTCGTCAC	ACCGGTTTCT	TAAACGGTTA	CCGTCCCCAA	TTCTACTTCC	1000
GTACTACAGA	CGTTACTGGT	TCGATTTCCT	TACCAGAAAA	CACCGAAATG	1050
GTGCTACCAG	GTGACAATAC	CTCGATTACA	GTTGAACTAA	TTGCACCAAT	1100
TGCTTGTGAA	AAAGGTAGTA	AGTTCTCCAT	CCGTGAAGGT	GGTCGAACGG	1150
TTGGTGCTGG	TTCAGTCACG	GAAGTGCTTG	AATAG		1185

2) INFORMATION FOR SEQ ID NO: 2098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098

CTGAGTCACA CCGACAAACG TC

22

2) INFORMATION FOR SEQ ID NO: 2099

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099

CCAGGACTGA ACGGGATACG AA

22

2) INFORMATION FOR SEQ ID NO: 2100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100

GCGAGACGAT AGGTTGTC

18

2) INFORMATION FOR SEQ ID NO: 2101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv
- (C) ACCESSION NUMBER: Z79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101

CAGCCCGCGA	GCGTAACCTG	GCTGCGATTT	CCGGCGCGGA	TTTTCGCAGT	50
GCGGTTACGC	TCGGAAAGCG	CGGGCCTCGC	CCACGCGGCG	GATGATGTCA	100
GCGGGGTGGT	CCTCGGCGAC	GACCCGGACC	ACGATCCACC	CGTAGCGGTG	150
CTGGACTTTC	TCGTGCCGGA	GGATGTCTTT	CCGGTAGTGG	TAGCGACTGG	200
TCAGATGGTG	GTCGCCGTCA	TACTCGGCCG	CGACCTTGAT	GTCTTGCCAG	250
CCCATATCCA	AATGGGCTTC	CGCCAGCCC	CATTCGTTGC	GCACCGCGAT	300
CTGCGTCTGG	GGGCGCGGAA	AGCCGGCGCG	GATCAACAAC	AAGCGCAGCC	350
AGGTTTCCTT	GGGGGACTGG	GCACCGCCGT	CGACGAGGTC	CAGAGCGGCT	400
CTTGCGGCCT	TCATGCCACG	GCGGCCCGGA	TAGCGCTCGA	TCAGCGGCTC	450
GACGTCGGCC	ACCTTCAAAT	CGGTGGCCTG	TATCAGGGCG	TCGACGGCCG	500
CGACGGCGGG	GTCCAATGGA	AATCGACTGG	TCAGGTCGAG	CGCCGTTCGC	550
TCCGGTGTGG	TCACGCGCAT	GCCCTCGATG	ACGCAGATCT	CGTCGGGCTC	600
GATGCGCTCT	TCCCAGACTT	GCAGCCCCGG	GGCACGGCGG	CGGTTGGTGT	650
CGATGATCGC	GGCGGGAAGA	TCCGCGTCGA	TCCACTTGGC	GCCATGGAAG	700
GCAGAAGCCG	AGTAGCCGGC	CAGCACGCCG	CGGCGGCGCG	AGCGCAGCCA	750
CAGCGCTTTT	GCACGCAATT	GCGCGGTCAG	TTCCACACCC	TGCGGCACGT	800

1084

ACACGTCTTT	ATGTAGCGCG	ACATACCTGC	TGCGCAATTC	GTAGGGCGTC	850
AATACACCCG	CAGCCAGGGC	CTCGCTGCCC	AGAAAGGGAT	CCGTCATGGT	900
CGAAGTGTGC	TGAGTCACAC	CGACAAACGT	CACGAGCGTA	ACCCCAGTGC	950
GAAAGTTCCC	GCCGGAAATC	GCAGCCACGT	TACGCTCGTG	GACATACCGA	1000
TTTCGGCCCC	GCCGCGGCGA	GACGATAGGT	TGTCGGGGTG	ACTGCCACAG	1050
CCACTGAAGG	GGCCAAACCC	CCATTCGTAT	CCCGTTCAGT	CCTGGTTACC	1100
GGAGGAAACC	GGGGGATCGG	GCTGGCGATC	GCACAGCGGC	TGGCTGCCGA	1150
CGGCCACAAG	GTGGCCGTCA	CCCACCGTGG	ATCCGGAGCG	CCAAAGGGGC	1200
TGTTTGGCGT	CGAATGTGAC	GTCACCGACA	GCGACGCCGT	CGATCGCGCC	1250
TTACAGGCGG	TAGAAGAGCA	CCAGGGTCCG	GTCGAGGTGC	TGGTGTCCAA	1300
CGCCGGCCTA	TCCGCGGACG	CATTCCTCAT	GCGGATGACC	GAGGAAAAGT	1350
TCGAGAAGGT	CATCAACGCC	AACCTCACCG	GGGCGTTCCG	GGTGGCTCAA	1400
CGGGCATCGC	GCAGCATGCA	GCGCAACAAA	TTCGGTCGAA	TGATATTTCAT	1450
AGGTTTCGGT	TCCGGCAGCT	GGGGCATCGG	CAACCAGGCC	AACTACGCAG	1500
CCTCCAAGGC	CGGAGTGATT	GGCATGGCCC	GCTCGATCGC	CCGCGAGCTG	1550
TCGAAGGCAA	ACGTGACCGC	GAATGTGGTG	GCCCCGGGCT	ACATCGACAC	1600
CGATATGACC	CGCGCGCTGG	ATGAGCGGAT	TCAGCAGGGG	GCGCTGCAAT	1650
TTATCCCAGC	GAAGCGGGTC	GGCACCCCCG	CCGAGGTTCG	CGGGGTGGTC	1700
AGCTTCCTGG	CTTCCGAGGA	TGCGAGCTAT	ATCTCCGGTG	CGGTCATCCC	1750
GGTCGACGGC	GGCATGGGTA	TGGGCCACTG	ACACAACACA	AGGACGCACA	1800
TGACAGGACT	GCTGGACGGC	AAACGGATTC	TGGTTAGCGG	AATCATCACC	1850
GACTCGTCGA	TCGCGTTTCA	CATCGCACGG	GTAGCCCAGG	AGCAGGGCGC	1900
CCAGCTGGTG	CTCACCGGGT	TCGACCGGCT	GCGGCTGATT	CAGCGCATCA	1950
CCGACCGGCT	GCCGGCAAAG	GCCCCGCTGC	TCGAACTCGA	CGTGCAAAAC	2000
GAGGAGCACC	TGGCCAGCTT	GGCCGGCCGG	GTGACCGAGG	CGATCGGGGC	2050
GGGCAACAAG	CTCGACGGGG	TGGTGCATTC	GATTGGGTTC	ATGCCGCAGA	2100
CCGGGATGGG	CATCAACCCG	TTCTTCGACG	CGCCCTACGC	GGATGTGTCC	2150
AAGGGCATCC	ACATCTCGGC	GTATTCGTAT	GCTTCGATGG	CCAAGGCGCT	2200
GCTGCCGATC	ATGAACCCCG	GAGGTTCCAT	CGTCGGCATG	GACTTCGACC	2250
CGAGCCGGGC	GATGCCGGCC	TACAACTGGA	TGACGGTCGC	CAAGAGCGCG	2300
TTGGAGTCGG	TCAACAGGTT	CGTGGCGCGC	GAGGCCGGCA	AGTACGGTGT	2350
GCGTTCGAAT	CTCGTTGCCG	CAGGCCCTAT	CCGGACGCTG	GCGATGAGTG	2400
CGATCGTCGG	CGGTGCGCTC	GGCGAGGAGG	CCGGCGCCCA	GATCCAGCTG	2450
CTCGAGGAGG	GCTGGGATCA	GCGCGCTCCG	ATCGGCTGGA	ACATGAAGGA	2500
TGCGACGCCG	GTCGCCAAGA	CGGTGTGCGC	GCTGCTGTCT	GACTIONGCTG	2550
CGGCGACCAC	GGGTGACATC	ATCTACGCCG	ACGGCGGCGC	GCACACCCAA	2600
TTGCTCTAG					2609

2) INFORMATION FOR SEQ ID NO: 2102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102

CACCTTCACC CTGACCGACG

20

2) INFORMATION FOR SEQ ID NO: 2103

1085

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103

CGAACCAGCG GAAATAGTTG GAC

23

2) INFORMATION FOR SEQ ID NO: 2104

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104

CTGGGCATGG CICGAGTC

18

2) INFORMATION FOR SEQ ID NO: 2105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37rv
- (C) ACCESSION NUMBER: U68480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105

ATGACACAGT	GCGCGAGCAG	ACGCAAAAGC	ACCCCAAATC	GGGCGATTTT	50
GGGGGCTTTT	GCGTCTGCTC	GCGGGACGCG	CTGGGTGGCC	ACCATCGCCG	100
GGCTGATTGG	CTTTGTGTTG	TCGGTGGCGA	CGCCGCTGCT	GCCCGTCGTG	150
CAGACCACCG	CGATGCTCGA	CTGGCCACAG	CGGGGGCAAC	TGGGCAGCGT	200
GACCGCCCCG	CTGATCTCGC	TGACGCCGGT	CGACTTTACC	GCCACCGTGC	250
CGTGCGACGT	GGTGCGCGCC	ATGCCACCCG	CGGGCGGGGT	GGTGCTGGGC	300
ACCGCACCCA	AGCAAGGCAA	GGACGCCAAT	TTGCAGGCGT	TGTTTCGTCT	350
CGTCAGCGCC	CAGCGCGTGG	ACGTCACCGA	CCGCAACGTG	GTGATCTTGT	400
CCGTGCCGCG	CGAGCAGGTG	ACGTCCCCGC	AGTGTCAACG	CATCGAGGTC	450

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ACCTCTACCC	ACGCCGGCAC	CTTCGCCAAC	TTCGTCGGGC	TCAAGGACCC	500
GTCGGGCGCG	CCGCTGCGCA	GCGGCTTCCC	CGACCCCAAC	CTGCGCCCCG	550
AGATTGTCGG	GGTGTTCCACC	GACCTGACCG	GGCCCGCGCC	GCCCGGGCTG	600
GCGGTCTCGG	CGACCATCGA	CACCCGGTTC	TCCACCCGGC	CGACCACGCT	650
GAAACTGCTG	GCGATCATCG	GGGCGATCGT	GGCCACCGTC	GTCGCACTGA	700
TCGCGTTGTG	GCGCCTGGAC	CAGTTGGACG	GGCGGGGCTC	AATTGCCCAG	750
CTCCTCCTCA	GGCCGTTCCG	GCCTGCATCG	TCGCCGGGCG	GCATGCGCCG	800
GCTGATTCCG	GCAAGCTGGC	GCACCTTCAC	CCTGACCGAC	GCCGTGGTGA	850
TATTCGGCTT	CCTGCTCTGG	CATGTCATCG	GCGCGAATTC	GTCGGACGAC	900
GGCTACATCC	TGGGCATGGC	CCGAGTCGCC	GACCACGCCG	GCTACATGTC	950
CAACTATTTT	CGCTGGTTCG	GCAGCCCAGA	GGATCCCTTC	GGCTGGTATT	1000
ACAACCTGCT	GGCGCTGATG	ACCCATGTCA	GCGACGCCAG	TCTGTGGATG	1050
CGCCTGCCAG	ACCTGGCCGC	CGGGCTAGTG	TGCTGGCTGC	TGCTGTGCGC	1100
TGAGGTGCTG	CCCCGCCTCG	GGCCGGCGGT	GGAGGCCAGC	AAACCCGCCT	1150
ACTGGGCGGC	GGCCATGGTC	TTGCTGACCG	CGTGGATGCC	GTTCAACAAC	1200
GGCCTGCGGC	CGGAGGGCAT	CATCGCGCTC	GGCTCGCTGG	TCACCTATGT	1250
GCTGATCGAG	CGGTCCATGC	GGTACAGCCG	GCTCACACCG	GCGGCGCTGG	1300
CCGTCGTTAC	CGCCGCATTC	ACACTGGGTG	TGCAGCCAC	CGGCCTGATC	1350
GCGGTGGCCG	CGCTGGTGGC	CGGCGGCCGC	CCGATGCTGC	GGATCTTGGT	1400
GCGCCGYCAT	CGCCTGGTCG	GCACGTTGCC	GTTGGTGTGC	CCGATGCTGG	1450
CCGCCGGCAC	CGTCATCCTG	ACCGTGGTGT	TCGCCGACCA	GACCCTGTCA	1500
ACGGTGTTGG	AAGCCACCAG	GGTTCGCGCC	AAAATCGGGC	CGAGCCAGGC	1550
GTGGTATACC	GAGAACCTGC	GTTACTACTA	CCTCATCCTG	CCCACCGTCG	1600
ACGGTTCGCT	GTCGCGGCGC	TTCGGCTTTT	TGATCACCGC	GCTATGCCTG	1650
TTACCCGCGG	TGTTTCATCAT	GTTGCGGCGC	AAGCGAATTC	CCAGCGTGGC	1700
CCGCGGACCG	GCGTGGCGGC	TGATGGGCGT	CATCTTCGGC	ACCATGTTCT	1750
TCCTGATGTT	CACGCCCACC	AAGTGGGTGC	ACCACTTCGG	GCTGTTTCGCC	1800
GCCGTAGGGG	CGGCGATGGC	CGCGCTGACG	ACGGTGTTGG	TATCCCCATC	1850
GGTGCTGCGC	TGGTCGCGCA	ACCGGATGGC	GTTCTTGCGC	GCGTTATTCT	1900
TCCTGCTGGC	GTTGTGTTGG	GCCACCACCA	ACGGCTGGTG	GTATGTCTCC	1950
AGCTACGGTG	TGCCGTTCAA	CAGCGCGATG	CCGAAGATCG	ACGGGATCAC	2000
AGTCAGCACA	ATCTTTTTCG	CCCTGTTTGC	GATCGCCGCC	GGCTATGCGG	2050
CCTGGCTGCA	CTTCGCGCCC	CGCGGCGCCG	GCGAAGGGCG	GCTGATCCGC	2100
GCGCTGACGA	CAGCCCCGGT	ACCGATCGTG	GCCGGTTTCA	TGGCGGCGGT	2150
GTTCGTGCGG	TCCATGGTGG	CCGGGATCGT	GCGACAGTAC	CCGACCTACT	2200
CCAACGGCTG	GTCCAACGTG	CGGGCGTTTG	TCGGCGGCTG	CGGACTGGCC	2250
GACGACGTAC	TCGTGAGGCC	TGATACCAAT	GCGGGTTTCA	TGAAGCCGCT	2300
GGACGGCGAT	TCGGGTTCCT	GGGGCCCCTT	GGGCCCCGCTG	GGTGGAGTCA	2350
ACCCGGTCGG	CTTCACGCCC	AACGGCGTAC	CGGAACACAC	GGTGGCCGAG	2400
GCGATCGTGA	TGAAACCCAA	CCAGCCCCGGC	ACCGACTACG	ACTGGGATGC	2450
GCCGACCAAG	CTGACGAGTC	CTGGCATCAA	TGGTTCTACG	GTGCCGCTGC	2500
CCTATGGGCT	CGATCCCCGCC	CGGGTACCGT	TGGCAGGCAC	CTACACCACC	2550
GGCGCACAGC	AACAGAGCAC	ACTCGTCTCG	GCGTGGTATC	TCCTGCCTAA	2600
GCCGGACGAC	GGGCATCCGC	TGGTCGTGGT	GACCGCCGCG	GGCAAGATCG	2650
CCGGCAACAG	CGTGCTGCAC	GGGTACACCC	CCGGGCAGAC	TGTGGTGCTC	2700
GAATACGCCA	TGCCGGGACC	CGGAGCGCTG	GTACCCGCCG	GGCGGATGGT	2750
GCCCGACGAC	CTATACGGAG	AGCAGCCCAA	GGCGTGCGCG	AACCTGCGCT	2800
TCGCCCCGAGC	AAAGATGCCC	GCCGATGCCG	TCGCGGTCCG	GGTGGTGGCC	2850
GAGGATCTGT	CGCTGACACC	GGAGGACTGG	ATCGCGGTGA	CCCCGCCGCG	2900
GGTACCGGAC	CTGCGCTCAC	TGCAGGAATA	TGTGGGCTCG	ACGCAGCCGG	2950
TGCTGCTGGA	CTGGGCGGTC	GGTTTGGCCT	TCCCGTGCCA	GCAGCCGATG	3000
CTGCACGCCA	ATGGCATCGC	CGAAATCCCG	AAGTTCCGCA	TCACACCGGA	3050
CTACTCGGCT	AAGAAGCTGG	ACACCGACAC	GTGGGAAGAC	GGCACTAACG	3100
GCGGCCCTGCT	CGGGATCACC	GACCTGTTGC	TGCGGGCCCA	CGTCATGGCC	3150
ACCTACCTGT	CCCGCGACTG	GGCCCGCGAT	TGGGGTTCCC	TGCGCAAGTT	3200
CGACACCCTG	GTCGATGCCC	CTCCCGCCCA	GCTCGAGTTG	GGCACCGCGA	3250
CCCGCAGCGG	CCTGTGGTCA	CCGGGCAAGA	TCCGAATTGG	TCCATAG	3297

2) INFORMATION FOR SEQ ID NO: 2106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106

GCGAGCAGAG CACGCCCTCC TCGCCGCTCG C

31

2) INFORMATION FOR SEQ ID NO: 2107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107

GCGAGCTCCC CATCTCTGGT TGGCACGCTC GC

32

2) INFORMATION FOR SEQ ID NO: 2108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108

GCGGGCAACT TCRTCAAGAA GGTGGTTAC AACCCGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109

GCGGGCCCAA TCTCTGGTTG GAAYGGTGAC AAGCCCGC

38

2) INFORMATION FOR SEQ ID NO: 2110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110

GCGGGCCCTT AACGATTTCA GCGAATCTGG ATTCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111

GCGGGCATGA TTGAAGCCAC CACCAACGCT TCCTGGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112

GCGGGCTTGA TGAAGTTTTG GGTTCCTTG ACAATTTGCC CGC

43

2) INFORMATION FOR SEQ ID NO: 2113

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113

GCGGGCACAA GGGTTGGACT AAGGAAACCA AGGCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2114

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114

GCGGGCATCG ATGCTATTGA ACCACCTGTC AGACCGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2115

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115

GCGGGCTTGA TGATTCCTC GAATCTAGAT TGGGCCCGC

39

2) INFORMATION FOR SEQ ID NO: 2116

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116

GCGGGCGGTA AGTCCACCGG TAAGACCTTG TTGGCCCGC

39

2) INFORMATION FOR SEQ ID NO: 2117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117

GCGGGCGACG CCATTGAGCC ACCTTCGAGA GCCCGC

36

2) INFORMATION FOR SEQ ID NO: 2118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118

GCGGGCTCCT TGACAATTTC TTCGTATCTG TTCTTGCCCC GC

42

2) INFORMATION FOR SEQ ID NO: 2119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119

GCGGGCTTAC AACCTAAGG CTGTTCCATT CGTTGCCCCG

40

2) INFORMATION FOR SEQ ID NO: 2120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120

GCGGGCAGAA ACCAAGGCTG GTAAGGTTAC CGGTAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121

CGACCGCIAG CCGCACACCA AGTTCCGGTC G

31

2) INFORMATION FOR SEQ ID NO: 2122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122

CCGAGCGAAT GTAGGAGTCC AGGGTCTCTG CTCGG

35

2) INFORMATION FOR SEQ ID NO: 2123

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123

TCTACCACTG AAGCATTAC

19

2) INFORMATION FOR SEQ ID NO: 2124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124

TAGGTACTGT AGGTTTATTG

20

2) INFORMATION FOR SEQ ID NO: 2125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125

CACGCGGATT TTGAATCTCT TCCTCTAGTA GCGCGTG

37

2) INFORMATION FOR SEQ ID NO: 2126

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126

ATATCAGAGA CTGATGAG

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2) INFORMATION FOR SEQ ID NO: 2127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127

TAGCATATTC AGAGAATATT GT

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2) INFORMATION FOR SEQ ID NO: 2128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128

CAACGCTGGA GAATCTATAT TTGTAGAAAC TGC GTTG

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2) INFORMATION FOR SEQ ID NO: 2129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8133 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X51797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129

ATGTCTTTAA	TATCTAAAGA	AGAGTTAATA	AAACTCGCAT	ATAGCATTAG	50
ACCAAGAGAA	AATGAGTATA	AAACTATACT	AACTAATTTA	GACGAATATA	100
ATAAGTTAAC	TACAAACAAT	AATGAAAATA	AATATTTGCA	ATTAAAAAAA	150
CTAAATGAAT	CAATTGATGT	TTTTATGAAT	AAATATAAAA	CTTCAAGCAG	200
AAATAGAGCA	CTCTCTAATC	TAAAAAAAGA	TATATTAAAA	GAAGTAATTC	250
TTATTAAAAA	TTCCAATACA	AGCCCTGTAG	AAAAAAATTT	ACATTTTGTA	300
TGGATAGGTG	GAGAAGTCAG	TGATATTGCT	CTTGAATACA	TAAAACAATG	350
GGCTGATATT	AATGCAGAAT	ATAATATTAA	ACTGTGGTAT	GATAGTGAAG	400
CATTCTTAGT	AAATACACTA	AAAAAGGCTA	TAGTTGAATC	TTCTACCACT	450
GAAGCATTAC	AGCTACTAGA	GGAAGAGATT	CAAAATCCTC	AATTTGATAA	500
TATGAAATTT	TACAAAAAAA	GGATGGAATT	TATATATGAT	AGACAAAAAA	550
GGTTTATAAA	TTATTATAAA	TCTCAAATCA	ATAAACCTAC	AGTACCTACA	600
ATAGATGATA	TTATAAAGTC	TCATCTAGTA	TCTGAATATA	ATAGAGATGA	650
AACTGTATTA	GAATCATATA	GAACAAATTC	TTTGAGAAAA	ATAAATAGTA	700
ATCATGGGAT	AGATATCAGG	GCTAATAGTT	TGTTTACAGA	ACAAGAGTTA	750
TTAAATATTT	ATAGTCAGGA	GTTGTAAAT	CGTGGAATT	TAGCTGCAGC	800

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ATCTGACATA	GTAAGATTAT	TAGCCCTAAA	AAATTTTGGC	GGAGTATATT	850
TAGATGTTGA	TATGCTTCCA	GGTATTCACT	CTGATTTATT	TAAAACAATA	900
TCTAGACCTA	GCTCTATTGG	ACTAGACCGT	TGGGAAATGA	TAAAATTAGA	950
GGCTATTATG	AAGTATAAAA	AATATATAAA	TAATTATACA	TCAGAAAAC	1000
TTGATAAACT	TGATCAACAA	TTAAAAGATA	ATTTTAAACT	CATTATAGAA	1050
AGTAAAAGTG	AAAAATCTGA	GATATTTTCT	AAATTAGAAA	ATTTAAATGT	1100
ATCTGATCTT	GAAATTAAAA	TAGCTTTCGC	TTTAGGCAGT	GTTATAAATC	1150
AAGCCTTGAT	ATCAAAACAA	GGTTCATATC	TTACTAACCT	AGTAATAGAA	1200
CAAGTAAAAA	ATAGATATCA	ATTTTAAAC	CAACACCTTA	ACCCAGCCAT	1250
AGAGTCTGAT	AATAACTTCA	CAGATACTAC	TAAAATTTTT	CATGATTCAT	1300
TATTTAATTC	AGCTACCGCA	GAAAACCTCTA	TGTTTTTAAAC	AAAAATAGCA	1350
CCATACTTAC	AAGTAGGTTT	TATGCCAGAA	GCTCGCTCCA	CAATAAGTTT	1400
AAGTGGTCCA	GGAGCTTATG	CGTCAGCTTA	CTATGATTTT	ATAAATTTAC	1450
AAGAAAATAC	TATAGAAAAA	ACTTTAAAG	CATCAGATTT	AATAGAATTT	1500
AAATTCCTAG	AAAATAATCT	ATCTCAATTG	ACAGAACAAG	AAATAAATAG	1550
TCTATGGAGC	TTTGATCAAG	CAAGTGCAAA	ATATCAATTT	GAGAAATATG	1600
TAAGAGATTA	TACTGGTGGA	TCTCTTTCTG	AAGACAATGG	GGTAGACTTT	1650
AATAAAAATA	CTGCCCTCGA	CAAAAACCTAT	TTATTAAATA	ATAAAATTCC	1700
ATCAAACAAT	GTAGAAGAAG	CTGGAAGTAA	AAATTATGTT	CATTATATCA	1750
TACAGTTACA	AGGAGATGAT	ATAAGTTATG	AAGCAACATG	CAATTTATTT	1800
TCTAAAAATC	CTAAAAATAG	TATTATTATA	CAACGAAATA	TGAATGAAAG	1850
TGCAAAAAGC	TACTTTTTTAA	GTGATGATGG	AGAATCTATT	TTAGAATTAA	1900
ATAAATATAG	GATACCTGAA	AGATTAAAAA	ATAAGGAAAA	AGTAAAAGTA	1950
ACCTTTATTG	GACATGGTAA	AGATGAATTC	AACACAAGCG	AATTTGCTAG	2000
ATTAAGTGTA	GATTCACTTT	CCAATGAGAT	AAGTTCATTT	TTAGATACCA	2050
TAAAATTAGA	TATATCACCT	AAAAATGTAG	AAGTAACTT	ACTTGGATGT	2100
AATATGTTTA	GTTATGATTT	TAATGTTGAA	GAACTTATC	CTGGGAAGTT	2150
GCTATTAAGT	ATTATGGACA	AAATTACTTC	CACTTTACCT	GATGTAAATA	2200
AAAATTCTAT	TACTATAGGA	GCAAATCAAT	ATGAAGTAAG	AATTAATAGT	2250
GAGGGAAGAA	AAGAACTTCT	GGCTCACTCA	GGTAAATGGA	TAAATAAAGA	2300
AGAAGCTATT	ATGAGCGATT	TATCTAGTAA	AGAATACATT	TTTTTTGATT	2350
CTATAGATAA	TAAGCTAAAA	GCAAAGTCCA	AGAATATTCC	AGGATTAGCA	2400
TCAATATCAG	AAGATATAAA	AACATTATTA	CTTGATGCAA	GTGTTAGTCC	2450
TGATACAAAA	TTTATTTTAA	ATAATCTTAA	GCTTAATATT	GAATCTTCTA	2500
TTGGGGATTA	CATTTATTAT	GAAAAATTAG	AGCCTGTAA	AAATATAATT	2550
CACAATTCTA	TAGATGATTT	AATAGATGAG	TTCAATCTAC	TTGAAAATGT	2600
ATCTGATGAA	TTATATGAAT	TAAAAAAATT	AAATAATCTA	GATGAGAAGT	2650
ATTTAATATC	TTTTGAAGAT	ATCTCAAAAA	ATAATTCAAC	TTACTCTGTA	2700
AGATTTATTA	ACAAAAGTAA	TGGTGAGTCA	GTTTATGTAG	AAACAGAAAA	2750
AGAAATTTTT	TCAAAATATA	GCGAACATAT	TACAAAAGAA	ATAAGTACTA	2800
TAAAGAATAG	TATAATTACA	GATGTTAATG	GTAATTTATT	GGATAATATA	2850
CAGTTAGATC	ATACTTCTCA	AGTTAATACA	TTAAACGCAG	CATTCTTTAT	2900
TCAATCATTA	ATAGATTATA	GTAGCAATAA	AGATGTACTG	AATGATTTAA	2950
GTACCTCAGT	TAAGGTTCAA	CTTTATGCTC	AACTATTTAG	TACAGGTTTA	3000
AATACTATAT	ATGACTCTAT	CCAATTAGTA	AATTTAATAT	CAAATGCAGT	3050
AAATGATACT	ATAAATGTAC	TACCTACAAT	AACAGAGGGG	ATACCTATTG	3100
TATCTACTAT	ATTAGACGGA	ATAAACTTAG	GTGCAGCAAT	TAAGGAATTA	3150
CTAGACGAAC	ATGACCCATT	ACTAAAAAAA	GAATTAGAAG	CTAAGGTGGG	3200
TGTTTTAGCA	ATAAATATGT	CATTATCTAT	AGCTGCAACT	GTAGCTTCAA	3250
TTGTTGGAAT	AGGTGCTGAA	GTTACTATTT	TCTTATTACC	TATAGCTGGT	3300
ATATCTGCAG	GAATACCTTC	ATTAGTTAAT	AATGAATTAA	TATTGCATGA	3350
TAAGGCAACT	TCAGTGGTAA	ACTATTTTAA	TCATTTGTCT	GAATCTAAAA	3400
AATATGGCCC	TCTTAAAACA	GAAGATGATA	AAATTTTAGT	TCCTATTGAT	3450
GATTTAGTAA	TATCAGAAAT	AGATTTTAA	AATAATTCTG	TAAAACCTAGG	3500
AACATGTAAT	ATATTAGCAA	TGGAGGGGGG	ATCAGGACAC	ACAGTGACTG	3550
GTAATATAGA	TCACTTTTTT	TCATCTCCAT	CTATAAGTTC	TCATATTCCT	3600
TCATTATCAA	TTTATTCTGC	AATAGGTATA	GAAACAGAAA	ATCTAGATTT	3650

TTCAAAAAAA	ATAATGATGT	TACCTAATGC	TCCTTCAAGA	GTGTTTTTGGT	3700
GGGAAACTGG	AGCAGTTCCA	GGTTTAAGAT	CATTGGAAAA	TGACGGAACT	3750
AGATTACTTG	ATTCAATAAG	AGATTTATAC	CCAGGTAAAT	TTTACTGGAG	3800
ATTCTATGCT	TTTTTTCGATT	ATGCAATAAC	TACATTAAAA	CCAGTTTATG	3850
AAGACACTAA	TATTAAAATT	AAACTAGATA	AAGATACTAG	AAACTTCATA	3900
ATGCCAACTA	TAACTACTAA	CGAAATTAGA	AACAAATTAT	CTTATTCATT	3950
TGATGGAGCA	GGAGGAACTT	ACTCTTTATT	ATTATCTTCA	TATCCAATAT	4000
CAACGAATAT	AAATTTATCT	AAAGATGATT	TATGGATATT	TAATATTGAT	4050
AATGAAGTAA	GAGAAATATC	TATAGAAAAT	GGTACTATTA	AAAAAGGAAA	4100
GTTAATAAAA	GATGTTTTTAA	GTAATAATTGA	TATAAATAAA	AATAAACTTA	4150
TTATAGGCAA	TCAAACAATA	GATTTTTTCAG	GCGATATAGA	TAATAAAGAT	4200
AGATATATAT	TCTTGACTTG	TGAGTTAGAT	GATAAAATTA	GTTTAATAAT	4250
AGAAATAAAT	CTTGTTGCAA	AATCTTATAG	TTTGTTATTG	TCTGGGGATA	4300
AAAATTATTT	GATATCCAAT	TTATCTAATA	CTATTGAGAA	AATCAATACT	4350
TTAGGCCTAG	ATAGTAAAAA	TATAGCGTAC	AATTACACTG	ATGAATCTAA	4400
TAATAAATAT	TTTGGAGCTA	TATCTAAAC	AAGTCAAAAA	AGCATAATAC	4450
ATTATAAAAA	AGACAGTAAA	AATATATTAG	AATTTTATAA	TGACAGTACA	4500
TTAGAATTTA	ACAGTAAAGA	TTTTATTGCT	GAAGATATAA	ATGTATTTAT	4550
GAAAGATGAT	ATTAATACTA	TAACAGGAAA	ATACTATGTT	GATAATAATA	5000
CTGATAAAAG	TATAGATTTT	TCTATTTCTT	TAGTTAGTAA	AAATCAAGTA	5050
AAAGTAAATG	GATTATATTT	AAATGAATCC	GTATACTCAT	CTTACCTTGA	5100
TTTTGTGAAA	AATTCAGATG	GACACCATAA	TACTTCTAAT	TTTATGAATT	5150
TATTTTTTGA	CAATATAAGT	TTCTGGAAAT	TGTTTGGGTT	TGAAAATATA	5200
AATTTTGTAA	TCGATAAATA	CTTTACCCTT	GTTGGTAAAA	CTAATCCTGG	5250
ATATGTAGAA	TTTATTTGTG	ACAATAATAA	AAATATAGAT	ATATATTTTG	5300
GTGAATGGAA	AACATCGTCA	TCTAAAAGCA	CTATATTTAG	CGGAAATGGT	5350
AGAAATGTTG	TAGTAGAGCC	TATATATAAT	CCTGATACGG	GTGAAGATAT	5400
ATCTACTTCA	CTAGATTTTT	CCTATGAACC	TCTCTATGGA	ATAGATAGAT	5450
ATATAAATAA	AGTATTGATA	GCACCTGATT	TATATACAAG	TTTAATAAAT	5500
ATTAATACCA	ATTATTATTC	AAATGAGTAC	TACCCTGAGA	TTATAGTTCT	5550
TAACCCAAAT	ACATTCCACA	AAAAAGTAAA	TATAAATTTA	GATAGTTCTT	5600
CTTTTGAGTA	TAAATGGTCT	ACAGAAGGAA	GTGACTTTAT	TTTAGTTAGA	5650
TACTTAGAAG	AAAGTAATAA	AAAAATATTA	CAAAAAATAA	GAATCAAAGG	5700
TATCTTATCT	AATACTCAAT	CATTTAATAA	AATGAGTATA	GATTTTAAAG	5750
ATATTAAAAA	ACTATCATTA	GGATATATAA	TGAGTAATTT	TAAATCATTT	5800
AATTCTGAAA	ATGAATTAGA	TAGAGATCAT	TTAGGATTTA	AAATAATAGA	5850
TAATAAAACT	TATTACTATG	ATGAAGATAG	TAAATTAGTT	AAAGGATTAA	5900
GCAAGTAATT	GACAATAATA	AGTATTATTT	CAATCCTGAC	ACTGCTATCA	5950
TCTCAAAAGG	TTGGCAGACT	GTTAATGGTA	GTAGATACTA	CTTTGATACT	6000
GATACCGCTA	TTGCCTTTAA	TGGTTATAAA	ACTATTGATG	GTAAACACTT	6050
TTATTTTGAT	AGTGATTGTG	TAGTGAAAAT	AGGTGTGTTT	AGTACCTCTA	6100
ATGGATTTGA	ATATTTTGCA	CCTGCTAATA	CTTATAATAA	TAACATAGAA	6150
GGTCAGGCTA	TAGTTTATCA	AAGTAAATTC	TTAACTTTGA	ATGGTAAAAA	6200
ATATTACTTT	GATAATAACT	CAAAGCAGT	TACCGGATTG	CAAACATTTG	6250
ATAGTAAAAA	ATATTACTTT	AATACTAACA	CTGCTGAAGC	AGCTACTGGA	6300
TGGCAAACCTA	TTGATGGTAA	AAAATATTAC	TTTAATACTA	ACACTGCTGA	6350
AGCAGCTACT	GGATGGCAAA	CTATTGATGG	TAAAAAATAT	TACTTTAATA	6400
CTAACACTGC	TATAGCTTCA	ACTGGTTATA	CAATTATTAA	TGGTAAACAT	6450
TTTTATTTTA	ATACTGATGG	TATTATGCAG	ATAGGAGTGT	TTAAAGGACC	6500
TAATGGATTT	GAATATTTTG	CACCTGCTAA	TACGGATGCT	AACAACATAG	6550
AAGGTCAAGC	TATACTTTAC	CAAATGAAT	TCTTAACTTT	GAATGGTAAA	6600
AAATATTACT	TTGGTAGTGA	CTCAAAAGCA	GTTACTGGAT	GGAGAATTAT	6650
TAACAATAAG	AAATATTACT	TTAATCCTAA	TAATGCTATT	GCTGCAATTC	6700
ATCTATGCAC	TATAAATAAT	GACAAGTATT	ACTTTAGTTA	TGATGGAATT	6750
CTTCAAAATG	GATATATTAC	TATTGAAAGA	AATAATTTCT	ATTTTGATGC	6800
TAATAATGAA	TCTAAAATGG	TAACAGGAGT	ATTTAAAGGA	CCTAATGGAT	6850
TTGAGTATTT	TGCACCTGCT	AATACTCACA	ATAATAACAT	AGAAGGTCAG	6900

GCTATAGTTT	ACCAGAACAA	ATTCTTAACT	TTGAATGGCA	AAAAATATTA	6950
TTTTGATAAT	GACTCAAAAG	CAGTTACTGG	ATGGCAAACC	ATTGATGGTA	7000
AAAAATATTA	CTTTAATCTT	AACACTGCTG	AAGCAGCTAC	TGGATGGCAA	7050
ACTATTGATG	GTAAAAAATA	TTACTTTAAT	CTTAACACTG	CTGAAGCAGC	7100
TACTGGATGG	CAAACCTATTG	ATGGTAAAAA	ATATTACTTT	AATACTAACA	7150
CTTTCATAGC	CTCAACTGGT	TATACAAGTA	TTAATGGTAA	ACATTTTTTAT	7200
TTTAATACTG	ATGGTATTAT	GCAGATAGGA	GTGTTTAAAG	GACCTAATGG	7250
ATTTGAATAC	TTTGCACCTG	CTAATACGGA	TGCTAACAAC	ATAGAAGGTC	7300
AAGCTATACT	TTACCAAAAT	AAATTCTTAA	CTTTGAATGG	TAAAAAATAT	7350
TACTTTGGTA	GTGACTCAAA	AGCAGTTACC	GGACTGCGAA	CTATTGATGG	7400
TAAAAAATAT	TACTTTAATA	CTAACACTGC	TGTTGCAGTT	ACTGGATGGC	7450
AAACTATTAA	TGGTAAAAAA	TACTACTTTA	ATACTAACAC	TTCTATAGCT	7500
TCAACTGGTT	ATACAATTAT	TAGTGGTAAA	CATTTTTTATT	TTAATACTGA	7550
TGGTATTATG	CAGATAGGAG	TGTTTAAAGG	ACCTGATGGA	TTTGAATACT	7600
TTGCACCTGC	TAATACAGAT	GCTAACAATA	TAGAAGGTCA	AGCTATACGT	7650
TATCAAAATA	GATTCCTATA	TTTACATGAC	AATATATATT	ATTTTGGTAA	7700
TAATTCAAAA	GCGGCTACTG	GTTGGGTAAC	TATTGATGGT	AATAGATATT	7750
ACTTCGAGCC	TAATACAGCT	ATGGGTGCGA	ATGGTTATAA	AACTATTGAT	7800
AATAAAAATT	TTTACTTTAG	AAATGGTTTA	CCTCAGATAG	GAGTGTTTAA	7850
AGGGTCTAAT	GGATTTGAAT	ACTTTGCACC	TGCTAATACG	GATGCTAACA	7900
ATATAGAAGG	TCAAGCTATA	CGTTATCAAA	ATAGATTCCT	ACATTTACTT	7950
GGAAAAATAT	ATTACTTTGG	TAATAATTCA	AAAGCAGTTA	CTGGATGGCA	8000
AACTATTAAT	GGTAAAGTAT	ATTACTTTAT	GCCTGATACT	GCTATGGCTG	8050
CAGCTGGTGG	ACTTTTCGAG	ATTGATGGTG	TTATATATTT	CTTTGGTGTT	8100
GATGGAGTAA	AAGCCCCTGG	GATATATGGC	TAA		8133

2) INFORMATION FOR SEQ ID NO: 2130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X53138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130

ATGAGTTTAG	TTAATAGAAA	ACAGTTAGAA	AAAATGGCAA	ATGTAAGATT	50
TCGTACTCAA	GAAGATGAAT	ATGTTGCAAT	ATTGGATGCT	TTAGAAGAAT	100
ATCATAATAT	GTCAGAGAAT	ACTGTAGTCG	AAAAATATTT	AAAATTAAAA	150
GATATAAATA	GTTTAACAGA	TATTTATATA	GATACATATA	AAAAATCTGG	200
TAGAAATAAA	GCCTTAAAAA	AATTTAAGGA	ATATCTAGTT	ACAGAAGTAT	250
TAGAGCTAAA	GAATAATAAT	TTAACTCCAG	TTGAGAAAAA	TTTACATTTT	300
GTTTGGATTG	GAGGTCAAAT	AAATGACACT	GCTATTAATT	ATATAAATCA	350
ATGGAAAGAT	GTAAATAGTG	ATTATAATGT	TAATGTTTTT	TATGATAGTA	400
ATGCATTTTT	GATAAACACA	TTGAAAAAAA	CTGTAGTAGA	ATCAGCAATA	450
AATGATACAC	TTGAATCATT	TAGAGAAAAC	TTAAATGACC	CTAGATTTGA	500
CTATAATAAA	TTCTTCAGAA	AACGTATGGA	AATAATTTAT	GATAAACAGA	550
AAAATTTTCAT	AAACTACTAT	AAAGCTCAAA	GAGAAGAAAA	TCCTGAACTT	600

ATAATTGATG	ATATTGTAAA	GACATATCTT	TCAAATGAGT	ATTCAAAGGA	650
GATAGATGAA	CTTAATACCT	ATATTGAAGA	ATCCTTAAAT	AAAATTACAC	700
AGAATAGTGG	AAATGATGTT	AGAAACTTTG	AAGAATTTAA	AAATGGAGAG	750
TCATTCAACT	TATATGAACA	AGAGTTGGTA	GAAAGGTGGA	ATTTAGCTGC	800
TGCTTCTGAC	ATATTAAGAA	TATCTGCATT	AAAAGAAATT	GGTGGTATGT	850
ATTTAGATGT	TGATATGTTA	CCAGGAATAC	AACCAGACTT	ATTTGAGTCT	900
ATAGAGAAAC	CTAGTTCAGT	AACAGTGGAT	TTTTGGGAAA	TGACAAAGTT	950
AGAAGCTATA	ATGAAATACA	AAGAATATAT	ACCAGAATAT	ACCTCAGAAC	1000
ATTTTGACAT	GTTAGACGAA	GAAGTTCAAA	GTAGTTTTGA	ATCTGTTCTA	1050
GCTTCTAAGT	CAGATAAATC	AGAAATATTC	TCATCACTTG	GTGATATGGA	1100
GGCATCACCA	CTAGAAGTTA	AAATTGCATT	TAATAGTAAG	GGTATTATAA	1150
ATCAAGGGCT	AATTTCTGTG	AAAGACTCAT	ATTGTAGCAA	TTTAATAGTA	1200
AAACAAATCG	AGAATAGATA	TAAAATATTG	AATAATAGTT	TAAATCCAGC	1250
TATTAGCGAG	GATAATGATT	TTAATACTAC	AACGAATACC	TTTATTGATA	1300
GTATAATGGC	TGAAGCTAAT	GCAGATAATG	GTAGATTTAT	GATGGAACTA	1350
GGAAAGTATT	TAAGAGTTGG	TTTCTTCCCA	GATGTTAAAA	CTACTATTAA	1400
CTTAAGTGGC	CCTGAAGCAT	ATGCCGCAGC	TTATCAAGAT	TTATTAATGT	1450
TTAAAGAAGG	CAGTATGAAT	ATCCATTTGA	TAGAAGCTGA	TTTAAGAAAC	1500
TTTGAAATCT	CTAAAACTAA	TATTTCTCAA	TCAACTGAAC	AAGAAATGGC	1550
TAGCTTATGG	TCATTTGACG	ATGCAAGAGC	TAAAGCTCAA	TTTGAAGAAT	1600
ATAAAAGGAA	TTATTTTGAA	GGTTCTCTTG	GTGAAGATGA	TAATCTTGAT	1650
TTTTCTCAAA	ATATAGTAGT	TGACAAGGAG	TATCTTTTAG	AAAAAATATC	1700
TTCATTAGCA	AGAAGTTCAG	AGAGAGGATA	TATACACTAT	ATTGTTCACT	1750
TACAAGGAGA	TAAAATTAGT	TATGAAGCAG	CATGTAACCT	ATTTGCAAAG	1800
ACTCCTTATG	ATAGTGTACT	GTTTCAGAAA	AATATAGAAG	ATTCAGAAAT	1850
TGCATATTAT	TATAATCCTG	GAGATGGTGA	AATACAAGAA	ATAGACAAGT	1900
ATAAAATTCC	AAGTATAATT	TCTGATAGAC	CTAAGATTAA	ATTAACATTT	1950
ATTGGTCATG	GTAAAGATGA	ATTTAATACT	GATATATTTG	CAGGTTTTGA	2000
TGTAGATTCA	TTATCCACAG	AAATAGAAGC	AGCAATAGAT	TTAGCTAAAG	2050
AGGATATTTT	TCCTAAGTCA	ATAGAAATAA	ATTTATTAGG	ATGTAATATG	2100
TTTAGCTACT	CTATCAACGT	AGAGGAGACT	TATCCTGGAA	AATTATTACT	2150
TAAAGTTAAA	GATAAAATAT	CAGAATTAAT	GCCATCTATA	AGTCAAGACT	2200
CTATTATAGT	AAGTGCAAAT	CAATATGAAG	TTAGAATAAA	TAGTGAAGGA	2250
AGAAGAGAAT	TATTGGATCA	TTCTGGTGAA	TGGATAAATA	AAGAAGAAAG	2300
TATTATAAAG	GATATTTTCAT	CAAAAGAATA	TATATCATTT	AATCCTAAAG	2350
AAAATAAAAT	TACAGTAAAA	TCTAAAAATT	TACCTGAGCT	ATCTACATTA	2400
TTACAAGAAA	TTAGAAATAA	TTCTAATTCA	AGTGATATTG	AACTAGAAGA	2450
AAAAGTAATG	TTAACAGAAT	GTGAGATAAA	TGTTATTTCA	AATATAGATA	2500
CGCAAATTGT	TGAGGAAAGG	ATTGAAGAAG	CTAAGAATTT	AACTTCTGAC	2550
TCTATTAATT	ATATAAAAGA	TGAATTTAAA	CTAATAGAAT	CTATTTCTGA	2600
TGCACTATGT	GACTTAAAC	AACAGAATGA	ATTAGAAGAT	TCTCATTTTA	2650
TATCTTTTGA	GGACATATCA	GAGACTGATG	AGGGATTTAG	TATAAGATTT	2700
ATTAATAAAG	AAACTGGAGA	ATCTATATTT	GTAGAACTG	AAAAACAAT	2750
ATTCTCTGAA	TATGCTAATC	ATATAACTGA	AGAGATTTCT	AAGATAAAAG	2800
GTACTATATT	TGATACTGTA	AATGGTAAGT	TAGTAAAAAA	AGTAAATTTA	2850
GATACTACAC	ACGAAGTAAA	TACTTTAAAT	GCTGCATTTT	TTATACAATC	2900
ATTAATAGAA	TATAATAGTT	CTAAAGAATC	TCTTAGTAAT	TTAAGTGTAG	2950
CAATGAAAGT	CCAAGTTTAC	GCTCAATTAT	TTAGTACTGG	TTTAAATACT	3000
ATTACAGATG	CAGCCAAAGT	TGTTGAATTA	GTATCAACTG	CATTAGATGA	3050
AACTATAGAC	TTACTTCCTA	CATTATCTGA	AGGATTACCT	ATAATTGCAA	3100
CTATTATAGA	TGGTGTAAGT	TTAGGTGCAG	CAATCAAAGA	GCTAAGTGAA	3150
ACGAGTGACC	CATTATTAAG	ACAAGAAATA	GAAGCTAAGA	TAGGTATAAT	3200
GGCAGTAAAT	TTAACAACAG	CTACAACCTG	AATCATTACT	TCATCTTTGG	3250
GGATAGCTAG	TGGATTTAGT	ATACTTTTAG	TTCCTTTAGC	AGGAATTTCA	3300
GCAGGTATAC	CAAGCTTAGT	AAACAATGAA	CTTGTACTTC	GAGATAAGGC	3350
AACAAAGGTT	GTAGATTATT	TTAAACATGT	TTCATTAGTT	GAAACTGAAG	3400
GAGTATTTAC	TTTATTAGAT	GATAAAATAA	TGATGCCACA	AGATGATTTA	3450

GTGATATCAG	AAATAGATTT	TAATAATAAT	TCAATAGTTT	TAGGTAAATG	3500
TGAAATCTGG	AGAATGGAAG	GTGGTTCAGG	TCATACTGTA	ACTGATGATA	3550
TAGATCACTT	CTTTTCAGCA	CCATCAATAA	CATATAGAGA	GCCACACTTA	3600
TCTATATATG	ACGTATTGGA	AGTACAAAAA	GAAGAAGTTG	ATTTGTCAAA	3650
AGATTTAATG	GTATTACCTA	ATGCTCCAAA	TAGAGTATTT	GCTTGGGAAA	3700
CAGGATGGAC	ACCAGGTTTA	AGAAGCTTAG	AAAATGATGG	CACAAAAGTG	3750
TTAGACCGTA	TAAGAGATAA	CTATGAAGGT	GAGTTTTATT	GGAGATATTT	3800
TGCTTTTATA	GCTGATGCTT	TAATAACAAC	ATTAAAACCA	AGATATGAAG	3850
ATACTAATAT	AAGAATAAAT	TTAGATAGTA	ATACTAGAAG	TTTTATAGTT	3900
CCAATAATAA	CTACAGAATA	TATAAGAGAA	AAATTATCAT	ATTCTTTCTA	3950
TGGTTCAGGA	GGAAGTTATG	CATTGTCTCT	TTCTCAATAT	AATATGGGTA	4000
TAAATATAGA	ATTAAGTGAA	AGTGATGTTT	GGATTATAGA	TGTTGATAAT	4050
GTTGTGAGAG	ATGTAAGTAT	AGAATCTGAT	AAAATTAAAA	AAGGTGATTT	4100
AATAGAAGGT	ATTTTATCTA	CACTAAGTAT	TGAAGAGAAT	AAAATTATCT	4150
TAAATAGCCA	TGAGATTAAT	TTTTCTGGTG	AGGTAAATGG	AAGTAATGGA	4200
TTTGTTTCTT	TAACATTTTC	AATTTTAGAA	GGAATAAATG	CAATTATAGA	4250
AGTTGATTTA	TTATCTAAAT	CATATAAATT	ACTTATTTCT	GGCGAATTAA	4300
AAATATTGAT	GTTAAATTCA	AATCATATTC	AACAGAAAAT	AGATTATATA	4350
GGATTCAATA	GCGAATTACA	GAAAAATATA	CCATATAGCT	TTGTAGATAG	4400
TGAAGGAAAA	GAGAATGGTT	TTATTAATGG	TTCAACAAAA	GAAGGTTTAT	4450
TTGTATCTGA	ATTACCTGAT	GTAGTTCTTA	TAAGTAAGGT	TTATATGGAT	4500
GATAGTAAGC	CTTCATTTGG	ATATTATAGT	AATAATTTGA	AAGATGTCAA	4550
AGTTATAACT	AAAGATAATG	TTAATATATT	AACAGGTTAT	TATCTTAAGG	4600
ATGATATAAA	AATCTCTCTT	TCTTTGACTC	TACAAGATGA	AAAAACTATA	4650
AAGTTAAATA	GTGTGCATTT	AGATGAAAGT	GGAGTAGCTG	AGATTTTGAA	4700
GTTCATGAAT	AGAAAAGGTA	ATACAAATAC	TTCAGATTCT	TTAATGAGCT	4750
TTTTAGAAAG	TATGAATATA	AAAAGTATTT	TCGTTAATTT	CTTACAATCT	4800
AATATTAAGT	TTATATTAGA	TGCTAATTTT	ATAATAAGTG	GTACTACTTC	4850
TATTGGCCAA	TTTGAGTTTA	TTTGTGATGA	AAATGATAAT	ATACAACCAT	4900
ATTTCAATTAA	GTTTAATACA	CTAGAAACTA	ATTATACTTT	ATATGTAGGA	4950
AATAGACAAA	ATATGATAGT	GGAACCAAAT	TATGATTTAG	ATGATTCTGG	5000
AGATATATCT	TCAACTGTTA	TCAATTTCTC	TCAAAAGTAT	CTTTATGGAA	5050
TAGACAGTTG	TGTTAATAAA	GTTGTAATTT	CACCAAATAT	TTATACAGAT	5100
GAAATAAATA	TAACGCCTGT	ATATGAAACA	AATAATACTT	ATCCAGAAGT	5150
TATTGTATTA	GATGCAAATT	ATATAAATGA	AAAAATAAAT	GTTAATATCA	5200
ATGATCTATC	TATACGATAT	GTATGGAGTA	ATGATGGTAA	TGATTTTATT	5250
CTTATGTCAA	CTAGTGAAGA	AAATAAGGTG	TCACAAGTTA	AAATAAGATT	5300
CGTTAATGTT	TTTAAAGATA	AGACTTTGGC	AAATAAGCTA	TCTTTTAACT	5350
TTAGTGATAA	ACAAGATGTA	CCTGTAAGTG	AAATAATCTT	ATCATTTACA	5400
CCTTCATATT	ATGAGGATGG	ATTGATTGGC	TATGATTTGG	GTCTAGTTTC	5450
TTTATATAAT	GAGAAATTTT	ATATTAATAA	CTTTGGAATG	ATGGTATCTG	5500
GATTAATATA	TATTAATGAT	TCATTATATT	ATTTTAAACC	ACCAGTAAAT	5550
AATTTGATAA	CTGGATTTGT	GACTGTAGGC	GATGATAAAT	ACTACTTTAA	5600
TCCAATTAAT	GGTGGAGCTG	CTTCAATTGG	AGAGACAATA	ATTGATGACA	5650
AAAATTATTA	TTTCAACCAA	AGTGGAGTGT	TACAAACAGG	TGTATTTAGT	5700
ACAGAAGATG	GATTTAAATA	TTTTGCCCCA	GCTAATACAC	TTGATGAAAA	5750
CCTAGAAGGA	GAAGCAATTG	ATTTTACTGG	AAAATTAATT	ATTGACGAAA	5800
ATATTTATTA	TTTTGATGAT	AATTATAGAG	GAGCTGTAGA	ATGGAAAGAA	5850
TTAGATGGTG	AAATGCACTA	TTTTAGCCCA	GAAACAGGTA	AAGCTTTTAA	5900
AGGTCTAAAT	CAAATAGGTG	ATTATAAATA	CTATTTCAAT	TCTGATGGAG	5950
TTATGCAAAA	AGGATTTGTT	AGTATAAATG	ATAATAAACA	CTATTTTGAT	6000
GATTCTGGTG	TTATGAAAGT	AGGTTACACT	GAAATAGATG	GCAAGCATTT	6050
CTACTTTGCT	GAAAACGGAG	AAATGCAAAT	AGGAGTATTT	AATACAGAAG	6100
ATGGATTTAA	ATATTTTGCT	CATCATAATG	AAGATTTAGG	AAATGAAGAA	6150
GGTGAAGAAA	TCTCATATTC	TGGTATATTA	AATTTCAATA	ATAAAATTTA	6200
CTATTTTGAT	GATTCATTTA	CAGCTGTAGT	TGGATGGAAA	GATTTAGAGG	6250
ATGGTTCAAA	GTATTATTTT	GATGAAGATA	CAGCAGAAGC	ATATATAGGT	6300

TTGTCATTAA	TAAATGATGG	TCAATATTAT	TTTAATGATG	ATGGAATTAT	6350
GCAAGTTGGA	TTTGTCACTA	TAAATGATAA	AGTCTTCTAC	TTCTCTGACT	6400
CTGGAATTAT	AGAATCTGGA	GTACAAAACA	TAGATGACAA	TTATTTCTAT	6450
ATAGATGATA	ATGGTATAGT	TCAAATTGGT	GTATTTGATA	CTTCAGATGG	6500
ATATAAATAT	TTTGCACCTG	CTAATACTGT	AAATGATAAT	ATTTACGGAC	6550
AAGCAGTTGA	ATATAGTGGT	TTAGTTAGAG	TTGGGGAAGA	TGTATATTAT	6600
TTTGGAGAAA	CATATACAAT	TGAGACTGGA	TGGATATATG	ATATGGAAAA	6650
TGAAAGTGAT	AAATATTATT	TCAATCCAGA	AACTAAAAAA	GCATGCAAAG	6700
GTATTAATTT	AATTGATGAT	ATAAAATATT	ATTTTGATGA	GAAGGGCATA	6750
ATGAGAACGG	GTCTTATATC	ATTTGAAAAT	AATAATTATT	ACTTTAATGA	6800
GAATGGTGAA	ATGCAATTTG	GTTATATAAA	TATAGAAGAT	AAGATGTTCT	6850
ATTTTGGTGA	AGATGGTGTC	ATGCAGATTG	GAGTATTTAA	TACACCAGAT	6900
GGATTTAAAT	ACTTTGCACA	TCAAAATACT	TTGGATGAGA	ATTTTGAGGG	6950
AGAATCAATA	AACTATACTG	GTTGGTTAGA	TTTAGATGAA	AAGAGATATT	7000
ATTTTACAGA	TGAATATATT	GCAGCAACTG	G TTCAGTTAT	TATTGATGGT	7050
GAGGAGTATT	ATTTTGATCC	TGATACAGCT	CAATTAGTGA	TTAGTGAATA	7100
G					7101

2) INFORMATION FOR SEQ ID NO: 2131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131

AAGCMATTGT TGTAATTTTT GAAAG

25

2) INFORMATION FOR SEQ ID NO: 2132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132

TCATATCCAT AGCAATAGTT CTA

23

2) INFORMATION FOR SEQ ID NO: 2133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid

1100

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133

CCACGCACAW AAAC TTGTTT TAGAAGTAGC AGCWCAGCGT GG

42

2) INFORMATION FOR SEQ ID NO: 2134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134

CGCGTGAAGC TTCTGTG

17

2) INFORMATION FOR SEQ ID NO: 2135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135

TCTCGCCGTT ATTCAGTTTC

20

2) INFORMATION FOR SEQ ID NO: 2136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136

CCAACGCGTC CTCAATCATT TCTAACTTCT ATGGCCGGCG TTGG

44

2) INFORMATION FOR SEQ ID NO: 2137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137

ATGATCACCG	GTGCTGCCCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
CGCCGATGGT	CCGATGCCrC	AAACCCGTGA	GCACATCCTG	CTGTCCCGTC	100
AGGTAGGCGT	TCCGTACATC	GTGGTCTTCC	TGAACAAGGC	CGACCTGGTA	150
GACGACGCTG	AGCTGCTGGA	ACTGGTCGAG	ATGGAAGTTC	GCGACCTGCT	200
GTCCACCTAC	GACTTCCCAG	GCGACGACAC	TCCGATCATC	ATCGGTTCGG	250
CTCGTATGGC	CCTGGAAGGC	AAAGACGACA	ACGAAATGGG	CACTACCGCT	300
GTCAAGAAGC	TGGTAGAAAC	TCTGGATGCC	TACATCCCTG	AGCCAGTTCG	350
TGCCATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCGTGG	TACCGTTGTT	ACCGGTCGTA	TCGAGCGTGG	CATCGTTTCG	450
GTTCAGGATC	CGCTGGAAAT	CGTTGGTCTG	CGTGACACCA	CCACCACCAC	500
CTGCACCGGT	GTTGAGATGT	TCCGCAAGCT	GCTGGACGAA	GGTCGTGCTG	550
GCGAGAACTG	CGGCGTTCTG	CTGCGTGGTA	CCAAGCGTGA	CGACGTTGAG	600
CGTGGCCAGG	TTCTGGTCAA	GCCAGGTTTCG	GTCAAGCCGC	ACACCAAGTT	650
CACCGCAGAA	GTCTACGTCC	TGTCGAAGGA	AGAAGGCGGC	CGTCACACTC	700
CGTTCTTCAA	AGGCTACCGT	CCACAGTTCT	ACTTCCGTAC	CACTGACGTG	750
ACCGGTA ACT	GCGAACTGCC	GGAAGGCGTT	GAAATGGTAA	TGCCAGGTGA	800
CAACATTCAG	ATGACTGTTA	CCCTGATCAA	GACCATCGCA	ATGGAAGACG	850
GTCTGCGCTT	CGCTATCCGT	GAAGGCGGTC	GTACCGTCG		889

2) INFORMATION FOR SEQ ID NO: 2138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (B) STRAIN: PAO-1
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138

AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
GGCTGCCGAC	GGCCCCATGC	CGCAGACCCG	CGAGCACATC	CTGCTGTCCC	100
GCCAGGTAGG	CGTTCCCTAC	ATCGTCGTGT	TCCTGAACAA	GGCCGACATG	150
GTCGACGACG	CCGAGCTGCT	GGAAGTGGTC	GAGATGGAAG	TTCGCGATCT	200
GCTGAACACC	TACGACTTCC	CGGGCGACGA	CACTCCGATC	ATCATCGGTT	250
CCGCGCTGAT	GGCGCTGGAA	GGCAAGGATG	ACAACGGCAT	CGGCGTAAGC	300
GCCGTGCAGA	AGCTGGTAGA	GACCCTGGAC	TCCTACATTC	CGGAGCCGGT	350
TCGTGCCATC	GACCAGCCGT	TCCTGATGCC	GATCGAAGAC	GTGTTCTCGA	400
TCTCCGGCCG	CGGTACCGTG	GTAACCGGTC	GTGTAGAGCG	CGGCATCATC	450
AAGGTCCAGG	AAGAAGTGGA	AATCGTCGGC	ATCAAGGCGA	CCACCAAGAC	500
TACCTGCACC	GGCGTTGAAA	TGTTCCGCAA	GCTGCTCGAC	GAAGGTCGTG	550
CTGGTGAGAA	CGTTGGTATC	CTGCTGCGTG	GCACCAAGCG	TGAAGACGTA	600
GAGCGTGGCC	AGGTTCTGGC	CAAGCCGGGC	ACCATCAAGC	CGCACACCAA	650
GTTCGAGTGC	GAAGTGTACG	TGCTGTCCAA	GGAAGAAGGT	GGTCGTCACA	700
CCCCGTTCTT	CAAGGGCTAC	CGTCCGCAGT	TCTACTTCCG	TACCACCGAC	750
GTGACCGGTA	ACTGCGAACT	GCCGGAAGGC	GTAGAGATGG	TAATGCCGGG	800
CGACAACATC	AAGATGGTTG	TCACCCTGAT	CGCTCCGATC	GCCATGGAAG	850
ATGGCCTGCG	CTTCGCGATC	CGCGAAGGCG	GCCGTACCGT	TGGCGCCGGC	900

2) INFORMATION FOR SEQ ID NO: 2139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni*
- (B) STRAIN: NCTC 11168
- (C) ACCESSION NUMBER: AL139074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139

ATGCAAGGAT	TTATTTTACA	GGTATTAGGT	CCGGTTGTTG	ATGTAGATTT	50
TAACGACTAT	TTGCCTCAAA	TTAATGAAGC	AATTGTTGTA	AATTTTGAAA	100
GCGAAGGAAA	AAAACATAAA	CTTGTTTTAG	AAGTAGCAGC	TCATTTAGGA	150
GATAATAGAG	TTAGAAGTAT	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	200
GGGCTTAAAA	GCTGAGGCTT	TAGGTGCTCC	CATTAGTGTT	CCTGTTGGTG	250
AGAAAGTTTT	AGGAAGAATT	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	300
GGTGAAGAAA	TTTCTTTCGA	TAAAAAATGG	GCAATTCATA	GAGATCCACC	350
AGCTTTTGA	GATCAAAGCA	CAAAAAGTGA	GATTTTGA	ACAGGGATTA	400
AAGTTGTAGA	TTTACTTGCT	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	450
TTTGGTGGTG	CAGGTGTTGG	TAAAACTGTT	ATTATTATGG	AGCTTATTCA	500
CAATGTTGCA	TTTAAGCATA	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	550
AGAGAACTCG	TGAAGGAAAT	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	600
GTTTTAGACA	AAGTTGCTCT	ATGTTATGGA	CAAATGAATG	AACCACCAGG	650
GGCAAGAAAT	CGTATTGCTT	TAACAGGTTT	AACAATGGCT	GAGTATTTTA	700
GAGATGAAAT	GGGTCTTGAT	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	750
TTTTTACAAT	CAGGTTCTGA	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	800
AGCTGTGGGT	TATCAACCAA	CCTTAGCAAG	TGAAATGGGT	AAATTCCAAG	850
AAAGAATTAC	TTCAACTAAA	AAAGGCTCAA	TCACTTCAGT	TCAAGCTGTT	900
TACGTTCCAG	CTGATGACTT	AACAGACCCA	GCTCCAGCAA	CTGTTTTTGC	950

TCACTTAGAT	GCTACAACGG	TTTTAAATAG	AGCTATTGCT	GAAAAGGGTA	1000
TTTATCCTGC	AGTTGACCCA	CTTGACTCAA	CTTCAAGAAT	GCTTGACCCA	1050
AATATCATTG	GAGAAGAACA	TTATAAAGTT	GCTCGTGGTG	TTCAATCAGT	1100
GCTTCAAAAA	TACAAAGATT	TACAAGATAT	CATCGCCATT	TTAGGTATGG	1150
ATGAGCTTAG	CGAAGAGGAT	AAACTTGTAG	TTGAAAGAGC	AAGAAAGATT	1200
GAAAAATTCT	TATCACAACC	ATTTTTCGTT	GCAGAAGTTT	TCACAGGTAG	1250
CCCAGGAAAA	TATATAAGCC	TTGAAGATAC	AATAGCAGGA	TTTAAGGGAA	1300
TTTTAGAAGG	TAAATATGAT	CATTTACCAG	AAAATGCTTT	CTATATGGTT	1350
GGAAATATAG	ATGAAGCTAT	TGCAAAAGCG	GATAAATTAA	AAGGTTAA	1398

2) INFORMATION FOR SEQ ID NO: 2140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 670
- (C) ACCESSION NUMBER: X67867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAGTT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAAC TCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400

TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCCAACGGTG	GAATTTACCA	CAAACCCATG	1500
TATATCAATA	AGGTCGTCTT	CAGTGACGGT	AGTAAAAAAG	AATTTTCAGA	1550
TGTAGGTACA	CGAGCTATGA	AAGAAACAAC	TGCTTACATG	ATGACCGAAA	1600
TGATGAAAAC	TGTCTTGGCA	TACGGAAGT	GTCGTGGAGC	CTATCTCCCA	1650
TGGTTAGCGC	AAGCTGGTAA	GACAGGTACT	TCTAACTACA	CAGATGATGA	1700
AATTGAAAAA	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCTG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGAATTTGT	ATTCAAAAAT	1950
GGAGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCGATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCA					2157

2) INFORMATION FOR SEQ ID NO: 2141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141

CACCAGTCAC AGAAAAGC

18

2) INFORMATION FOR SEQ ID NO: 2142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142

GCCTTAATTT CGGATAGTGC

20

2) INFORMATION FOR SEQ ID NO: 2143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1105

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143

GAGAAAGAGC CCAATTATCT AATGT

25

2) INFORMATION FOR SEQ ID NO: 2144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3075 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: J2870
- (C) ACCESSION NUMBER: X75439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144

TTGACAAAGA	AATATTTAAA	CACCCAGAAT	GAAATATCAG	CATTTTGGAA	50
TACTCAAAAG	ATATTTAAAA	AATCAATTGA	CAATAGAAAA	GGACAGGAAA	100
GTTTTGTTTT	TTATGACGGC	CCCCCAACTG	CAAATGGCCT	TCCTCATGCT	150
GGCCATGTTC	TTGGAAGAGT	AATCAAGGAT	TTAGTTGCAA	GATTAAAAAC	200
TATGCAAGGT	TTTTATGTAG	AAAGAAAAGC	AGGATGGGAT	ACCCATGGCT	250
TACCAGTTGA	ATTAGAGGTT	GAAAAAATAA	TTGGAATTAA	AGGAAAACAA	300
GACATTGAAA	AGTATGGAAT	AGAAAATTTT	ATAAATGAAT	GTAAAAAAG	350
TGTATTTAAT	TATGAAAAAG	AATGGCGGGA	TTTTTCTAAA	GATTTAGGAT	400
ACTGGGTTGA	CATGGACTCC	CCCTATATAA	CTCTTGAGAA	TAATTATATT	450
GAAAGTGTAT	GGAATATATT	ATCTACATTC	CATAAAAAAG	GACTATTATA	500
TAAGGGACAT	AAGGTGACTC	CTTATTGTAC	ACATGATCAA	ACCGCTTTAA	550
GTTCTCATGA	AGTAGCGCAA	GGCTATAAAA	ACGTTAAAGA	TTTATCAGCT	600
GTTGTTAAT	TTCAACTTAC	AAATAGTAAA	GATACTTATT	TCTTAAGTTG	650
GACTACCACT	CCCTGGACTT	TGCCTGCAAA	TGTAGCATT	GCTATAAATA	700
AAGATCTTAA	TTATTCAAAA	ATTCGGGTAG	AAAATGAGTA	TTATATCTTA	750
GCTACAGATC	TAATTAATTC	TATAATAACT	GAAAAATACG	AAATTATTGA	800
TACCTTTTCA	GGAAGTAATT	TAATTAATTT	AAAATACATT	CCTCCTTTTG	850
AAAGCGACGG	TTAGTTAAT	GCATATTACG	TTGTTGATGG	AGAATTTGTT	900
ACTAACTCAG	AAGGAACTGG	TATTGTTTAT	ATAGCACCAG	CTCATGGGGA	950
AGATGACTAC	CAATTGGTTT	TAGAGCGTGA	TTTGGATTTC	TTAAATGTTA	1000
TAACAAGAGA	AGGAGTATAT	AATGATAGGT	TCCCTGAATT	AGTTGGTAAT	1050
AAAGCTAAAA	ATAGTGATAT	AGAAATCATA	AAATTATTAT	CCAAAAACA	1100
ACTTTTATAT	AAAAAACAAA	AATATGAGCA	TAATTATCCT	CATTGTTGGA	1150
GATGTGGTAA	TCCTTTGATA	TATTATGCGA	TGGAAGGTTG	GTTTATTAAA	1200
ACAATAATT	TTAAGAATGA	AATTATTAAC	AATAATAATA	ATATAGAGTG	1250
GTTTCCTTCT	CATATTAAGG	AAGGGAGAAT	GGGAAATTTT	TTAGAAAATA	1300
TGGTTGATTG	GAACATTGGT	AGAAATAGAT	ATTGGGGAAC	ACCATTAAT	1350
GTATGGATTT	GCAATGATTG	TAATCACGAA	TACGCACCAA	GTAGTATTAA	1400
GGATTTACAA	AATAATTCCA	TCAATAAAAT	TGATGAAGAT	ATTGAGTTGC	1450
ATAGACCTTA	TGTTGATAAT	ATCACTCTTA	GTTGCCCTAA	GTGTAATGGG	1500

1106

AAAATGTCTC	GAGTAGAAGA	AGTAATCGAT	GTTTGGTTTG	ATAGCGGCTC	1550
TATGCCGTTT	GCTCAGCATC	ATTATCCTTT	TGATAACCAG	AAAATTTTTA	1600
ATCAACACTT	TCCAGCTGAT	TTTATTGCAG	AAGGAGTTGA	TCAAACGAGA	1650
GGCTGGTTTT	ACAGTTTACT	AGTAATTTCT	ACTATTCTAA	AAGGAAAATC	1700
TTCTTATAAA	CGTGCTTTAT	CTTTAGGACA	TATTCTAGAC	AGTAATGGTA	1750
AAAAAATGTC	TAAAAGTAAA	GGAAACGTTA	TTAATCCAAC	TGAATTAATT	1800
AATAAGTACG	GAGCCGATTC	TTTAAGATGG	GCCTTAATTT	CGGATAGTGC	1850
TCCATGGAAT	AACAAAAGAT	TCTCAGAAAA	TATAGTAGCT	CAGACCAAAT	1900
CGAAATTTAT	AGATACGCTT	GATAATATTT	ATAAATTTTA	TAATATGTAT	1950
AATAAAATAG	ATCACTATAA	TCCTAATAAT	GAAATTACAA	AAAGTAGAAA	2000
TACATTAGAT	AATTGGGCTC	TTTCTCGCTT	AAACACCTTA	ATAAAAGAAA	2050
GTAATATTTA	TGTAAATAAT	TACGATTTCA	CTTCCGCAGC	CAGATTAATT	2100
AACGAATATA	CCAATACAAT	AAGTAATTGG	TATATCGGAG	ATTCGAGAGG	2150
ACGATTTTGG	GAACAAGGAA	TTTCTAACGA	TAAAAAAGAT	GCGTACAATA	2200
CGCTTTATGA	AATTTTAACA	ACTTTATCAA	GACTAGTGGC	TCCATTTGTT	2250
CCATTTATAT	CTGAAAAAAT	CCATTATAAT	TTGACTGGAA	AAAGTGTGCA	2300
TTTACAAGAT	TATCCACAAT	ATAAAGAAAG	TTTTATTAAT	CAAGCATTGG	2350
AAGATGAAAT	GCATACCGTT	ATAAAAATTG	TAGAATTATC	TAGACAGGCT	2400
CGCAAAAATG	CAGATTTAAA	AATTAAGCAA	CCTTTATCGA	AAATGGTGAT	2450
TAAACCTAAT	AGTCAATTAA	ACTTAAGTTT	TTTACCTAAT	TACTATTCAA	2500
TAATAAAAGA	CGAATTAAAT	ATAAAAAACA	TTGAATTAAC	TGATAATATT	2550
AATGACTATA	TTACCTATGA	GCTTAAATTG	AATTTTTCTT	CTGTGGGACC	2600
AAAAC TAGGG	AACAAAACGA	AAAATATTCA	AACATTGATA	GACTCCCTAT	2650
CAGAGTATGA	TAAAAAAAGT	TTAATTGAGT	CTAATAACTT	CAAAAGTTTA	2700
TCTTCTGATG	CTGAGTTAAC	TAAGGATGAT	TTTATAATTA	AAACCTTACC	2750
TAAGGATAGT	TATCAACTCA	GTGAAGATAA	TGACTGCGTT	ATATTATTAG	2800
ATAAAAATTT	ATCTCCTGAA	TTAATTCGCG	AAGGACATGC	TAGAGAGCTC	2850
ATTAGATTAA	TTCAACAATT	AAGAAAAAAG	AAAAATTTAC	CAATAAATCA	2900
ACGTATTGAT	ATTTATATCG	GTGTAAGTGG	GGAATTATTA	GAATCAATAA	2950
AAACCAATAA	AAATATGTTT	AAAGAAAATT	TCGTGATTAA	AAATATACAC	3000
TTAAATGTTA	TAGATGAATA	TGAAAATACT	ATTCATTTTA	ATAATAAAGA	3050
AATAAAAATT	TCCTTATTAT	ATTAA			3075

2) INFORMATION FOR SEQ ID NO: 2145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145

GCAAGATGTG GCGTGTTACG GT

22

2) INFORMATION FOR SEQ ID NO: 2146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1107

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146

GGGGCGAAGA AGTTGTCCAT ATT

23

2) INFORMATION FOR SEQ ID NO: 2147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: V00622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147

ATGGAGAAAA	AAATCACTGG	ATATAACCACC	GTTGATATAT	CCCAATGGCA	50
TCGTAAAGAA	CATTTTGAGG	CATTTTCAGTC	AGTTGCTCAA	TGTACCTATA	100
ACCAGACCGT	TCAGCTGGAT	ATTACGGCCT	TTTTAAAGAC	CGTAAAGAAA	150
AATAAGCACA	AGTTTTATCC	GGCCTTTATT	CACATTCTTG	CCCGCCTGAT	200
GAATGCTCAT	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT	GAGCTGGTGA	250
TATGGGATAG	TGTTCAACCCT	TGTTACACCG	TTTTCCATGA	GCAAACCTGAA	300
ACGTTTTTCAT	CGCTCTGGAG	TGAATACCAC	GACGATTTC	GGCAGTTTCT	350
ACACATATAT	TCGCAAGATG	TGGCGTGTTA	CGGTGAAAAC	CTGGCCTATT	400
TCCCTAAAGG	GTTTATTGAG	AATATGTTTT	TCGTCTCAGC	CAATCCCTGG	450
GTGAGTTTCA	CCAGTTTTGA	TTTAAACGTG	GCCAATATGG	ACAACTTCTT	500
CGCCCCCGTT	TTCACCATGG	GCAAATATTA	TACGCAAGGC	GACAAGGTGC	550
TGATGCCGCT	GGCGATTCAG	GTTTCATCATG	CCGTCTGTGA	TGGCTTCCAT	600
GTCGGCAGAA	TGCTTAATGA	ATTACAACAG	TACTGCGATG	AGTGGCAGGG	650
CGGGGCGTAA					660

2) INFORMATION FOR SEQ ID NO: 2148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148

CAGATTAAAT GCGGATTCAG CC

22

2) INFORMATION FOR SEQ ID NO: 2149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149

ATCAGGTAAA TCATCAGCGG ATA

23

2) INFORMATION FOR SEQ ID NO: 2150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: K12
- (C) ACCESSION NUMBER: X53796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150

ATGAATTTTA	CCCGGATTGA	CCTGAATACC	TGGAATCGCA	GGGAACACTT	50
TGCCCTTTAT	CGTCAGCAGA	TTAAATGCGG	ATTCAGCCTG	ACCACCAAAC	100
TCGATATTAC	CGCTTTGCGT	ACCGCACTGG	CGGAGACAGG	TTATAAGTTT	150
TATCCGCTGA	TGATTTACCT	GATCTCCCGG	GCTGTTAATC	AGTTTCCGGA	200
GTTCCGGATG	GCACTGAAAG	ACAATGAACT	TATTTACTGG	GACCAGTCAG	250
ACCCGGTCTT	TACTGTCTTT	CATAAAGAAA	CCGAAACATT	CTCTGCACTG	300
TCCTGCCGTT	ATTTTCCGGA	TCTCAGTGAG	TTTATGGCAG	GTTATAATGC	350
GGTAACGGCA	GAATATCAGC	ATGATACCAG	ATTGTTTCCG	CAGGGAAATT	400
TACCGGAGAA	TCACCTGAAT	ATATCATCAT	TACCGTGGGT	GAGTTTTGAC	450
GGATTTAACC	TGAACATCAC	CGGAAATGAT	GATTATTTTG	CCCCGGTTTT	500
TACGATGGCA	AAGTTTCAGC	AGGAAGGTGA	CCGCGTATTA	TTACCTGTTT	550
CTGTACAGGT	TCATCATGCA	GTATGTGATG	GCTTTCATGC	AGCACGGTTT	600
ATTAATACAC	TTCAGCTGAT	GTGTGATAAC	ATACTGAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

1109

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151

ATATTTTCAGC ATTACCTTGG GTT

23

2) INFORMATION FOR SEQ ID NO: 2152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152

TACACAACCTC TTGTAGCCGA TTA

23

2) INFORMATION FOR SEQ ID NO: 2153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
- (C) ACCESSION NUMBER: X07848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153

ATGAACTATA	CAAAATTTGA	TGTAAAAAAT	TGGGTTCGCC	GTGAGCATTT	50
TGAGTTTTAT	CGGCATCGTT	TACCATGTGG	TTTTAGCTTA	ACAAGCAAAA	100
TTGATATCAC	GACGTTAAAA	AAGTCATTGG	ATGATTCAGC	GTATAAGTTT	150
TATCCGGTAA	TGATCTATCT	GATTGCTCAG	GCCGTGAATC	AATTTGATGA	200
GTTGAGAATG	GCGATAAAAG	ATGATGAATT	GATCGTATGG	GATTCAGTCG	250
ACCCACAATT	CACCGTATTC	CATCAAGAAA	CAGAGACATT	TTCAGCACTG	300
AGTTGCCCAT	ACTCATCCGA	TATTGATCAA	TTTATGGTGA	ATTATTTATC	350
GGTAATGGAA	CGTTATAAAA	GTGATACCAA	GTTATTTTCCT	CAAGGGGTAA	400
CACCAGAAAA	TCATTTAAAT	ATTTTCAGCAT	TACCTTGGGT	TAATTTTGAT	450
AGCTTTAATT	TAAATGTTGC	TAATTTTACC	GATTATTTTG	CACCCATTAT	500
AACAATGGCA	AAATATCAGC	AAGAAGGGGA	TAGACTGTTA	TTGCCGCTCT	550
CAGTACAGGT	TCATCATGCA	GTTTGTGATG	GCTTCCATGT	TGCACGCTTT	600
ATTAATCGGC	TACAAGAGTT	GTGTAACAGT	AAATTAAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2154

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154

CGCCATTCAG AGTTTAGGAC

20

2) INFORMATION FOR SEQ ID NO: 2155

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155

TTCCATACCG TTGCGTATCA CTT

23

2) INFORMATION FOR SEQ ID NO: 2156

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
(B) STRAIN: CP590
(C) ACCESSION NUMBER: M74769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156

ATGGTATTTG	AAAAAATTGA	TAAAAATAGT	TGGAACAGAA	AAGAGTATTT	50
TGACCACTAC	TTTGCAAGTG	TACCTTGTA	ATACAGCATG	ACCGTTAAAG	100
TGGATATCAC	ACAAATAAAG	GAAAAGGGAA	TGAAACTATA	TCCTGCAATG	150
CTTTATTATA	TTGCAATGAT	TGTAAACCGC	CATTCAGAGT	TTAGGACGGC	200
AATCAATCAA	GATGGTGAAT	TGGGGATATA	TGATGAGATG	ATACCAAGCT	250

1111

ATACAATATT	TCACAATGAT	ACTGAAACAT	TTTCCAGCCT	TTGGACTGAG	300
TGTAAGTCTG	ACTTTAAATC	ATTTT TAGCA	GATTATGAAA	GTGATACGCA	350
ACGGTATGGA	AACAATCATA	GAATGGAAGG	AAAGCCAAAT	GCTCCGGAAA	400
ACATTTTTAA	TGTATCTATG	ATACCGTGGT	CAACCTTCGA	TGGCTTTAAT	450
CTGAATTTGC	AGAAAGGATA	TGATTATTTG	ATTCCTATTT	TTACTATGGG	500
GAAATATTAT	AAAGAAGATA	ACAAAATTAT	ACTTCCTTTG	GCAATTCAAG	550
TTCATCACGC	AGTATGTGAC	GGATTT CACA	TTTGCCGTTT	TGTAAACGAA	600
TTGCAGGAAT	TGATAAATAG	TTAA			624

2) INFORMATION FOR SEQ ID NO: 2157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157

CCACAGAAAT TGATATTAGT GTTTTAT

27

2) INFORMATION FOR SEQ ID NO: 2158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158

TCGCTATTGT AACCAGTTCT A

21

2) INFORMATION FOR SEQ ID NO: 2159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159

ATGAACTTTA	ATAAAATTGA	TTTAGACAAT	TGGAAGAGAA	AAGAGATATT	50
TAATCATTAT	TTGAACCAAC	AAACGACTTT	TAGTATAACC	ACAGAAATTG	100
ATATTAGTGT	TTTATACCGA	AACATAAAAC	AAGAAGGATA	TAAATTTTAC	150
CCTGCATTTA	TTTTCTTAGT	GACAAGGGTG	ATAAACTCAA	ATACAGCTTT	200
TAGAACTGGT	TACAATAGCG	ACGGAGAGTT	AGGTTATTGG	GATAAGTTAG	250
AGCCACTTTA	TACAATTTTT	GATGGTGTAT	CTAAAACATT	CTCTGGTATT	300
TGGACTCCTG	TAAAGAATGA	CTTCAAAGAG	TTTTATGATT	TATACCTTTC	350
TGATGTAGAG	AAATATAATG	GTTCGGGGAA	ATTGTTTCCC	AAAACACCTA	400
TACCTGAAAA	TGCTTTTTTCT	CTTTCTATTA	TTCCATGGAC	TTCATTTACT	450
GGGTTTAACT	TAAATATCAA	TAATAATAGT	AATTACCTTC	TACCCATTAT	500
TACAGCAGGA	AAATTCATTA	ATAAAGGTAA	TTCAATATAT	TTACCGCTAT	550
CTTTACAGGT	ACATCATTCT	GTTTGTGATG	GTTATCATGC	AGGATTGTTT	600
ATGAACTCTA	TTCAGGAATT	GTCAGATAGG	CCTAATGACT	GGCTTTTATA	650
A					651

2) INFORMATION FOR SEQ ID NO: 2160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160

TTTTGAACAC TATTTTAACC AGC

23

2) INFORMATION FOR SEQ ID NO: 2161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161

GATTTAACTT ATCCCAATAA CCT

23

2) INFORMATION FOR SEQ ID NO: 2162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

1113

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: X02166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162

ATGACTTTTA	ATATTATCAA	ATTAGAAAAT	TGGGATAGAA	AAGAATATTT	50
TGAACACTAT	TTTAACCAGC	AAACTACGTA	TAGCATTACT	AAAGAAATTG	100
ATATTACTTT	GTTTAAAGAT	ATGATAAAAA	AGAAAGGATA	TGAAATTTAT	150
CCTTCTTTGA	TTTATGCAAT	TATGGAAGTT	GTAAATAAAA	ATAAAGTGTT	200
TAGAACAGGA	ATTAATAGTG	AGAATAAATT	AGGTTATTGG	GATAAGTTAA	250
ATCCTTTGTA	TACAGTTTTT	AATAAGCAAA	CTGAAAAATT	TACTAACATT	300
TGGACTGAAT	CTGATAACAA	CTTCACTTCT	TTTTATAATA	ATTATAAAAA	350
TGACTTGCTT	GAATATAAAG	ATAAAGAAGA	AATGTTTCCT	AAAAAACCGA	400
TACCTGAAAA	CACCATACCG	ATTTCAATGA	TTCCTTGGAT	TGATTTTAGT	450
TCATTTAATT	TAAACATTGG	TAACAATAGC	AACTTTTTAT	TGCCTATTAT	500
TACGATAGGT	AAATTTTATA	GTGAGAATAA	TAAAATTTAT	ATACCAGTTG	550
CTTTGCAGCT	TCATCATGCT	GTATGTGATG	GTTACCATGC	TTCATTATTT	600
ATGAATGAAT	TTCAAGATAT	AATTCATAAG	GTAGATGATT	GGATTTAG	648

2) INFORMATION FOR SEQ ID NO: 2163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163

ACCTTCATCC TACCGATGTG GGTT

24

2) INFORMATION FOR SEQ ID NO: 2164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164

CAACGACACC AGCACTGCCA TTG

23

2) INFORMATION FOR SEQ ID NO: 2165

1114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
- (B) STRAIN: H3380
- (C) ACCESSION NUMBER: AF071555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165

ATGACCACCA	CACGCCCCGC	GTGGGCCTAT	ACGCTGCCGG	CAGCACTGCT	50
GCTGATGGCT	CCTTTCGACA	TCCTCGCTTC	ACTGGCGATG	GATATTTATC	100
TCCCTGTCGT	TCCAGCGATG	CCCGGCATCC	TGAACACGAC	GCCCGCTATG	150
ATCCAACTCA	CGTTGAGCCT	CTATATGGTG	ATGCTCGGCG	TGGGCCAAGT	200
GATTTTTTGGT	CCGCTCTCAG	ACAGAATCGG	GCGACGGCCA	ATTCTACTTG	250
CGGGCGCAAC	GGCTTTCGTC	ATTGCGTCTC	TGGGAGCAGC	TTGGTCTTCA	300
ACTGCACCGG	CCTTTGTCGC	TTTCCGTCTA	CTTCAAGCAG	TGGGCGCGTC	350
GGCCATGCTG	GTGGCGACGT	TCGCGACGGT	TCGCGACGTT	TATGCCAACC	400
GTCCTGAGGG	TGTCGTCATC	TACGGCCTTT	TCAGTTCGAT	GCTGGCGTTC	450
GTGCCTGCGC	TCGGCCCTAT	CGCCGGAGCA	TTGATCGGCG	AGTTCTTGGG	500
ATGGCAGGCG	ATATTCATTA	CTTTGGCTAT	ACTGGCGATG	CTCGCACTCC	550
TAAATGCGGG	TTTCAGGTGG	CACGAAACCC	GCCCTCTGGA	TCAAGTCAAG	600
ACGCGCCGAT	CTGTCTTGCC	GATCTTCGCG	AGTCCGGCTT	TTTGGGTTTA	650
CACTGTCGGC	TTTAGCGCCG	GTATGGGCAC	CTTCTTCGTC	TTCTTCTCGA	700
CGGCTCCCCG	TGTGCTCATA	GGCCAAGCGG	AATATTCCGA	GATCGGATTC	750
AGCTTTGCCT	TCGCCACTGT	CGCGCTTGTA	ATGATCGTGA	CAACCCGTTT	800
CGCGAAGTCC	TTTGTCGTCA	GATGGGGCAT	CGCAGGATGC	GTGGCGCGTG	850
GGATGGCGTT	GCTTGTTTGC	GGAGCGGTCC	TGTTGGGGAT	CGGCGAACTT	900
TACGGCTCGC	CGTCATTCCT	CACCTTCATC	CTACCGATGT	GGGTTGTTCG	950
GGTCGGTATT	GTCTTCACGG	TGTCCGTTAC	CGCGAACGGC	GCTTTGGCAG	1000
AGTTGACGA	CATCGCGGGA	TCAGCGGTCG	CGTTCTACTT	CTGCATCCAA	1050
AGCCTGATAG	TCAGTATCGT	CGGGACATTG	GCGGTGACGC	TGTTAAACGG	1100
CGATACAGCG	TGGCCCGTGA	TTTGTTACGC	CACGGCAATG	GCAGTGCTGG	1150
TGTCGTTGGG	GCTGGCGCTC	CTTCGATCCC	GTGATGCTGC	CACCGAGAAG	1200
TCGCCAGTCG	TCTAG				1215

2) INFORMATION FOR SEQ ID NO: 2166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166

GACAAACCAT TCCTGCTG

18

2) INFORMATION FOR SEQ ID NO: 2167

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167

CAGCAGCTGG GCGGCGGT

18

2) INFORMATION FOR SEQ ID NO: 2168

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168

CATCAAAGTT GGTGAAGAAG TTG

23

2) INFORMATION FOR SEQ ID NO: 2169

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169

CCCGTTTGCG AAAGGTGG

18

2) INFORMATION FOR SEQ ID NO: 2170

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1116

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170

ACGTGACGTT GACAAACCA

19

2) INFORMATION FOR SEQ ID NO: 2171

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171

TCGTTGGATT AACTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 2172

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172

GTGTTGAAAT GTTCCGTAAA

20

2) INFORMATION FOR SEQ ID NO: 2173

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173

AAGAAAAAAT CTTCGAACTG GCTA

24

2) INFORMATION FOR SEQ ID NO: 2174

1117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174

TCTACACGGC CGGTG

15

2) INFORMATION FOR SEQ ID NO: 2175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175

CCGCCATACC CCGTTT

16

2) INFORMATION FOR SEQ ID NO: 2176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176

CGGCATTACC ATTTCCACAC CTTT

24

2) INFORMATION FOR SEQ ID NO: 2177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177

GGCACGGACA AACCATTCTT GCTGCCTATC GAAGACGTGT TCCCGTGCC 49

2) INFORMATION FOR SEQ ID NO: 2178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178

GGCACGACAA ACCATTCTTG CTGCCTATCG AACGTGCC 38

2) INFORMATION FOR SEQ ID NO: 2179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179

GGCAGCTCTA CTTCCGTACC ACTGACGTAA CCGGCTGCC 39

2) INFORMATION FOR SEQ ID NO: 2180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180

TTCGCCGGCG TGGGC 15

2) INFORMATION FOR SEQ ID NO: 2181

(i) SEQUENCE CHARACTERISTICS:

1119

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181

AGCGCCACGC GCAGG

15

2) INFORMATION FOR SEQ ID NO: 2182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182

GCGCGCCAAC GACTTCTACC ACGAAATGGA AGAGTCGCGC GC

42

2) INFORMATION FOR SEQ ID NO: 2183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
- (B) STRAIN: ATCC 8750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183

TATCTTGGTT	WGCTCGGCCG	CTGACGGCCC	AATGCCTCAG	ACTCGCGAGC	50
ACATCCTGCT	GAGCCGTCAG	GTTGGCGTTC	CTTACATCAT	CGTGTTCCTG	100
AACAAGGCCG	ACATGGTTGA	TGACGAAGAG	CTGATCGAAC	TGGTTGAAAT	150
GGAAGTTCGC	GAGCTGTTGT	CCAAGTACGA	CTTCCCTGGC	GACGACACCC	200
CGATCATCAA	GGGTTCGGCC	AAACTGGCTC	TGGAAGGCCG	CGAAGGCCCA	250
CTGGGCAGCC	AAGCCGTTCT	GGCTCTGGCC	GAAGCGCTGG	ACAACTACAT	300
TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	GTTCTTGATG	CCTGTTGAAG	350
ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
CACGGTCAAG	ACCATTGTGA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700

1120

CGTACAACTG	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
GGTTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
TCGCCATGGA	AGAAGGT				817

2) INFORMATION FOR SEQ ID NO: 2184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
- (B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2184

TACAATTGAA	GTTGAAAGAT	CTATGCGTGT	TCTTGATGGT	GCTGTTGCGG	50
TATTTTGTTT	AGTGGGTGGG	GTGCAGCCTC	AAAGTGAAAC	AGTTTGGAGA	100
CAAGCAAATA	AATATGGTGT	TCCAAGAATA	GTATTTGTAA	ATAAAATGGA	150
TAGAATCGGT	GCAAATTTCT	ACAATGTAGA	AGATCAAATT	CGCAACCGTT	200
TAAAAGCTAA	TCCAGTTCCA	CTTCAAATTC	CAATCGGTGC	TGAGGATAAT	250
TTTAAAGGCG	TAATCGATCT	TGTAACATATG	AAAGCTTTAG	TTTGGGAAGA	300
TGATACTAAG	CCAACGGATT	ATGTAGAAAA	AGAAATTCCA	GCTGAACTTA	350
AAGAAAAGGC	AGAAGAATAT	CGCACAAAAA	TGATAGAAGC	AGTTTCTGAA	400
ACTTCAGATG	AGTTGATGGA	AAAATATTTA	GGTGGAGAAG	AATTAAGCCT	450
TGAAGAGATT	AAAACAGGGA	TTAAAGCAGG	ATGTTTAAAGT	CTTTCATATCG	500
TTCTATGCT	TTGCGGTACA	GCGTTTAAAA	ATAAAGGGGT	TCAACCTTTG	550
CTTGATGCTG	TTGTGGCTTA	TTTACCAGCT	CCTGATGAAG	TTGCTAATAT	600
CAAAGGGGAA	TATGAAGACG	GCACAGAAGT	TTCTGTAAAA	TCAACTGATG	650
ATGGCGAATT	TGCAGGACTT	GCATTTAAAA	TTATGACAGA	TCCATTTGTA	700
GGACAACTTA	CTTTCGTGCG	TGTTTATCGT	GGATGTTTAG	AAAGCGGTTC	750
TTATGCTTAT	AACTCAACCA	AAGATAAAAA	AGAAAGAATT	GGTCGTTTGT	800
TAAAAATGCA	CTCTAATAAA	AGAGAAGAAA	TTAAAGTTCT	TTACGCAGGA	850
GAAATCGGTG	CAGTTGTAGG	ACTTAAAGAT	ACTTTAACAG	GGGATACTCT	900
TGCAAGTGAA	AAAGATAAAG	TAATTCTTGA	AAGAATGGAT	TTCCCAGACC	950
CAGTTATTTT	TGTTGCAGTA	GAMCCAAAAA	CTAAAGCAGA	TCAAGAAAAA	1000
ATGTCTATTG	CACTAAATAA	ATTAGCTCAA	GAAGATCCAA	GCTTTAGAGT	1050
TTCTACGGAT	GAAGAAAGTG	GTCAAACAT	CATTTTCAGG	ATGGGTGAAT	1100
TACACCTTGA	AATTATTGTT	GATCGTATGC	TTCGTGAATT	TAAAGTGGAA	1150
GCTGAAGTGG	GACAACCTCA	AGTTGCTTAT	CGTGAAACTA	TCAGAAAAAC	1200
TGTTGAGCAA	GAATACAAAT	ACGCTAAGCA	ATCAGGCGGT	CGTGGTCAGT	1250
ATGGACATGT	ATTCTTACGC	CTTGAGCCAC	TTGAGCCAGG	AAGTGGATAC	1300
GAGTTTGTTA	ACGACATCAA	AGGTGGGGTA	ATTCCAAAAG	AATATATTCC	1350
TGCAGTAGAT	AAGGGTGTTT	AAGAAGCATT	GCAAAATGGT	GTTTTAGCAG	1400
GTTATCCAGT	AGAAGATGTT	AAAGTAACTG	TTTATGATGG	AAGTTATCAC	1450
GAGGTGGATT	CATCTGAGAT	GGCATTTAAA	CTTGCTGCTT	CTATGGGATT	1500
TAAAGAGGGT	GCTAGAAAAG	CAGGTGCTGT	GATCTTAGAG	CCTATGATGA	1550
AAGTTGAAGT	AGAAACTCCT	GAAGATTACA	TGGGCGATGT	TATTGGCGAT	1600
CTTAATAAGC	GTCGTGGTCA	AGTAAATAGC	ATGGATGAAA	GAGGTGGTAA	1650
TA					1652

2) INFORMATION FOR SEQ ID NO: 2185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185

GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTC	ATACATTCCA	300
GAGCCAAAGC	GTGATATCGA	TGATCCATTC	CTATTACCAA	TCGAAGATAT	350
CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
AGGTCGTGCA	GGTGATAACG	TTGGTGTTCT	ACTACGTGGT	ACCAAGCGTG	550
ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
TATGGCTGAA	GGCGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 2186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186

ACGCGCTCAA AGCAGAAGTA TACGTATTAT CAAAAGACGC GCGT

44

2) INFORMATION FOR SEQ ID NO: 2187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1612 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187

CAGTGGGTGG	GGTGCAGCCT	CAAAGTGAAA	CAGTTTGGAG	ACAAGCAAAT	50
AAATATGGTG	TTCCAAGAAT	AGTATTTGTA	AACAAAATGG	ATAGAATCGG	100
TGCAAATTTT	TACAATGTAG	AAGATCAAAT	TCGCAACCGT	TTAAAAGCTA	150
ATCCAGTTCC	ACTTCAAATT	CCAATCGGTG	CTGAGGATAA	TTTTAAAGGC	200
GTAATCGATC	TTGTAACAT	GAAAGCTTTA	GTTTGGGAAG	ATGATACTAA	250
GCCAACGGAT	TATGTAGAAA	AAGAAATTCC	AGCTGAACTT	AAAGAAAAGG	300
CAGAAGAATA	TCGCACAAAA	ATGATAGAAG	CAGTTTCTGA	AACTTCAGAT	350
GAGTTGATGG	AAAAATATTT	AGGCGGAGAA	GAATTAAGCC	TTGAAGAGAT	400
TAAAACAGGG	ATTAAAGCAG	GATGTTTAAG	TCTTTCTATC	GTTCCCTATG	450
TTTGCGGTAC	AGCGTTTAAA	AATAAAGGGG	TTCAACCTTT	ACTTGATGCT	500
GTTGTGGCTT	ATTTACCAGC	TCCTGATGAA	GTGGCAAATA	TCAAGGGTGA	550
ATATGAAGAT	GGCACAGAAG	TTTCTGTAAA	ATCAACTGAT	GATGGCGAGT	600
TTGCAGGACT	TGCATTTAAA	ATTATGACAG	ATCCATTTGT	AGGACAACTT	650
ACTTTCGTGC	GTGTTTATCG	CGGTTGTTTA	GAAAGTGGTT	CTTATGCTTA	700
TAAGTCAACT	AAAGATAAAA	AAGAAAGAAT	TGGTCGTTTG	TTAAAAATGC	750
ACTCTAACCA	AAGAGAAGAG	ATTAAAGTGC	TTTACGCAGG	CGAAATTGGT	800
GCTGTTGTAG	GACTTAAAGA	TACTTTAACA	GGGGATACTC	TTGTAAGTGA	850
AAAAGATAAG	GTAATCCTTG	AAAGAATGGA	TTTTCCAGAT	CCAGTTATTT	900
CTGTTGCAGT	TGAGCCAAAA	ACTAAAGCAG	ATCAAGAAAA	AATGTCTATT	950
GCTTTAAATA	AATTAGCACA	AGAAGATCCA	AGTTTTAGAG	TTTCTACAGA	1000
TGAAGAAAGT	GGCCAAACTA	TCATTTTCAG	TATGGGTGAG	TTACACCTTG	1050
AAATTATCGT	TGATAGAATG	CTTCGTGAAT	TTAAAGTTGA	AGCTGAAGTA	1100
GGTCAACCAC	AAGTTGCTTA	TCGCGAAACT	ATTAGAAAAA	CTGTTGAACA	1150
AGAATACAAA	TACGCTAAAC	AATCAGGTGG	TCGTGGTCAG	TATGGACATG	1200
TATTCTTACG	CCTTGAACCA	CTTGAGCCAG	GTAGTGGATA	TGAATTTGTT	1250
AATGATATCA	AAGGTGGAGT	AATTCCAAAA	GAATACATTC	CTGCAGTTGA	1300
TAAAGGTGTT	CAAGAAGCAT	TACAAAATGG	TGTTTTAGCA	GGTTATCCTG	1350
TGGAAGATGT	TAAAGTAACT	GTTTATGATG	GAAGTTATCA	CGAGGTGGAT	1400
TCATCTGAGA	TGGCGTTTAA	ACTTGCTGCT	TCTATGGGCT	TTAAAGAAGG	1450
TGCTAGAAAA	GCAGGTGCTG	TGATCTTAGA	GCCTATGATG	AAAGTTGAAG	1500
TAGAACTCC	TGAAGATTAC	ATGGGTGATG	TTATTGGAGA	TCTTAACAAA	1550
CGCCGTGGTC	AAGTAAATAG	CATGGATGAG	CGTGGTGGAA	ATAAAATCAT	1600
CACAGCATTT	TG				1612

2) INFORMATION FOR SEQ ID NO: 2188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188

ACAATTGAAG	TTGAAAGATC	TATGCGTGTT	CTTGATGGTG	CTGTTGCGGT	50
ATTTTGTTCA	GTGGGTGGGG	TGCAGCCTCA	AAGTGAAACA	GTTTGGAGAC	100
AAGCAAATAA	ATATGGTGTT	CCAAGAATAG	TATTTGTAAA	TAAAATGGAT	150
AGAATCGGTG	CAAATTTCTA	CAATGTAGAA	GATCAAATTC	GCAACCGTTT	200
AAAAGCTAAT	CCAGTTCCAC	TTCAAATTCC	AATTGGTGCT	GAGGATAATT	250
TTAAAGGCGT	AATCGATCTT	GTAACATATGA	AAGCTTTAGT	TTGGGAAGAT	300
GATACTAAGC	CAACGGATTA	TGTAGAAAAA	GAAATTCCAG	CTGAACTTAA	350
AGAAAAGGCA	GAAGAATATC	GCACAAAAAT	GATAGAAGCA	GTTTCTGAAA	400
CTTCAGATGA	GTTGATGGAA	AAATATTTAG	GCGGAGAAGA	ATTAAGCCTT	450
GAAGAGATTA	AAACAGGGAT	TAAAGCAGGA	TGTTTAAGTC	TTTCTATCGT	500
TCCTATGCTT	TGCGGTACAG	CGTTTAAAAA	TAAAGGGGTT	CAACCTTTGC	550
TTGATGCTGT	TGTGGCTTAT	TTACCAGCTC	CTGATGAAGT	GGCAAATATC	600
AAGGGTGAAT	ATGAAGATGG	CACAGAAGTT	TCTGTAAAAT	CAACTGATGA	650
TGGCGAGTTT	GCAGGACTTG	CATTTAAAAT	CATGACAGAT	CCATTTGTAG	700
GACAACTTAC	TTTCGTGCGT	GTTTATCGCG	GTTGTTTAGA	AAGCGGTTCT	750
TATGCGTATA	ACTCAACTAA	AGATAAAAAA	GAAAGAATTG	GTCGTTTGTT	800
AAAAATGCAC	TCTAACAAAA	GAGAAGAGAT	TAAAGTGCTT	TACGCAGGCG	850
AAATTGGTGC	TGTTGTAGGA	CTTAAAGATA	CTTTAACAGG	GGATACTCTT	900
GCAAGTGAAA	AAGATAAGGT	AATCCTTGAA	AGAATGGATT	TTCCAGATCC	950
AGTTATTTCT	GTTGCAGTTG	AGCCAAAAAC	TAAAGCTGAT	CAAGAAAAAA	1000
TGTCTATTGC	TTTAAATAAA	TTAGCACAAAG	AAGATCCAAG	TTTTAGAGTT	1050
TCTACAGATG	AAGAAAGTGG	TCAAACATATC	ATTTCAGGTA	TGGGTGAGTT	1100
ACACCTTGAA	ATTATCGTTG	ATAGAATGCT	TCGTGAATTT	AAAGTTGAAG	1150
CTGAAGTAGG	TCAACCACAA	GTTGCTTATC	GCGAAACTAT	TAGAAAAACT	1200
GTTGAACAAG	AATACAAATA	CGCTAAACAA	TCAGGTGGTC	GTGGTCAGTA	1250
TGGACATGTA	TTCTTACGCC	TTGAACCACT	TGAGCCAGGT	AGTGGATATG	1300
AATTTGTTAA	TGATATCAAA	GGTGGGGTAA	TTCCAAAAGA	ATACATTCCT	1350
GCAGTTGATA	AAGGTGTTCA	AGAAGCATTA	CAAAATGGTG	TTTTAGCAGG	1400
TTATCCTGTG	GAAGATGTTA	AAGTAACTGT	TTATGATGGA	AGTTATCACG	1450
AGGTGGATTC	ATCTGAGATG	GCGTTTAAAC	TTGCTGCTTC	TATGGGCTTT	1500
AAAGAAGGTG	CTAGAAAAGC	AGGCGCTGTG	ATCTTAGAGC	CTATGATGAA	1550
AGTTGAAGTA	GAAACTCCTG	AAGATTATAT	GGGTGATGTT	ATTGGAGATC	1600
TTAACAAACG	CCGTGGTCAA	GTAAATAGCA	TGGATGAGCG	TGGTGGAAT	1650
AAAATCATCA	CAGCATT				1667

2) INFORMATION FOR SEQ ID NO: 2189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189

TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
TGCAAGGGCG	GCAAGATCGG	CCTGTTCCGG	GGTGCCGGTG	TGGGCAAGAC	400
TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
ACCAGCCGAC	GCTTGCGGAG	GATCTTGGCA	TGCTGCAGGA	GCGCATTACG	800
TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCTT	1150
GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 2190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190

GCCCTTGACG	TTGTTGACAA	ACTTGGCCGT	GATGAGCCTC	TTACTCTTGA	50
GATCGTGACG	CATCTTGACG	CCCACACGGG	CCGCTGTATC	GCGATGCAAA	100
CGACGGATCT	CCTCAAAGTG	AAGGCAAAGG	TCGTTTCGAC	AGGTGGCAAC	150
ATTTCCGTTC	CTGTCGGCCG	GGAAACACTA	GGTCGTATCT	TCAACGTGCT	200
TGGAGACGCT	ATTGACCAGC	GCGGCCCCGT	TGGTGAGAAA	CTGCGCATGC	250
CCATCCATGC	CGTGGCTCCC	AAGCTTGCGG	ACCAGGCCGC	TGAGGATGCG	300
GTGCTCACAA	CTGGTATTAA	GGTGATTGAT	CTCATTCTCC	CTTACTGCAA	350

AGGTGGAAAA	ATTGGCCTCT	TTGGGGGTGC	GGGTGTGGGC	AAAACCGTCA	400
TTATTATGGA	GCTCATTAAC	AACGTTGCCA	AGGGTCACGG	TGGTTTCTCT	450
GTCTTCGCTG	GTGTTGGTGA	GCGTACCCGT	GAGGGAACGG	ATTTGTATCT	500
TGAGATGATG	CAGTCTAAGG	TTATTGACCT	TAAGGGTGAG	TCCAAATGTG	550
TGTTGGTGTA	CGGTCAGATG	AACGAGCCCC	CAGGTGCCCC	TGCGCGTGTT	600
GCGCAGTCGG	CTCTGACGAT	GGCTGAGTAC	TTCCGTGATG	TGGAGGGCCA	650
AGATGTGCTT	CTTTTTATCG	ACAATATTTT	TCGTTTCACT	CAGGCTAACT	700
CCGAGGTGTC	GGCGCTTCTG	GGTCGTATTC	CCGCCGCTGT	TGGCTACCAG	750
CCTACCCTCG	CTGAGGATCT	AGGGCAGTTG	CAGGAGCGTA	TTACCTCAAC	800
AACGAAAGGC	TCCATTACTT	CTGTGCAGGC	CGTATACGTG	CCGGCCGATG	850
ACATTACCGA	TCCAGCTCCA	GCAACAACCT	TCTCACATCT	GGACGCCACA	900
ACTGTGTTGG	ACCGTGCTGT	TGCCGAGTCT	GGTATCTACC	CCGCTGTTAA	950
CCCCTGGAA	TGCGCCTCGC	GTATCATGGA	CCCCGACGTT	ATCAGTGTGG	1000
ATCACTACAA	TGTTGCACAA	GATGTGGTAC	AGATGCTCAC	CAAGTACAGG	1050
GAATTACAGG	ATATCATTCG	TGTCCTTGGT	ATCGACGAGC	TAAGCGAGGA	1100
GGACAAACTT	ATCGTGGACC	GTGCGCGTAA	GTTGGTGAAG	TTCTCTCCC	1150
AGCCATTCCA	AGTTGCTGAG	GTCTTCACAG	GAATGACTGG	CCATTACGTG	1200
CAGTTGGATG	ACACCATCGA	TTCTTTTCT	GGTCTCCTCA	TGGGTACG	1248

2) INFORMATION FOR SEQ ID NO: 2191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191

GAGCTGATTG	TAAGTCATCG	ACCACTTGAT	ATATGAATAC	ATCTAACAGT	50
AGTAGAACAA	CATCGCCAAG	GCTCACGGTG	GTTACTCCGT	CTTCACTGGT	100
GTCGGTGAGC	GTACTCGTGA	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	150
GACTGGTGTC	ATTCAGCTCG	ACGGCGAATC	CAAGGTGTCT	CTTGTGTTCT	200
GTCAGATGAA	CGAGCCCCCA	GGTGCTCGTG	CCCGTGTCTG	CCTTACTGGT	250
CTGACCATCG	CCGAATACTT	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	300
CTTCATTGAC	AACATTTTCC	GTTTCACCCA	GGCCGGTTCC	GAGGTGTCTG	350
CCCTTCTTGG	TCGTATCCCC	TCTGCCGTCG	GTTACCAGCC	CACTCTGGCC	400
GTCGACATGG	GTGGTATGCA	GGAACGTATT	ACCACCACCA		440

2) INFORMATION FOR SEQ ID NO: 2192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania panamensis*

(B) STRAIN: ATCC 50158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192

GCTGACGGCG	CTGGACGTGA	CGGAGGACCT	CGGCCGCGAT	GAGCCGCTGA	50
CGCTGGAGAT	CGTGCAGCAC	TTGGATGCGA	ACACCGGCCG	CTGCATTGCG	100
ATGCAGACGA	CGGACCTGCT	GAAGCTGAAG	TCGAAGGTTG	TGTCGACCGG	150
CGGCAACATC	TCCGTGCCGG	TGGGCCGCGA	GACGCTGGGC	CGCATCTTCA	200
ACGTGCTGGG	CGACGCGATT	GACCACCGCG	GCCCCGTGTG	CGAGAAGATG	250
CGCATGGCGA	TCCACGCCGA	GGCGCCGAAG	CTGGCGGACC	AGGCTGCGGA	300
GGACACGATC	CTGACGACCG	GCATCAAGGT	GATCGACCTG	ATTCTGCCCT	350
ACTGCAAGGG	CGGCAAGATC	GGCCTGTTCG	GCGGTGCCGG	TGTGGGCAAG	400
ACTGTGATCA	TCATGGAGCT	GATCAACAAC	GTCGCGAAGG	GGCACGGCAG	450
CTTCTCCGTG	TTCGCCGGCG	TTGGCGAGCG	CACGCGCGAG	GGCACGGACC	500
TGTACCTGGA	GATGATGCAG	TCAAAGGTGA	TTGACCTGAA	GGGCGAGTCG	550
AAGTGCGTGC	TTGTGTACGG	GCAGATGAAC	GAGCCCCCGG	GTGCGCGCGC	600
GCGCGTTGCG	CAGTCTGCGC	TGACGATGGC	CGAGTACTTC	CGCGACGTGG	650
AGGGCCAGAA	CGTGCTGCTG	TTCATCGACA	ACATCTTCCG	CTTCACGCAG	700
GCGAACTCCG	AGGTGTCTGC	GCTGCTGGGC	CGCATCCCCG	CCGCCGTGGG	750
TTACCAGCCG	ACGCTTGCGG	AGGATCTTGG	CATGCTGCAG	GAGCGCATTA	800
CGTCGACGAC	GAAGGGATCG	ATTACGTCTG	TGCAGGCTGT	GTACGTGCCT	850
GCGGATGATA	TCACGGACCC	CGCGCCCCGCG	ACGACGTTCT	CGCACCTGGA	900
CGCGACGACT	GTGCTGGACC	GCGCGGTGGC	GGAGTCGGGC	ATCTACCCTG	950
CCGTGAACCC	GCTGGAGTGC	GCGTCGCGCA	TCATGGACCC	CGATGTGATC	1000
GACGTGGACC	ATTACAACGT	TGCACAGGAT	ATCGTCCAGA	TGCTGACCAA	1050
GTACAAGGAG	CTGCAGGACA	TCATTGCGGT	GCTTGGCATC	GACGAGCTGA	1100
GCGAGGAGGA	CAAGGTCGTG	GTGGACCGCG	CGCGCAAGGT	GACGCGGTTC	1150
CTGTGCGCAG	CGTTCCAGGT	TGCGGAGGTG	TTCACCGGCA	TGACGGGCCA	1200
CTACGTGCAG	CTGAGCGACA	CGGTGGAGTC	GTTCTCTGGC	CTGCTGATGG	1250
GGTCGTACGA	CC				1262

2) INFORMATION FOR SEQ ID NO: 2193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus nidulans*

(B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193

TTCCGATGGT	CAAATGTACG	ATTGATATTC	CTTCCAGCCA	GTCAGGATAA	50
CAGCTGATAC	CAGTTGCAAA	TAGGCCCCAG	ACTCGTGAGC	ACTTGTTGCT	100
TGCCCCGTCAG	GTTGGTGTCC	AGAAGATCGT	TGTCTTCGTC	AACAAGGTTG	150
ACGCTGTCTGA	TGACCCTGAG	ATGTTGGAGC	TTGTTGAGCT	CGAGATGCGT	200

GAGCTCCTCA	ACACTTACGG	TTTCGAGGGA	GAGGAGACCC	CTATCATCTT	250
CGGTTCCGCC	CTGTGCGCTC	TCGAAGGCCG	CCGCGAGGAC	ATTGGTACTC	300
AGCGTATTGA	CTCCCTCCTC	GAGGCCGTTG	ACACTTGGAT	CCCTACCCCC	350
CAGCGTGACT	TGGACAAGCC	CTTCCTGATG	TCCATTGAGG	AAGTTTTCTC	400
CATTGGTGGT	CGTGGTACCG	TCGCCTCTGG	TCGTGTCGAG	CGTGGTCTCC	450
TCAAGAAGGA	TACCGAAGTT	GAAATTCACG	GTGCTGATGG	TATTCTGAAG	500
ACCAAGGTCA	CCGACATTGA	GACCTTCAAG	AAGAGCTGCG	ATGAGTCTCG	550
TGCTGGTGAC	AACTCCGGTC	TTCTCCTCCG	TGGTATCCGT	CGTGAGGATG	600
TTCTGTCGTG	TATGGTCATC	GCTGCCCCCTG	GCTCCATCAA	GGCCTCCAAG	650
AAGTTCATGG	TCTCCATGTA	CGTCTTGACT	GAGGCTGAAG	GTGGCCGCAA	700
GAACGGCTTC	GGTGCCAACT	ACCGCCCCCA	GGCTTTTCATC	CGCACTGCTG	750
GTAAGTTTCG	AACTATTTGA	TTCATTGATC	ACGTCCCTAA	CTGTTACTTT	800
AGACGAGGCT	TGCGACCTTC	ATTTCCCTGA	TGAGGCCGAC	AAGGACCGCC	850
ACGTCATGCC	CGGTGACAAC	GTCGAAATGG	TCCTCAACCT	CAACAACCCC	900
GTGCTGCTG	AG				912

2) INFORMATION FOR SEQ ID NO: 2194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194

TCATCGTCGT	CGCCGCTTCT	GACGGTCAGA	TGCCCCAGAC	CAGAGAGCAC	50
TTGCTTCTCG	CCCGTCAGGT	CGGTATCCAG	AAGATTGTCG	TCTTCGTCAA	100
CAAGGTCGAC	GCCATCGAGG	ACAAGGAGAT	GCTTGAGCTC	GTCGAGATGG	150
AGATGCGTGA	GCTCCTCAGC	AGCTACGGCT	TCGAGGGTGA	CGAGACCCCC	200
ATCGTCATGG	GTTCCGCTCT	TTGTGCCCTT	GAGAACCGCC	AGCCCGAGAT	250
TGGAACCACC	CAGATCGACA	ACCTGATGAA	CGCTGTGCGAC	GAGTGGATCC	300
CCACTCCCCA	GAGAGATCTT	GAGAAGCCCT	TCCTCATGTC	CGTTGAGGAT	350
GTCTTCTCTA	TCCCCGGTCG	TGGTACTGTC	GTTTCTGGCC	GTGTTGAGCG	400
TGGTACCCTG	AAGAAGGATT	CCGAAATCGA	GCTTGTCGGC	AAGAACAAGG	450
TCCCCATCAA	GACCAAGGTC	ACCGACATCG	AGACCTTCAA	GAAGTCTTGC	500
GACGAGTCCC	GCGCTGGTGA	CAACTCCGGT	CTTCTGCTCC	GTGGTATCAA	550
GCGTGAGGAT	GTCAACCGTG	GTATGGTTGT	CGTCAAGCCC	GGTACCGTCA	600
CCTCGCACAA	GAAGTTCCTC	GTCTCCATGT	ACGTCCTGAC	CAAGGAGGAG	650
GGTGGTCGTC	ACACTGGTTT	CCACGGAAAC	TACCGTCCCC	AGATCTTCAT	700
CCGTACCGCT	GGTAAGTCCT	GACTTTGAAC	TGCTGACCAA	TTTTCGCATC	750
TCTAACATGT	TTTACAGACG	AGGCTGCCGC	TATTGACTGG	CCCGAAGGCA	800
CCGAGGACGC	TGACTCCAAG	ATGGTCATGC	CCGGTGACAA	CGTCGAGATG	850
GTCTGCTCTC	TTCACAGACC	TCTTGCCGTT	GAACAGG		887

2) INFORMATION FOR SEQ ID NO: 2195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
- (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195

TGACGGCCAA	ATGTAGGACT	CTTGCGCGGG	ACTGACTGAT	TGGGGGGAAT	50
CCATTTTTC	TTTTTCTTT	TTCTTTTGA	GTACATGATT	ATACTAATAT	100
TTGGATAACG	TACCAGGCCT	CAAACACGTG	AACATTTACT	CCTTGCCCGA	150
CAAGTCGGTG	TCCAGAAGAT	CGTCGTTTTC	GTAAACAAGG	TCGATGTTCT	200
CGAAGATAAG	GAGATGTTGG	AGCTTGTCGA	GTTGGAAATG	AGAGAGCTCT	250
TGAACACCTA	CGGATTTCGAG	GGTGAGGAAA	CGCCCATCAT	CTTCGGTTCT	300
GCCCTTTGTG	CCATGGAGGG	CCGCGAGCCT	GAGCTGGGCG	AGAAGAGAAT	350
TGATGAATTG	CTCGACGCTG	TTGATAGCTG	GATCCCTACG	CCGCAACGTG	400
ATACGGAAAA	ACCCTTCCTA	ATGTCCATTG	AGGAAGTGTT	CTCCATCTCC	450
GGTCGTGGAA	CCGTTGCCTC	CGGCCGTGTT	GAGCGTGGTG	TCCTCAAGAA	500
GGATTCCGAA	GTCGAGCTTG	TTGGCGGCGG	CGTCGCCCCA	ATCAGGACCA	550
AGGTAACCGA	TATCGAAACC	TTCAAGAAGT	CCTGCGACGA	GTCCAGGGCT	600
GGAGACAACT	CTGGCCTTTT	GTTGCGTGGT	GTCAAGCGTG	AGGATATCCG	650
CCGTGGTATG	GTCGTTGTCG	TTCTTGGCAG	CGTCAAGGCC	CACGACAAGT	700
TCTTGGTGTC	CATGTATGTT	CTGACCGAAG	CCGAGGGTGG	TCGCCGAACT	750
GGATTTCGGCC	AAAACATATCG	TCCTCAAATG	TTTATCCGCA	CAGCTGGTAC	800
GTAACGTATA	ATGCCTCTCC	TCTTCATATA	TACCACCCCC	CCCACCACTG	850
ACTCCCTGAC	TCTTCGATTA	CAGACGAGGC	CGCCGATCTC	AGCTTCCCTG	900
ACGCAGCAGA	CGAAACCAAA	CTGGTTATGC	CCGGTGACAA	CGTCGAGATG	950
ATCCTCAAGA	CACACCGCCC	CATAGCTGCC	GAAG		984

2) INFORMATION FOR SEQ ID NO: 2196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exserohilum rostratum*
- (B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196

GCCGCCTCTG	ACGGCCAAAT	GCCCCAGACC	CGTGAGCACT	TGCTGCTTGC	50
TCGCCAGGTC	GGTGTTCAGA	AGATTGTTGT	TTTTGTCAAC	AAGGTCGATG	100
CCGTCGAGGA	CAAGGAGATG	TTGGAGCTCG	TTGAGATGGA	GATGCGTGAG	150
TTGCTCAGCA	GCTATGGCTT	CGAGGGCGAT	GAGACTCCCA	TTGTCATGGG	200

CTCCGCTCTC	TGCGCCATCG	AGGGCCGTGA	GCCCGAAATT	GGTGTCAACC	250
GTATTGATGA	GCTGCTCGAG	GCTGTCGACA	CCTGGATCCC	CACCCCTCAG	300
CGTGATACCG	ACAAGCCCTT	CCTCATGGCT	GTTGAGGACG	TCTTCTCCAT	350
TGCTGGCCGT	GGTACCGTCG	TTTCTGGCCG	TGTCGAGCGA	GGTGTCTTGA	400
AGCGCGATGC	CGAAGTCGAG	CTGGTTGGCA	AGGGCACTGC	GCCCATCAAG	450
ACCAAGGTTA	CCGACATTGA	AACCTTCAAG	AAGTCGTGTG	AAGAGTCTCG	500
CGCCGGTGAC	AACTCGGGTC	TCCTCCTCCG	TGGTGTCAAG	CGTGACGACG	550
TCCGCCGTGG	CATGGTCGTT	TCTGTTCTTG	GACAAGTCAA	GGCCCACAAG	600
AAGTTCCTCG	TCTCCATGTA	TGTGTTGAGC	AAAGAGGAAG	GTGGCCGCCA	650
CACGGGCTTC	GGCGAGAACT	ACAGGCCACA	AATGTTTCATC	CGTACTGCTG	700
ACGAGTCATG	CGCGCTGCAC	TGGCCAGAAG	GTACCCCAAG	TGCTCACGAC	750
AAGCTTGTTA	TGCCTGGTGA	TAACGTTGAG	ATGGTTTGTG	AGCTTCACGT	800
GCCACA					806

2) INFORMATION FOR SEQ ID NO: 2197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197

ACCCGTGAAC	ACTTGCTCCT	CGCTCGTCAG	GTTGGTGTTC	AGCGAATTGT	50
CGTCTTTGTC	AACAAGGTCG	ATGCCATTGA	TGACCCCGAG	ATGCTTGAGC	100
TCGTCGAGAT	GGAGATGCGC	GAGCTTCTTA	ACACCTATGG	CTTCGAAGGC	150
GACGACACTC	CCGTCATCAT	GGGCTCGGCT	CTCATGTCTC	TCCAGAACCA	200
GCGCCCTGAG	ATTGGCACCG	AGAAGATTGA	TGAGCTTCTT	GCTGCCGTCG	250
ACGAGTGGAT	CCCAACCCCC	GAGCGTGACC	TTGACAAGCC	CTTCCTTATG	300
TCCGTCGAGG	ATGTCTTCTC	CATTGCTGGC	CGTGGTACCG	TCGTGTCTGG	350
CCGTGTGGAG	CGTGGTGTTC	TGAAGCGTGA	CCAGGAGATC	GAGCTTGTTG	400
GAAAGGGTCA	GGAGGTTATC	AAGACCAAGG	TTACCGACAT	CGAGACCTTC	450
AAGAAGTCTT	GTGAGCAGTC	CCAGGCTGGT	GACAACTCTG	GTCTCCTCAT	500
CCGAGGTGTT	CGCCGTGAGG	ATGTCCGCCG	TGGTATGGTC	GTCTGCGCTC	550
CTGGCACCGT	GAAGTCTCAC	ACCCAGTTCC	TCGCTTCCCT	CTATGTCCTC	600
TCCAAGGAGG	AGGGTGGCCG	ACACACCGGT	TTCCAGGAGC	ACTACCGACC	650
CCAGCTCTAC	CTCCGAACCG	CAGATGAGTC	CATTGACCTG	ACTTTCCCTG	700
AGGGTACTGA	GGATGCCTCC	AGCAAGATGG	TCATGCCTGG	CGACAACACC	750
GAGATGGTTG	TCACCATGGG	TCACCCCAAT	GCCATCGAGG	TTGGTCAGC	799

2) INFORMATION FOR SEQ ID NO: 2198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
(B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198

CTCTGACGGT	CAGATGCCCC	AGACCCGTGA	GCACTTGCTG	CTTGCCCGTC	50
AGGTCGGTGT	CCAGAAGATT	GTCGTCTTCG	TCAACAAGGT	CGATGCCATT	100
GACGACCCTG	AGATGCTTGA	GCTCGTCGAG	ATGGAGATGC	GTGAGCTCCT	150
CAACACCTAC	GGCTTCGAGG	GTGACGAGAC	CCCTGTTCATC	ATGGGCTCTG	200
CTCTCATGTC	CCTCCAGAAC	CAGCGCCCCG	AGATCGGTAG	CCAGAAGATT	250
GACGAGCTCC	TTGCCGCCGT	TGACGAGTGG	ATCCCTACCC	CCGAGCGTGA	300
CCTTGACAAG	CCCTTCCTCA	TGTCCGTTGA	GGATGTCTTC	TCCATTGCCG	350
GCCGTGGTAC	CGTCGTCTCT	GGCCGTGTCG	AGCGTGGTGT	CCTGAAGCGC	400
GACCAGGAGA	TTGAGCTCGT	CGGCAAGGGT	AACGAGGTCA	TCAAGACCAA	450
GGTCACCGAC	ATTGAGACCT	TCAAGAAGTC	TTGCGAGCAG	TCCCAGGCTG	500
GTGACAACCTC	TGGTCTCCTC	ATCCGAGGTG	TCCGCCGTGA	GGATGTCCGC	550
CGTGGTATGG	TCGTCTGCGC	CCCCGGCACT	GTCAAGTCCC	ACACTCAGTT	600
CCTTTCTTCC	CTCTACGTCC	TCACCAAGGA	GGAGGGTGGC	CGACACACTG	650
GCTTCCAGGA	GCACTACCGA	CCCCAGCTCT	ACCTCCGAAC	TGCTGATGAG	700
TCCATCGACC	TGACCTTCCC	CGAGGGTACC	GAGGACGCCA	GCAGCAAGAT	750
GGTCATGCCC	GGTGACAACA	CCGAGATGGT	CATCACCATG	GGCCACCCCA	800
ACGCCATTGA	GGTCGGTCA				819

2) INFORMATION FOR SEQ ID NO: 2199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199

TGCTGACGGC	CAAATGTAAG	ACGCCGCGAG	GGAGTGCTGA	AGGTTTTTATG	50
CTTTTTAGGC	CCTTTGTTTC	TGAGAGCATG	ATGATACTAA	TACTCGGAAA	100
CGTATCTATT	AGGCCTCAAA	CACGTGAGCA	TTTGCTCCTT	GCCCGACAGG	150
TCGGTGTCCA	AAAGATCGTC	GTTTTTCGTGA	ACAAAGTCGA	CGCCCTTGAG	200
GACAAGGAGA	TGTTGGAGCT	TGTCGAGTTA	GAAATGAGAG	AGCTCTTAAA	250
CACCTACGGA	TTTGAGGGTG	AAGAGACACC	CATCATCTTT	GGTTCTGCCC	300
TTTGCGCCAT	GGAAGGCCGT	GAGCCTGAGT	TGGGAGAAAA	GAAAATTGAT	350
GAATTGCTGG	AGGCTGTTGA	TACTTGGATC	CCAACACCAC	AACGTGATAC	400
CGAAAAACCT	TTCTTGATGT	CCGTTGAGGA	AGTATTCTCT	ATCTCCGGTC	450
GTGGAACCGT	TGCCTCCGGT	CGTGTTGAGC	GCGGTGTCCT	CAAGAAGGAT	500

TCAGAAAGTCG	AGCTAATTGG	GGGCGGCTCC	ACCCCCATCA	GGACGAAGGT	550
AACTGATATC	GAAACTTTCA	AGAAATCCTG	TGACGAGTCT	AGAGCTGGGG	600
ACAACTCCGG	TCTTTTATTG	CGTGGTATCA	AGCGTGAAGA	TATCCGCCGT	650
GGTATGGTAG	TTGCCGTTCC	TGGCAGCGTC	AAGGCCACG	ACAAGTTCTT	700
GGTGTCGATG	TATGTCCTGA	CCGAAGCTGA	GGGTGGTCGC	CGAACCGGAT	750
TCGGCCAGAA	CTATCGTCCT	CAAATGTTCA	TCCGCACAGC	TGGTATGTCA	800
AAATGGGGCC	CCTTTTCATA	ATCCTTTCTT	TTTTTCCTTT	TCCTCTCTCT	850
ATCTCTCTCT	CTGTTTCTTT	TCAACTCGCC	TGATTCACGA	AATTAATAA	900
CCCCTTTGAT	TATAGACGAA	GCCGCCCATC	TCAGCTTCCC	TAGTGGAGCA	950
GATGAAAGCA	AACTCGTTAT	GCCTGGTGAC	AACGTCGAGA	TGATCCTCCA	1000
GACACACCGC	CCCGTGGCTG	CTGAG			1025

2) INFORMATION FOR SEQ ID NO: 2200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kocuria kristinae*
- (B) STRAIN: ATCC 27570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200

AGCACGTGCT	GCTCGCCCGC	CAGGTCGGCG	TGCCGACCCT	GCTGGTCGCC	50
CTGAACAAGG	CCGACATGGT	CGAGGACGAG	GAGCTGCTGG	ACCTCGTCGA	100
GATGGAGGTC	CGCGAGCTGC	TGTCCTCCCA	GGAGTTCGAC	GGCGACAACG	150
CCCCCGTCAT	CCGCGTCTCC	GCGCTGAAGG	CGCTGGAGGG	CGACGAGAAG	200
TGGGTCAAGT	CCATCGAGGA	GCTCATGGAG	GCCGTGGACG	AGTACATCCC	250
GGACCCCGTG	CGCGACAAGG	ACAAGCCGTT	CCTGATGCCC	ATCGAGGACG	300
TCTTCACCAT	CACCGGGCGC	GGCACCGTGG	TGACCGGTCG	CGCCGAGCGC	350
GGGACCCTGG	CCCTGAACTC	CGAGGTCGAG	ATCGTCGGCA	TCCGCCCGAT	400
CCAGAAGACC	ACGGTCACCG	GGATCGAGAT	GTTCCACAAG	CAGCTCGACG	450
AGGCCTGGGC	CGGCGAGAAC	TGCGGTCTGC	TGCTGCGCGG	CCTGAAGCGC	500
GACGACGTCG	AGCGCGGCCA	GGTCGTGGTG	AAGCCGGGTT	CCATCACCCC	550
GCACACCAAC	TTCGAGGCGA	ACGTCTACAT	CCTGTCCAAG	GACGAGGGTG	600
GGCGTCACAA	CCCGTTCTAC	TCGAACTACC	GTCCGCAGTT	CTACTTCCGG	650
ACCACCGACG	TCACCGG				667

2) INFORMATION FOR SEQ ID NO: 2201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Vibrio mimicus*

(B) STRAIN: ATCC 33653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201

TGCTGCAACA	GATGGTCCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTGCTGG	50
GTCGCCAAGT	AGGTATTCCT	TACATCATCG	TATTCATGAA	CAAATGTGAC	100
ATGGTTGACG	ATGAAGAGCT	TCTAGAGCTG	GTTGAGATGG	AAGTTCGTGA	150
GCTTCTGTCT	GAGTACGATT	TCCCAGGTGA	TGACCTGCCA	GTAATCCAAG	200
GTTCAGCACT	AGGCGCGCTA	AACGGCGAAG	CACAGTGGGA	AGCGAAGATT	250
GTTGAACTAG	CAGAAGCACT	AGATTCATAC	ATTCCAGAGC	CAGAGCGTGC	300
AGTAGACATG	GCATTCCTGA	TGCCAATCGA	AGACGTATTC	TCAATCCAAG	350
GTCGTGGTAC	AGTAGTAACT	GGCCGTATCG	AGCGCGGCAT	CCTGAAAGTG	400
GGTGACGAAG	TTGCGATCGT	TGGTATCAAA	GACACAGTAA	AAACTACCTG	450
TACAGGTGTA	GAAATGTTCC	GTAAGCTGCT	TGACGAAGGT	CGTGCAGGTG	500
AGAACGTTGG	TGCACTGCTA	CGTGGTACTA	AGCGTGAAGA	AGTAGAGCGT	550
GGTCAAGTAC	TGGCGAAGCC	AGGTTCAATC	ACCCACACAC	CTAAGTTCGA	600
ATCAGAAGTA	TACGTACTGT	CAAAAGACGA	AGGTGGCCGT	CATACTCCAT	650
TCTTCAAAGG	TTACCGTCCA	CAGTTCTACT	TCCGTACAAC	TGACGTAACA	700
GGCAGCATCG	AGCTTCCAGA	AGGCGTAGAA	ATGGTAATGC	CAGGCGACAA	750
CATCAAGATG	GTTGTAGACC	TGATTGCA			778

2) INFORMATION FOR SEQ ID NO: 2202

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter freundii*

(B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202

AACGCTGACC	CTGCAGGTTA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCATTTAT	CGATGCAGAA	CACGCACTGG	ACCCGGTCTA	TGCCCCGTAAG	100
CTTGCGCTTG	ATATCGATAA	CCTGCTGTGT	TCTCAGCCGG	ATACCGGTGA	150
ACAAGCGCTG	GAAATCTGTG	ATGCACTGGC	GCGCTCCGGT	GCGGTTGACG	200
TTATCGTTGT	CGACTCCGTT	GCCGCATTGA	CGCCGAAGGC	AGAAATCGAA	250
GGCGAGATTG	GCGACTCTCA	CATGGGCCTT	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCCG	GTAACCTGAA	GCAGTCCAAC	ACGCTGCTGA	350
TTTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTTATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2203

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases

1133

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:1.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203

TTTAGATCCA	TCTTATGCTA	GAAATTTAGG	TGTTGATATA	GATAACCTAA	50
TAGTTTCTCA	ACCAGATACA	GGAGAACAGG	CTTTAGAGAT	AACAGAAGCT	100
TTAGTAAGAT	CAGGAGCAGT	AGATGTTATA	GTTGTAGACT	CTGTAGCAGC	150
TTTAGTTCCT	AGGGCAGAAA	TAGAAGGAGA	AATGGGAGAC	TCACATGTAG	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCCC	TAAGAAAATT	AGCAGGATCT	250
ATAAATAAAT	CTAAGTGTGT	AGCTATATTT	ATAAACCAAT	TAAGAGAAAA	300
GGTTGGTATA	ATGTTTGGAA	ATCCAGAAAC	AACTCCT		337

2) INFORMATION FOR SEQ ID NO: 2204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
- (B) STRAIN: ATCC 29684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204

AAAGCAAGGC	GGTACTGCAG	CATTTGTTGA	TGCTGAGCAT	GCACTAGATC	50
CAAAATATGC	AAAGCTTTTA	GGTGTTGATG	TTGATAATCT	GATCGTGTCA	100
CAGCCGGATA	CGGGTGAGCA	AGCTTTAGAG	ATTGCTGATA	TGTTGGTACG	150
TTCTGGAGGA	GTTGATATTG	TAGTAATTGA	CTCTGTTGCT	GCACTTACGC	200
CAAAGGCAGA	GATTGAGGGT	GACATGGGCG	ACTCGCACAT	GGGCTTACAA	250
GCAAGATTAA	TGTCACAAGC	ACTAAGAAAA	CTAACGGCAA	ATATCAAGCG	300
CTCAAATACT	CTAGTGATAT	TCATTAACCA	AATTCGTATG	AAGATCGGGG	350
TTATGTTTGG	TAACCCTGAA	ACTACAAC			379

2) INFORMATION FOR SEQ ID NO: 2205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*

(B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205

ACTTGACCCA	GTATATGCAA	GGGCTCTTGG	AGTGGATATA	GACAACCTAG-	50
TCATATCTCA	GCCAGATACA	GGAGAACAGG	CCCTAGATAT	AGCAGAGTCC-	100
CTTATAAGAT	CAGGAGCTGT	AGATATACTA	GTAATAGACT	CAGTAGCTGC-	150
CCTAGTACCT	AAGGCAGAAA	TAGAAGGTGA	CATGGGAGAT	TCTCACGTAG-	200
GTCTACAGGC	TAGACTTATG	TCACAGGCAC	TTAGAAAATT	GACTGGATCT-	250
ATAAAGAAGT	CAAACGTGTG	TGTTATATTT	ATCAACCAGT	TGAGAGAAAA-	300
AGTAGGGGTT	ATGTTTCGGTA	ATCCAGAGAC	AACAACA		337

2) INFORMATION FOR SEQ ID NO: 2206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus asaccharolyticus*

(B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206

TCTTGATGCT	GGATATGCAA	AAAACCTTGG	AGTAGATGTA	GAAAATTTAA-	50
TTATTTCTCA	ACCTGATACA	GGTGAGCAAG	CCTTAGAAAT	AACTGAAGCT-	100
CTTGTAAGAT	CTAACGCTGT	TGATTTAATT	ATTATAGACT	CAGTTGCCGC-	150
ACTTGTAACCA	AAAGCAGAAA	TCGATGGTGA	CATGGGAGCT	GCACAAATAG-	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCTC	TTAGAAAATT	AACTGGGGCA-	250
ATCAACAAGT	CAAAATGTAC	CGTTGTATTT	ATTAACCAAC	TTAGAGAAAA-	300
AGTTGGTATC	ATGTTTGGTA	ACCCAGAAAC	TACAACA		337

2) INFORMATION FOR SEQ ID NO: 2207

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207

CTCACGTTGC	AAGTTATTGC	AGCAGCACAA	CGTAGCGGAA	AAACCTGTGC	50
ATTTATCGAC	GCTGAACATG	CGCTAGATCC	AATCTATGCG	AAAAAACTGG	100
GTGTTGATAT	CGATAACCTT	CTATGTTCTC	AACCTGATAC	TGGTGAGCAA	150
GCATTAGAGA	TTTGTGATGC	ACTGACGCGT	TCAGGCGCTG	TTGATGTCAT	200
TATCGTTGAC	TCCGTGGCCG	CATTAACACC	AAAAGCTGAA	ATTGAAGGTG	250
AAATCGGTGA	CTCACACATG	GGCTTAGCGG	CTCGTATGAT	GAGCCAAGCG	300
ATGCGTAAAT	TAGCGGGTAA	CTTAAAGAAC	TCGAATACAC	TTTTAATCTT	350
CATTAACCAA	ATCCGTATGA	AGATTGGCGT	TATGTTTGGT	AACCCAGAAA	400
CCACTACA					408

2) INFORMATION FOR SEQ ID NO: 2208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi A
- (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208

GCTGCAGGTG	ATTGCCGCTG	CGCAGCGTGA	AGGTAAAACC	TGTGCGTTTA	50
TCGATGCGGA	ACACGCGCTT	GACCCTGTTT	ACGCACGCAA	GCTGGGCGTC	100
GATATCGATA	ACCTGCTTTG	TTCTCAGCCG	GATACCGGCG	AGCAGGCGCT	150
GGAAATCTGT	GACGCGCTGG	CGCGTTCAGG	CGCGGTGGAC	GTCATTGTGG	200
TCGACTCCGT	AGCGGCGCTA	ACGCCGAAAG	CGGAAATCGA	AGGCGAAATT	250
GGCGACTCTC	ACATGGGCCT	CGCGGCGCGT	ATGATGAGCC	AGGCGATGCG	300
TAAGCTGGCG	GGGAACCTAA	AACAGTCCAA	CACGCTGTTG	ATTTTCATCA	350
ACCAGATCCG	TATGAAGATT	GGCGTGATGT	TCGGTAACCC	GGAAACCACC	400
ACC					403

2) INFORMATION FOR SEQ ID NO: 2209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Typhimurium
(B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209

GACCCTGACG	CTGCAGGTGA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCGTTTAT	CGATGCGGAA	CACGCGCTTG	ACCCTGTTTA	CGCACGCAAG	100
CTGGGCGTCG	ATATCGATAA	CCTGCTCTGC	TCTCAGCCGG	ATACCGGCGA	150
GCAGGCGCTG	GAAATCTGTG	ACGCGCTGGC	GCGTTCAGGC	GCGGTGGACG	200
TCATTGTGGT	CGACTCCGTA	GCGGCGCTAA	CGCCGAAAGC	GGAAATCGAA	250
GGCGAAATCG	GCGACTCTCA	CATGGGCCTC	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCGG	GGAACCTGAA	ACAGTCCAAC	ACGCTGTTGA	350
TTTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTGATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210

ATTAGATCCT	GTTTACGCAG	AAGCTTTAGG	CGTAGATATA	CAAAATTTAT-	50
ATTTATCTCA	ACCTGATCAT	GGGGAACAAG	GTTTAGAAAT	TGCCGAAGCA-	100
TTTGTTAGAA	GTGGCGCTGT	TGATATCGTT	GTGGTCGATT	CAGTTGCTGC-	150
GCTTACACCT	AAAGCTGAAA	TTGAAGGTGA	AATGGGAGAT	ACGCACGTTG-	200
GTTTGCAAGC	ACGTCTTATG	TCCAAGCCT	TGAGAAAGCT	TTCCGGTGCA-	250
ATTTCAAAAT	CAAATACAAC	AGCAGTATTT	ATCAACCAAA	TCCGTGAAAA-	300
AGTTGGTGTG	ATGTTCCGTA	ATCCTGAAGT	TACACCA		337

2) INFORMATION FOR SEQ ID NO: 2211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
(B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211

GACACTGACA	TTACAGGTTA	TCGCCGCCGC	ACAGCGTGAA	GGCAAAACGT	50
GTGCATTTAT	CGATGCCGAA	CATGCCCTTG	ACCCAATCTA	TGCCAAGAAA	100
TTGGGTGTAG	ATATTGATAA	CCTACTGTGT	TCTCAGCCAG	ATACTGGCGA	150
GCAGGCACTG	GAAATTTGTG	ATGCGCTGAC	TCGCTCTGGT	GCGGTTGACG	200
TTATCATCGT	TGACTCCGTA	GCGGCATTGA	CACCAAAAGC	TGAAATTGAA	250
GGTGAAATTG	GCGATTCTCA	TATGGGCCTT	GCCGCGCGTA	TGATGAGCCA	300
GGCTATGCGT	AAGCTGGCGG	GTAACCTGAA	GAATGCGAAT	ACCTTACTGA	350
TTTTTATCAA	CCAAATCCGC	ATGAAAATTG	GCGTGATGTT	TGGTAACCCA	400
GAAACCACTA	CC				412

2) INFORMATION FOR SEQ ID NO: 2212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212

CACGCTCACC	TTGCAAACCA	TCGCGGAAAT	GCAAAAACCTG	GGCGGCACCT	50
GCGCGTTTAT	CGACGCCGAG	CACGCACTGG	ACGTCACGTA	CGCGCAAAAG	100
CTGGGCGTCA	ACCTGAGCGA	TCTGCTGATC	TCGCAACCGG	ACACCGGCGA	150
ACAAGCGCTG	GAAATCTGCG	ACGCCCTGGT	GCGTTCGGT	TCGGTGGACA	200
TGGTCGTGAT	CGACTCGGTC	GCCGCGCTGA	CCCCGCGCGC	CGAGATCGAA	250
GGCGACATGG	GCGATTGCT	GCCAGGTTTG	CAGGCACGTT	TGATGTCGCA	300
AGCACTGCGC	AAGCTTACCG	GTTTCGATCAA	CCGCACCAAC	ACCCTGGTCA	350
TCTTCATCAA	CCAGATCCGC	ATGAAAATCG	GCGTCATGTT	CGGCAGCCCG	400
GAAA					404

2) INFORMATION FOR SEQ ID NO: 2213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213

CGTGCCATTG	ACATGATTTC	CGAAGAAGAC	GCTGAAGGCA	CG	42
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2) INFORMATION FOR SEQ ID NO: 2214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214

CAACTACATT ACGTTCTGCA ACACAAGGTC GTGGTACTTT CAGTATGACA	50
TTTGACCACT ATGAAGATGT TCCTAAGAGC ATTGCAGAAG AAATCATCAA	100
GAAAAATGGC GGTAACGGAG AATAA	125

2) INFORMATION FOR SEQ ID NO: 2215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215

CGACTCAAAT GCGTTCTATG TCTCAAGGTC GTGCGACATA CTCAATGGAA	50
TTTGCTAAAT ATGCTGAAAC TCCACGTAAC GTGGCTGAAG GCATCATCGC	100
TAAATTCCAA GCTGGCGGTA AAAAAGGTGA CGACGAGTAA	140

2) INFORMATION FOR SEQ ID NO: 2216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
(B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216

CCGGTGACCT GCGTTCTAAG ACGCAGGGTC GCGCTGTCTA CTCCATGGAG	50
TTCGACAGCT ACGCCGAGGT TCCGCGCGCG GTCGCGGATG AGATCGTCGG	100
CAAGTCTCGG GGCAACTGA	119

2) INFORMATION FOR SEQ ID NO: 2217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
(B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217

CGACCGACGT TCGCTCCATG TCCCAGGGTC GCGCAAGCTA CTCTATGGAA	50
TTCAAAAAAT ACAACACAGC TCCGGCGCAC ATCGCTGAAA CTGTATCCAA	100
AAAACAAGGC TGA	113

2) INFORMATION FOR SEQ ID NO: 2218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218

GCGACCTGCG TTCCCGTACC CAGGGCCGTG CAAACTACAC CATGATCTTC	50
GACTCCTACG CTGAGGTTCC TACCAACGTG GCAGCTGAGA TCGTGGCAGA	100
GCGCAACGGC ACTGCCTAA	119

2) INFORMATION FOR SEQ ID NO: 2219

1140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCTAACAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AGTAA	115

2) INFORMATION FOR SEQ ID NO: 2220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCGAACAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AATAA	115

2) INFORMATION FOR SEQ ID NO: 2221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221

CAACTCACCT TCGTTCAGGT ACGCAAGGTC GTGGTGTATA CACTATGCAA	50
TTTGACCACT ATGAAGAAGT TCCTAAATCT ATTGCTGAAG AAATCATTA	100
AGCTAATGGT GGA	113

2) INFORMATION FOR SEQ ID NO: 2222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222

CGGCGACCTG CGGTCCAAGA CCCAAGGCCG GCGGAAGTAC TCCATGGTCT	50
TCGACTCCTA CGCCGAAGTG CCGGCCAACG TGTCGAAGGA GATCATCGCG	100
AAGGCGACGG GTCAGTGA	118

2) INFORMATION FOR SEQ ID NO: 2223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223

CCGGCGACCT GCGGTCCAAG ACGCAAGGCC GGGCGAAGTCT CTCCATGGTG	50
TTGACTCGT ACGCCGAAGT TCCGGCGAAC GTGTCGAAGG AGATCATCGC	100
GAAGGCGACG GGCGAATAG	119

2) INFORMATION FOR SEQ ID NO: 2224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

1142

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224

CGGCGACCTG	CGGTCCAAGA	CTCAAGGCCG	GGCGAACTAC	TCGATGGTGT	50
TCGATTCCTA	CGCCGAAGTG	CCGGCTCAGG	TGTCGAAGGA	GATCATCGCG	100
AAGGCGACTG	GCGAGTGA				118

2) INFORMATION FOR SEQ ID NO: 2225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225

CGGAGACTTG	CGGTCGAAGA	CCCAGGGCCG	GGCGAACTAC	TCCATGGTGT	50
TCGACTCCTA	CGCCGAAGTG	CCGGCGCAGG	TGGCGAAGGA	GATTATCGCG	100
AAGGCAACGG	GCGAGTAA				118

2) INFORMATION FOR SEQ ID NO: 2226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226

GACCGACCTG	CGTTCTGCAA	CCCAAGGCCG	CGCTACTTAC	TCTATGGAGT	50
TCAAGAAATA	TTCTGAAGCT	CCTGCCACA	TAGCTGCTGC	TGTAAGTAA	100
GCCCGTAAAG	GCTAA				115

2) INFORMATION FOR SEQ ID NO: 2227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227

AACTTCATTA CGTTCTAACA CGCAAGGTCG CGGTACTTAC ACAATGTACT	50
TTGACCACTA TGCAGAAGTT CCTAAATCAA TTGCTGAAGA AATCATCAAG	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228

AACTTCATTA CGTTCTAACA CTCAAGGTCG CGGTACTTAC ACTATGTACT	50
TCGATCACTA TGCAGAAGTT CCAAATCAA TTGCTGATGA TATCATCAAA	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229

CGTTCAATGC	GTGTTCTAGA	CGGTGCAGTT	ATGGTTTACT	GTGCTGTGGG	50
TGGTGTTTCAG	CCTCAGTCTG	AAACCGTTTG	GAGACAGGCT	CAGAAGTACA	100
AGGTTCCCTCG	TATTGCTTTC	GTTAATAAGA	TGGACCGTAC	TGGTGCTAAT	150
TTCTTACGTG	TTGTAGAGCA	GATTAAGACC	CGTCTAAAGG	GTAACCCCTGT	200
TCCTCTAATG	TTACCTATCG	GTAAGAGAGGA	CAGCTTTGTT	GGTGTAGTTG	250
ACCTAATCAA	GCGTAAGGCT	ATCGACTGGG	ATGAGGCATC	TCAGGGTATG	300
AAGTTTGAGT	ACGTTGACAT	TCCAGCAGAT	ATGGTTGAGG	AAGTTGAAGA	350
GTGGCGTGCA	AAGCTTGTAG	AAGCAGCTGC	AGAAGCTAAC	GACGAGCTGA	400
TGGATAAATT	CTTCGGTGGT	GAAGAGCTGA	CCGAGGAAGA	GATCAAGGCT	450
GCTCTACGTG	AGCGTACTCT	TCGCAACGAA	ATTATTCCTA	TGTGCTGCGG	500
TTCAGCATTT	AAGAACAAGG	GTGTTCAGGC	AATGCTTGAC	GCTGTTGTTG	550
AGTATCTTCC	ATCTCCAGCA	GATGTTCTTG	CTGTTGAGGG	TAAGACCCTA	600
ACCGGTGAAG	CTGATACTCG	TAAGGCTGAC	GATAAAGAGC	CATTCTCTGC	650
TTTAGCATTT	AAGCTAGCAA	ATGACCCATT	CGTAGGTAAC	TTAACATTCT	700
TACGTTGCTA	CTCAGGCTTT	ATTAAGTCTG	GTGACACTGT	AATGAACTCA	750
GATAAGCAGA	AGCGTGAGCG	TTTCGGCCGT	CTAGTTCAGA	TGCACGCTAA	800
TGCTCGTAAT	GAGGTTAGCG	AGGTTTATGC	AGGTGACATC	GTTGCTGCTA	850
TTGGTCTGAA	GGAAACCGTT	ACCGGTGATA	CCTTATGTGA	CCCAGAGCAT	900
CCAATCATTC	TTGAGTCAAT	CGACTTTGCA	GAGCCAGTTA	TCTCTGTAGC	950
AGTTGAGCCT	AAGACCAAGG	ACGATCAGGA	GAAGATGGCT	CTTGCTTTAC	1000
AGCGTTTAGC	AAAAGAAGAT	CCTTCATTCC	GCGTTCGTAC	AGACGAAGAG	1050
TCTGGCCAGA	CCATTATTTT	TGGTATGGGT	GAGCTTCACC	TAGACATCAT	1100
TGTTGACCGT	CTACGCCGTG	AGTTCAAGGT	TGAGTGTAAT	CAGGGTAAGC	1150
CACAGGTTGC	ATACCGTGAG	ACCATTAAGA	GCAAGGTTGA	ACAGCAAGGT	1200
AAGTTTGCTC	GTCAGTCTGG	TGGTCGTGGT	CAGTACGGTG	ACTGCTGGTT	1250
ACGTATGGAA	CCTCTTGAGC	CAGGTAAGGG	CTACGAATTC	GTGAATGAGA	1300
TTGTTGGTGG	TGTAATTCCT	AAGGAATATA	TCCCTGCAAT	TGATAAGGGC	1350
TGTCAGGAGC	AGATCGCTAA	CGGTGTTCTA	GCTGGTTTCC	CAGTTGTTGA	1400
CATCAAGATC	ACTGTATTCT	ATGGTTCTTA	CCACGAAGTT	GACTCTTCAG	1450
AAATGGCATT	CAAGATTGCT	GCTTCTATGG	CATTCAAAGA	GGGCTTCAAG	1500
AAGGCAAATC	CTGTTCTTCT	AGAGCCTTTA	ATGAAGGTAG	AAGTTGATAC	1550
TCCTGAAGAC	TACATGGGTG	ACGTTATTGG	TGACTTAAAC	CGTCGTCGTG	1600
CTATCGTTGA	AGGCATGGAA	GATGGTCCTA			1630

2) INFORMATION FOR SEQ ID NO: 2230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230

TTGAAGTGCA	ACGTTTCATTG	CGTGTGCTAG	ACGGTTCAGT	TACTGTCTTG	50
GACTCACAAAT	CAGGTGTTGA	ACCACAAACT	GAAACAGTTT	GGCGTCAAGC	100
AACAGAATAT	CAAGTACCTC	GTATTGTATT	CTGTAATAAA	ATGGATAAGG	150
TTGGCGCAGA	TTTCTTATAT	TCTGTCCGAT	CATTGCATGA	TCGTTTAGAA	200
GCTAATGCAC	AACCTATCCA	ATTGCCAATT	GGTGCTGAAG	ATAACTTTGA	250
AGGTATCATC	GACCTTGTGA	AGATGAAAGC	TGAATTTTAT	AAAGATGATT	300
TAGGGACTAC	TTTCGAAGAA	ACTGAAATCC	CAGATGAATA	TAAAGAAACA	350
GCTCAAGAAT	GGCATAATAA	TTTGGTAGAA	TCTGTAGCTG	ATTTTGATGA	400
AGATATCATG	ATGAAATACT	TGGAAGGTGA	AGAAATTACA	CCTGAAGAGT	450
TACAAGCAGG	TATTCGTAAA	GCAACATTAT	CTGTTGAATT	TTACCCAGTA	500
TTATGTGGTT	CTGCATTTAA	AAACAAAGGT	GTTCAAATGA	TGTTGGATGC	550
AGTAATTGAT	TACTTGCTTT	CTCCAACCGA	CGTTCCCCCA	ATTAAAGGGA	600
TCGATCCGAA	AACAGATGAA	GAAACTGAAC	ATCCTGCTGA	TGATAGTGAG	650
CCTTTTTTCAT	CACTTGCTTT	TAAAGTTATG	TCAGACCCTT	ATGTTGGCCG	700
CTTAACTTTC	TTCCGTGTTT	ATTCAGGTGT	GTTGGATACA	GGTTCCTTATG	750
TATTGAATGC	TACTAAGGGT	TCACGTGAAC	GAATTGGTCG	TATTTTGCAA	800
ATGCATGCCA	ATTCTCGTTC	TGAGATCGAT	AAGGTTTATT	CAGGTGACAT	850
TGCAGCTGCT	GTAGGCTTGA	AGAACACTAC	AACAGGGGAT	ACCCTTTGTG	900
ATGAGAAAAA	TCCAGTTATT	TTGGAAACTA	TCAACTTCCC	TGAACCAGTA	950
ATTCAAGTTG	CTGTTGAACC	TAAGTCAAAA	GCTGACCAAG	ATAAAATGAG	1000
CGTAGCACTA	CAAAAACCTG	CAGAAGAAGA	CCCATCTTTT	AAAGTGGAAA	1050
CCAACGCTGA	AACTGGCGAA	ACTGTAATTG	CTGGTATGGG	TGAACTTCAA	1100
TTAGACGTTT	TTATTGACCG	TATGAAGACT	GAATTTAAAG	TGGATGCCAA	1150
TATTGGTGCA	CCACAAGTTT	CTTATCGTGA	AACTTTCCGT	TCATCAACTA	1200
AAGCTGAAGG	GAAATTTATC	CGCCAATCTG	GTGGTAGAGG	TCAATACGGT	1250
CACGTATGGG	TTGAATTTAC	TCCAAACGAA	GAAGGAGCAG	GATTCGAATT	1300
TAAAAACTCC	ATTGTTGGTG	GGGTTGTCCC	TCGTGACTAT	ATACCTGCAG	1350
TACAAAAAGG	ACTGGAAGAC	GCCATGGAAA	ATGGTGTGTT	AGCTGGTTAT	1400
CCATTAGTTG	ACGTAAAGGC	AGAACTGTTT	GATGGTTCTT	ACCATGACGT	1450
CGACTCTAAT	GAAACAGCCT	TCCGTATTGC	GGCTTCAATG	TCTCTACGTG	1500
AAGCTGCGAA	AAAGGCAGAT	CCAGTTATTG	TTGAACCGAT	GATGAAAGTA	1550
ACAATTAGTA	TCCCTGAAGA	ATATCTAGGT	GATATTATGG	GACATGTTAC	1600
AGCTCGTCGT	GGTCGTGTTG	AAGGAATGGA	TGCTCACGGT	AATGCACAAA	1650
CTGTAAATGC	GT				1662

2) INFORMATION FOR SEQ ID NO: 2231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
- (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2231

AAGTAGAACG	TTCTCTACGT	GTAATTGACG	GTTCTGTTGC	GGTGTTTCAGT	50
GCTAAAGGTG	GCGTTGAACC	TCAATCCGAA	ACAGTATGGC	GTCAGGCTTC	100
TAACTACGGC	GTACCTCGTA	TCGCTTATGT	AAATAAGATG	GATACTGTAG	150

GTGCTGACTT	CTTCAACGTA	GTTGACATGA	TGAAAGCTCG	TTTGGGTGCA	200
AATTCCGTAG	CTATCCAAGT	ACCAATCGGT	GCTGAAGATA	CTTTCGAAGG	250
CATCATTGAC	TTGATGACTA	TGAAAGCGGA	AATTTATAAA	TCCGATGACG	300
GTAAAGAATA	TGAAATCACT	GATATCCCTG	CTGAATATCA	AGAAGTAGCA	350
GAAGCTCGTC	GCGAAATGAT	GATCGATGCT	ATCGCTGAAA	CAGATGATGA	400
TATCATGATG	AAATATTTGG	AAGGCGAAGA	AATTTCTGTG	GAAGAATTGA	450
AAGCGGCATT	GCGTAAAGCT	GTTATTGCTA	ACCAATTATT	CCCAGTTCTT	500
TGTGGTTCTT	CCTATAAAAA	TAAAGGTGTT	CAAATGTTAT	TGGATGCTGT	550
TATCGATTAC	ATGCCAGCTC	CAATCGACAT	CCCACCTATT	AAAGGTGTTG	600
TTCTTGGTAC	TGAAGAAGAA	ACAACCTCGT	CTTCTTCCGA	TGAAGAGCCA	650
TTCTCTGCAT	TGGCATTCAA	AATCATGGCT	GACCCTTATG	TTGGTAAATT	700
AGCGTTCTTC	CGTGTGTACT	CCGGTACATT	GGAATCTGGC	TCCTACGTTT	750
TCAACTCCAC	TAAAGGTAAA	AAAGAACGTA	TCGGTCGTAT	TCTTCAAATG	800
CACGCTAACT	CCCGTAAAGA	AATCGAACGC	GTATATTCTG	GTGACATCGC	850
TGCGGCGGTT	GGCTTAAAGG	ATACTACTAC	AGGCGACACA	TTGTGTGATG	900
AAAAATCTCC	TGTAATCCTT	GAGTCCATGG	AATTCCTTGA	ACCAGTTATC	950
TCCGTTGCTG	TTGAACCTAA	AACAAAAGCT	GACCAAGAAA	AAATGGGTAC	1000
AGCTCTTGCT	CGTTTGGCAG	AAGAAGATCC	TACTTTCAAA	GTTTCGTACTG	1050
ATGAAGAAAC	AGGTCAAAC	ATTATCTCTG	GTATGGGCGA	ACTTCACTTG	1100
GATATCATCG	TTGACCGTAT	GAACCGTGAA	TTCAAAGTAG	ATTGTAACGT	1150
AGGTAAACCT	CAAGTAGCAT	ACCGCGAAAC	TATCCGTAAA	GCTGTTAAGG	1200
CTGAAGGTAA	ATTCGTACGT	CAATCTGGTG	GTCGTGGTCA	ATATGGTCAC	1250
TGCTGGTTGG	AATTGATTCC	TCAAGAACCA	GGTGCTGGCT	TCGAGTTTGA	1300
AAACAAGGTT	GTAGGTGGTG	CGATTCCCTCG	TGAATACATC	GGACCTGTTG	1350
AAAGCGGTGT	TAAAGAAGCT	ATGGAATCCG	GTGTTATCGC	TGGGTACCCT	1400
ATGGTTGATG	TTAAAGTTAT	CGTATTTGAT	GGTTCTTACC	ATGACGTTGA	1450
CTCCAACGAA	ATGGCCTTCA	AAATTGCTGG	TTCTATGGGC	TTCAAAGAAG	1500
GTGCTCGCAA	AGCAGACCCT	GCATTGCTTG	AACCATATAT	GGCTGTAGAA	1550
GTAGACGTTT	CTGAAGAATA	CATGGGCGAC	GTTATCGGTG	ACTTGAAGTC	1600
TCGTCGTGGT	CGCATGGACG	GCATGGAAGC	TCGTAATGGT	TCCCAACATA	1650
TC					1652

2) INFORMATION FOR SEQ ID NO: 2232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232

AGTAGAGCGT	TCCATGCGTG	TTCTTGACGG	CGCGGTAATG	GTTTACTGTG	50
CAGTTGGTGG	TGTTCAAGCA	CAGTCTGAAA	CCGTATGGCG	TCAGGCTAAT	100
AAATATAAAG	TTCCACGTAT	TGCGTTTCGTT	AACAAAATGG	ACCGTATGGG	150
TGCGAACTTC	CTGCGCGTAG	TTGGTCAACT	GAAATCTCGC	CTTGGTGCGA	200
ACCCAGTTCC	ACTGCAGTTG	GCAATTGGCG	CAGAAGAAAA	ATTCACCGGT	250
ATTATCGATC	TGGTGAAAAT	GAAAGCGATC	AACTGGAACG	AAGCTGATCA	300
GGGCGTGACC	TTCGAATATG	AAGAAATCCC	TGCTGATATG	GCTGAACTGG	350

CTGCTGAATG	GCACCAGAAT	CTGGTTGAAT	CTGCGGCAGA	AGCGTCTGAC	400
GAGCTGATGG	ACAAATACTT	GGGTGGCGAA	GAGCTGACCG	AAGAAGAAAT	450
CAAGAAAGCT	TTACGTCAAC	GTGTTCTGAA	AAGCGAAATT	ATTCTTGTTA	500
CCTGTGGTTC	TGCGTTTAAA	AACAAAGGCG	TACAGGCAAT	GCTGGATGCG	550
GTTATTGAGT	ACCTGCCTGC	ACCAACTGAC	GTTGAATCAA	TCAACGGCAT	600
CTTGGATGAT	GGCAAAGATA	CTCCGGCTGT	TCGTCATTCT	GACGACAAAG	650
AGCCGTTCTC	TGCTCTGGCG	TTCAAAATCG	CTACCGACCC	ATTCGTGGGT	700
AACCTGACGT	TCTTCCGCGT	GTACTCTGGT	ATTGTTAATT	CCGGTGATAC	750
CGTTCTGAAC	TCAGTGAAAT	CGCAACGTGA	ACGCTTAGGT	CGTATCGTAC	800
AGATGCACGC	TAACAAGCGT	GAAGAGATCA	AAGAAGTTCA	CGCCGGTGAT	850
ATCGCAGCCG	CTATCGGTCT	GAAAGATGTG	ACTACGGGTG	ACACTTTGTG	900
TGACCCGAAT	AATCCGATCA	TCTTGGAACG	TATGGAGTTC	CCAGAGCCGG	950
TAATCTCTGT	TGCTGTTGAA	CCAAAAACCA	AAGCTGACCA	AGAAAAAATG	1000
GGTATGGCTC	TGGGGCGTTT	GGCGAAAGAA	GATCCATCAT	TCCGCGTTTG	1050
GACTGACGAA	GAATCTGGTC	AGACTATCAT	CGCTGGTATG	GGTGAGTTGC	1100
ATTTGGATAT	CCTGGTTGAC	CGTATGCGCC	GCGAATTTAA	CGTGGAAGCA	1150
AACGTCGGTA	AACCTCAGGT	TGCGTACCGT	GAAACTATCC	GCGAAACCGT	1200
TAAGGATGTG	GAAGGTAAGC	ACGCTAAGCA	GTCAGGCGGT	CGTGGTCAGT	1250
ATGGTCATGT	TGTTATCGAC	ATGTCTCCAT	TGCCACCGGG	TGGTGTTGGG	1300
TATGAATTCG	TCAACGAAAT	CGTTGGTGGT	TCTATTCCTA	AAGAATTCAT	1350
TCCGGCCGTT	GATAAAGGTA	TTCAAGAACA	GCTGAAATCT	GGCCCTCTGG	1400
CAGGTTACCC	AGTTGTTGAC	GTTAAAGTGC	GTCTGCACTA	CGGTTCTTAC	1450
CATGACGTTG	ACTCCTCAGA	ATTGGCATT	AAATTAGCTG	GTTCTATCGC	1500
CTTTAAAGAA	GGTTTCAAAC	GAGCTAAACC	AGTTCTGCTT	GAGCCAATCA	1550
TGAAGGTTGA	AGTCGAAACC	CCTGAAGATT	ACATGGGTGA	CGTAATGGGC	1600
GACCTGAACC	GTCGTCGCGG	TATC			1624

2) INFORMATION FOR SEQ ID NO: 2233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233

GAACGCTCGA	TGCGCGTGCT	TGACGGTGCT	TGCATGGTTT	ACTGCGCAGT	50
GGGCGGTGTT	CAGCCACAGT	CGGAAACCGT	GTGGCGTCAG	GCTAACAAGT	100
ACAAAGTGCC	ACGTCTGGCC	TTCGTCAACA	AGATGGACCG	TACCGGCGCC	150
AACTTCTTCA	AGGTGTACGA	GCAGATGCGT	GCTCGCCTGA	AGGCCAACCC	200
GGTCCTGATC	CAGATCCCTA	TCGGCGCTGA	AGACAACTTC	AAAGGCGTGA	250
TCGATCTGGT	CAAGATGAAG	GCTATCCTGT	GGGACGAAGC	GTCGCAAGGC	300
ATGAAATTCG	ACTACGTCTGA	TATTCCTGCA	GAGCTGGCTG	ATTCGGCCGC	350
CGAGTGGCGC	GAAAAGATGG	TTGAAGCTGC	TGCTGAAGCC	ACCGAAGAGC	400
TGATGAACAA	GTACCTGGAA	GAAGGCGACC	TGACCGAAGC	CGAGATCAAG	450
CAGGCGCTGC	GTACCCGTAC	CATCGCTTCG	GAAATCGTTC	CGATGATGTG	500
CGGTACCGCC	TTCAAGAACA	AGGGCGTACA	GGCCATGCTG	GACGCGGTCA	550
TCGAATACCT	GCCATCGCCA	CTGGACATCG	ACGATGTCCG	CGGTACGGAC	600

GAAGACGACC	AGCCAACCAC	CCGTCGCGCA	GCTGACGACG	AGAAATTCTC	650
GGCGCTGGCC	TTCAAGATCA	TGACCGACCC	GTTTCGTCGGT	CAATTGGCCT	700
TCTTCCGCGT	GTACTCGGGC	GCCGTCAATT	CGGGCGACAC	CGTGTACAAC	750
TCGGTCAAAG	GTCGTAAAGA	GCGTCTGGGC	CGTATTCTGC	AGATGCACGC	800
GAATCAGCGC	GAAGAGATCA	AAGAAGTGCG	CGCCGGCGAC	ATCGCCGCTG	850
CGGTGCGCCT	GAAAGACGTG	ACCACGGGCG	AAACCCTGTG	CGATCCGACC	900
GCCATCATCA	CGCTGGAAAA	AATGATCTTC	CCTGAGCCTG	TGATTCAACA	950
GGCAGTCGAG	CCAAAAACCA	AGGCCGACCA	GGAAAAAATG	GGCCTGGCAC	1000
TGAACCGCCT	GGCACAGGAA	GATCCTTCGT	TCCGCGTGAA	GACCGATGAA	1050
GAATCGGGCC	AGACCATCAT	CGGTGGWATG	GGCGAGCTGC	ACCTGGAAAT	1100
TATCGTTGAC	CGCATGAAGC	GCGAATTTCG	CGTGGAAGCA	ACCGTCGGCA	1150
AGCCACAAGT	GGCTTACCGC	GAAACGATCC	GTAAAACCTG	CGAAGAATCG	1200
GAAGGCAAGT	TCGTCAAGCA	ATCCGGTGGT	CGTGGTCAAT	ACGGTCACGT	1250
TGTGCTGAAG	ATCGAGCCGC	AAGAACCAGG	CAAGGGCTTC	GAGTTCGTTG	1300
ACGCCATCAA	GGGCGGTACC	GTTCTTCGCG	AGTACATCCC	TGCGGTGGAA	1350
AAAGGCGTGC	GCGGCACCCT	GAACACCGGC	GTGCTGGCTG	GTTACCCGGT	1400
CGTGGAACGC	AAGGTCACGC	TGTTCTTCGG	TTCGTACCAC	GATGTGGACT	1450
CGAACGAAAA	CGCGTTCCAG	ATGGCCGCTT	CGATGGCATT	CAAAGAAGGC	1500
TGCCGCAAAG	CATCGCCAGT	CATTCTGGAG	CCAATGATGG	CTGTGGAAGT	1550
GGAAACGCCG	GAAGACTACG	CCGGTACCGT	GATGGGCGAC	CTGTCGTCCC	1600
GCCGCGGTAT	GGTGCAGGGC	ATGGACGAAA	TCCCAG		1636

2) INFORMATION FOR SEQ ID NO: 2234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234

GGCACGAACG	ATCTTGCCGG	ACGGGCCATC	TTCCATACCT	TCGATCAGGC	50
CACGACGACG	G TTCAGGTCA	CCGATCACGT	CGCCCATATA	GTCTTCCGGA	100
GTCTCGACTT	CTACTTTCAT	GATCGGTTCG	AGCAGAACCG	GGTTGGCCTT	150
CATGAAGCCA	GCCTTAAAGG	CCATGGAAGC	AGCGATCTTG	AACGCCAGTT	200
CGGAAGAGTC	GACATCGTGG	TAGGAACCGA	AGTGCAGACG	CACGCCCAGA	250
TCCATAACCG	GATAACCTGC	CAGCGGGCCG	GACTTCAGTT	GCTCGCGGAT	300
ACCCTTGTCA	ACACCCGGGA	TGAACTCACC	AGGAATGACG	CCGCCCTTGA	350
TGTCGTTGAC	GAATTCGTAG	GCTTTGCCTT	CTTCCAGCGG	GTACATGTCG	400
ATCACAACGT	GACCGTACTG	ACCACGACCA	CCGGACTGCT	TGGCGTGCTT	450
ACCTTCGATA	TCCTTGACGG	TGTTACGAAT	GGTTTCACGG	TAGGCAACCT	500
GCGGCTTACC	TACGTTTCGCT	TCTACCTTGA	ACTCGCGACG	CATACGGTCA	550
ACGATGATGT	CCAGGTGCAG	CTCACCCATA	CCGGCGATGA	TGGTTTGGCC	600
AGACTCTTCG	TCAGTCCATA	CGCGGAAGGA	CGGGTCTTCC	TGAGCCAGAC	650
GGCCCAGAGC	CAGGCCCATC	TTCTCTTGGT	CAGCCTTGGT	TTTCGGCTCA	700
ACTGCGATGG	AGATTACCGG	TTCCGGGAAT	TCCATACGCT	CGAGGATGAT	750
CGGCGCTTTT	TCGTACACAC	GGGTGTCACC	GGTGGTCACG	TCTTTCAGAC	800
CAATGGCGGC	AGCGATGTCG	CCTGCGCGAA	CTTCTTTGAT	CTCTTCACGC	850

TTGTTGGCGT	GCATCTGAAC	GATACGGCCA	AAACGCTCGC	GCTTCTCTTT	900
AACGGAGTTC	AGCACGGAGT	CACCGGAGTT	AACCACACCG	GAGTAAACGC	950
GGAAGAAGGT	CAGGTTGCCT	ACGAACGGGT	CGGTAGCAAT	CTTGAATGCC	1000
AGAGCAGCAA	ACGGCTCGTC	ATCAGAAGCA	TGACGCTCGT	CTTTGGTCTC	1050
GCCATCCAGC	TTCAGACCGT	CGATGGCTGC	TACGTCGGTC	GGCGCCGGCA	1100
GATAGTCAAC	CACGGCATCC	AGCATGGCCT	GTACGCCCTT	GTTCTTGAAC	1150
GCGGAGCCAC	AGGTAACCAG	GATGATTTCG	TTGTTCAGAA	CACGCTGACG	1200
AAGAGCTTTC	TTGATCTCTT	CCTCGGTCAG	TTCTTCACCA	CCCAGGTATT	1250
TTTCCATCAG	GTCTTCAGAC	GCTTCAGCAG	CGGCTTCAAC	CAGGGTCATG	1300
CGCATTTCTT	GCGCTTTTTC	CAGCAGCTCA	GCCGGGACGT	CTTCGTAATC	1350
GAAGGATACG	CCCTGGTCAG	CTTCGCTCCA	GTTGATGGCT	TTCATCTTGA	1400
CCAGGTTCGAT	AACGCCCTTG	AAGTTCTCTT	CTGAACCGAT	GTTTCAGTTGC	1450
AGCGGAACCG	GGTTACCTTT	CAGACGGGTC	TTGATGTGCT	CAACGCAGCG	1500
CAGGAAGTTG	GCACCGGTAC	GGTCCATCTT	GTTGACGAAC	GCGATACGGG	1550
GAACCTTGTA	CTTGTTAGCC	TGACGCCATA	CGGTTTCAGA	CTGTGGCTGT	1600
ACGCCACHTA	CGGCACAGTA	CACCATCACG	GCGCCGTCCA	GAACACGCAT	1650
GGAACG					1656

2) INFORMATION FOR SEQ ID NO: 2235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235

TCTCCTCCCC	ATTTGATAAC	TACCAAATGA	ACGCTATCGA	CTGGTTATGT	50
CAGTCATAAC	CAGTTGATTT	TTAAGAGAGT	TCTTTGGTAT	AATTACAATC	100
GGTAGATACT	GTTATAGAAT	CTAACAAAAC	TCAATTAATA	GGAGGAATCA	150
TTTAA					155

2) INFORMATION FOR SEQ ID NO: 2236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236

TCTTTCGATT ACTATAAGCC CTAAC TAATT CTTAGTTAAA AACCAAGTGC	50
TCATGGAGCG ACCCTCCATG AGTAGTTAAT AAAGGAAGAT CATC	94

2) INFORMATION FOR SEQ ID NO: 2237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237

GTCCCACCGG GGGTGAGTGG GGGCCGGGCA ATCGGCCCT GCGAGCCGCC	50
TCACACACCA GTAATCCCAG TAGGTCTCAT GCCCATGGG TGTAAAGTG	100
ACACCTAGCC GTAGGCTGAG AATTCTACC CGAGTCCAGG AGGACGAAA	150

2) INFORMATION FOR SEQ ID NO: 2238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238

TTCAGTCCTT TAGGCAAGGA GTTAATTGTC	30
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2) INFORMATION FOR SEQ ID NO: 2239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium diphtheriae*

(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2239

CAACTAGCCT	CTCGCTTATC	TCCCTATGCA	AAATTTCTAG	TCAGTTACAG	50
GGCATAGGGG	GAGCGTAGGC	GGGGGTAGCG	GCTTGCTGAG	CACTTCCTCT	100
ACATCAAAGG	GAATGTTGAG	CCGGCCGTTA	CCCTGTACGA	TCCCATCTGG	150
TTTCTTCGGT	GGTTTGATAA	ATACCCCGTT	GTGACCCTAG	GATCATGTAA	200
CTGGCACAAT	GTAAATAGCT	GTACTGCCAG	GCTGCCGAAT	TAGCAGTCAG	250
AAATGTACAG	CACTGTCAAC	TCGTGGCTGC	GAAATCGTAG	CCACCACGAA	300
GTCCAGGAGG	ACACACA				317

2) INFORMATION FOR SEQ ID NO: 2240

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter cloacae*

(B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCTGAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2241

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*

(B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCGAAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242

AACAACAAAG AAGATTAATT GATTTTTTTC GCAACATCAA GTATAACTTT	50
AGTTAGAAGT ATTACTTAGT TTAAATTTAA GCTAAGTAAA AAATAATTAT	100
CGAATTATCG AGGAGGATAT TTAAA	126

2) INFORMATION FOR SEQ ID NO: 2243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2243

GTGTCAACTC ACTGGCTCGG AGCCGAGCAA TCGGCTCAGC GAAGGCGACG	50
GGTCAGTAGC TACTGGCAGC GGAGTAATCT TGCCGGGTCA TTGGAATGCC	100
TTGGGCGCGG CACAACTGAA AACACCAACA CTGCTTTAAC AAGCACCAAC	150
TAGTCCAGGA GGACACAGAA	170

2) INFORMATION FOR SEQ ID NO: 2244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1153

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244

GGCCGGCAAG CCTGCGAGTA AGCTGACGCG GTTAGCACCG CGGCAAAACC	50
AAGAAAAATC AACACTGCTT TTTTAAGCAC CAACAGTCCA GGAGGACAAC	100
AAA	103

2) INFORMATION FOR SEQ ID NO: 2245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245

GCCGAGCGTT GCGCGTAAGC TAGCTCGGTT ACCACGGCGG CAAAACTAGA	50
AAAACATCAA CACTGCTTTT ATAAGCACCA ACAGTCCAGG AGGACACAGA	100
A	101

2) INFORMATION FOR SEQ ID NO: 2246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246

CCAGCTTCCC GCCCGTGCCG CTACGGTGGC ACAAACCCAA AAAGATCAAT	50
CCTGCTGTAA CCCAGCACCA ACAAGTCCAG GAGGACAAGA A	91

2) INFORMATION FOR SEQ ID NO: 2247

1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247

TCAGGCAAAT AGGCCGTCTG AAAGGCTGAA ATGATTTTTC AGACGGCATT	50
GTTCTTTAAT CGATCTTTAA TGTAAGGAA TTAGCTC	87

2) INFORMATION FOR SEQ ID NO: 2248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248

TATAACTTGT TAAGACTAGC TATGCTAGGT TAAAATACAG GTTGAGCTTA	50
TTTATAAGCT GACATTTTAA TGATTTGATT TTTAGGGGTA AATGCATTAT	100
AAAAGAATTA TAAATTCTTT TATGCTACAC TCAATCAATT TTCTTCTCAT	150
GATGGTGAGA AACTATCATG AGAGATAAAT TTGAAATAAC TTTTATTAAG	200
AATAGGAGAG ATTTAATA	218

2) INFORMATION FOR SEQ ID NO: 2249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249

TTAAACTTGT	TTTAGCTAGA	ATTTCTAGGT	AAAATACAGC	GTAAGCTTAT	50
TAATTAAGCT	AACATCTTTA	TGAATTGATT	TTTTACTGAA	AATGCATTAT	100
AAATGAATTA	TGAATTCTAA	CAATCATTAT	GTCTCATGAT	GGTGAGAAAC	150
TATCATGAGA	GATAATATTG	AAATAACTTT	TACTAGAATA	GGAGAGATTT	200
AATA					204

2) INFORMATION FOR SEQ ID NO: 2250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250

CCGTCGGATG	GTGTCGTATA	CCGCGGAGTC	GCCGACGG	38
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2) INFORMATION FOR SEQ ID NO: 2251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2251

CGGAGCCGTT	CTCGCTGCGT	TACATGCTGG	TGGCTCCG	38
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2) INFORMATION FOR SEQ ID NO: 2252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252

CCACATACAG	TGTCTCTC	18
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2) INFORMATION FOR SEQ ID NO: 2253

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253

CATTACCCAA CCGAAAGTA

19

2) INFORMATION FOR SEQ ID NO: 2254

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254

ACCTGAACAG AGAGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2255

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2255

ATGGCAAAAG	AAAAATTTGA	CCGTTCAAAA	CCACACGTTA	ACATTGGTAC	50
AATCGGCCAC	GTTGACCACG	GTAAAACAAC	ATTAAGTGCT	GCTATCACAA	100
CTGTTTTAGC	TAAGAAAGGT	TTCGCGCAAG	CTCAAGATTA	CGGTTCAATC	150
GATAAAGCTC	CAGAAGAACG	CGAACGTGGT	ATCACAATCA	ACACTTCTCA	200
CGTTGAGTAC	GAAACAGACA	CTCGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCGGA	CTACGTTAAA	AAC			273

1157

2) INFORMATION FOR SEQ ID NO: 2256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256

ATGGCTAAAG	CCAAGTTTGA	ACGTAATAAA	CCACACGTAA	ACGTGGGTAC	50
AATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACTGCT	GCGATTGCAA	100
CAATTTGTGC	AAAAACTTAC	GGCGGTGAAG	CGAAAGATTA	CTCACAAATC	150
GACTCAGCAC	CTGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACATCACA	200
CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTT	GACTGCCCAG	250
GCCACGCCGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257

GTGGCGAAGG	CCAAGTTTGA	GCGCACCAAG	CCGCACGTCA	ACATCGGCAC	50
GATTGGTCAC	GTTGACCACG	GCAAGACGAC	GCTGACGGCA	GCTATCACCA	100
AGGTGCTGCA	TGACAAGTAC	CCCGAACTGA	ACGAGTTCAC	CCCCTTCGAT	150
CAGGTCGACA	ACGCTCCCGA	GGAGCGCGAT	CGTGGCATCA	CGATCAACGT	200
CTCTCACGTT	GAGTACCAGA	CCGAGGCGCG	TCACTACGCG	CACGTTGACG	250
CTCCCGGCCA	CGCCGACTAC	GTCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2258

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases

1158

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258

GTGGCTAAAG	AAAAATTTGA	TCGTTCCCTA	CCGCACGTCA	ACGTTGGCAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTCTGACTC	100
GCGTTTGCTC	CGAAGTATTC	GGTTCGCAA	TCGTTGATTT	CGATAAAATC	150
GACAGCGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCGCGCA	200
CGTTGAATAC	AACTCGCTGA	TCCGTCACTA	CGCTCACGTT	GACTGCCCAG	250
GTCACGCTGA	CTATGTGAAG	AAC			273

2) INFORMATION FOR SEQ ID NO: 2259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259

GTGGCAAAGG	CTAAGTTCGA	GCGTACCAAG	CCGCACGTCA	ACATCGGCAC	50
CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCT	GCTATCACCA	100
AGGTTTTTGGC	AGACGCTTAC	CCAGAGCTGA	ACGAAGCTTT	CGCTTTCGAT	150
GCCATCGATA	AGGCACCGGA	AGAGAAAGAG	CGTG GTATTA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAGA	CCGAGAAGCG	CCACTACGCA	CACGTTGACG	250
CTCCAGGTCA	CGCTGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAACTAC	CCTGACTGCT	GCAATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CTCGTGCATT	CGACCAGATC	150
GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
GTCACGCCGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAACTAC	CCTGACTGCT	GCCATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCCG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GACTGCCCCG	250
GCCACGCCGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262

ATGGCAAAAG	AAAAATTTGA	CCGCTCTAAA	CCCCATGTTA	ACATTGGTAC	50
TATTGGACAC	GTTGACCATG	GTAAACAAC	TTTAACTGCT	GCAATTACAA	100

CTGTACTTGC	TAAAAAAGGC	TATGCTGATG	CACAAGCTTA	TGACCAAATT	150
GATGGTGCTC	CAGAAGAAAG	AGAACGTGGA	ATCACAATCT	CTACTGCTCA	200
CGTTGAGTAC	CAAACGTACA	GCCGTCATA	TGCACACGTT	GACTGCCAG	250
GACATGCCGA	TTACGTAAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2263

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCCG	CGCGTTCGAC	150
CAGATCGACA	ACGCGCCCGA	GGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCACGTG	GAGTACCAGA	CCGACAAGCG	GCACTACGCT	CACGTCGACG	250
CCCCGGGTCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	TCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCAA	GGCGTTCGAC	150
CAGATCGACA	ACGCGCCTGA	GGAGCGTCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAATACCAGA	CCGAGAAGCG	TCACTACGCG	CACGTCGACG	250
CCCCGGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCCCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	CCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	TGACAAGTTC	CCGGACCTGA	ACGAGTCGAA	GGCGTTCGAC	150
CAGATCGACA	ACGCTCCTGA	GGAGCGCCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTATGCA	CACGTCGACG	250
CGCCGGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266

GTGGCGAAGG	CGAAGTTCTGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTCA	ACGAGTCGCG	TGCGTTCGAC	150
CAGATCGACA	ACGCTCCCGA	AGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTACGCC	CACGTCGACG	250
CTCCTGGTCA	CGCTGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267

ATGGCTAAGG	AAAAATTCGA	ACGTAGCAAA	CCGCACGTAA	ACGTTGGCAC	50
CATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTTTGACTA	100
CTATTTTGGC	TAAAAAATTC	GGCGGTGCTG	CAAAAGCTTA	CGACCAAATC	150
GACAACGCAC	CCGAAGAAAA	AGCACGCGGT	ATTACCATTA	ACACCTCGCA	200
CGTAGAATAC	GAAACCGAAA	CCCGCCACTA	CGCACACGTA	GACTGCCCCG	250
GTCACGCCGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2268

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268

ATGGCAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTTG	CACAATCATA	CGATATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATTACAATCA	ATACTGCACA	200
TATCGAATAC	CAAACTGACA	AACGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCTGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2269

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269

ATGGCAAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACTAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTAG	CACAATCATA	TGACATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATCACAATCA	ATACTGCACA	200
CATCGAGTAT	CAAACCTGACA	AACGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCTGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270

CGATCCTGGT	AGTAGCAGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTCAT	100
GAACAAGTGT	GACATGGTAG	ATGACGAAGA	GCTGCTGGAA	CTGGTCGAGA	150
TGGAAGTTTCG	CGAACTGCTG	TCCGAGTACG	ACTTCCCGGG	TGATGACCTG	200
CCGGTAGTCC	GTGGTTCYGC	ACTGAAAGCG	CTGGAAGGCG	AAGCTCAGTG	250
GGAAGAGAAG	ATCCTGGAAC	TGGCTGGCCA	CCTGGACACC	TACATTCCGG	300
AGCCGGAGCG	TGCCATCGAC	CTGCCGTTCC	TGATGCCTAT	CGAAGACGTA	350
TTCTCCATCG	CTGGCCGYGG	TACCGTAGTG	ACCGGTCGTG	TAGAGCGCGG	400
TATCGTCAAA	GTTGGTGAAG	AAGTGGAAT	CGTKGGTATC	AAAGATACCA	450
CCAAGACCAC	CTGTACCGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
GGTCGTGCAG	GCGAGAACAT	CGGTGCACTG	CTGCGTGGCG	TGAAGCGTGA	550
AGACGTAGAG	CGTGGTCAGG	TACTGGCCAA	GCCGGGCACC	ATCAAGCCGC	600
ACACCAAGTT	YGAATCTGAA	GTGTACGTGC	TGTCCAAAGA	AGAAGGTGGT	650
CGTCATACCC	CGTTCTTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
TACCGACGTG	ACCGGTACCA	TCGAACTGCC	GGAAGGCGTA	GAGATGGTAA	750
TGCCGGGCGA	CAACATCAAG	ATGGTTGTTA	CCCTGATTGC	GCCGATCGCG	800
ATGGACGACG	GC				812

2) INFORMATION FOR SEQ ID NO: 2271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bilophila wadsworthia*

(B) STRAIN: ATCC 49260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271

CGACGGTCCC	ATGCCCCAGA	CCCGTGAGCA	CATCCTGCTC	GCCCGTCAGG	50
TCGGCGTGCC	TCACCTCGTC	GTGTTTCATGA	ACAAGTGTGA	CCTCGTCGAC	100
GACCCCGAAC	TGCTCGAACT	CGTCGAAATG	GAAGTCCGCG	AACTGCTGAG	150
CTCCTACGGC	TACCCCGGCG	ATGAAATCCC	GGTTGTCCGC	GGTTCCGCTC	200
TGAAGGCTCT	GGAATCCGAT	AGCGCTGATT	CCCCTGACGC	CCAGTGCGTG	250
CTCGAACTGC	TCGCCGCTTG	CGACAGCTAC	TCCCCGGATC	CGGTCCGCGA	300
AACCGACAAG	CCCTTCCTGA	TGCCCATCGA	AGACGTGTTC	TCCATCTCCG	350
GCCGCGGTAC	CGTGGTCACC	GGTCGTGTGG	AACGTGGCAT	CATCAAGGTC	400
GGCGAAGAAG	TCGAAATCGT	GGGTATCCGT	CCCACCGTGA	AGACGACCTG	450
CACCGGCGTC	GAAATGTTCC	GCAAGCTGCT	CGATCAGGGC	CAGGCCGGCG	500
ACAACATCGG	CGCTCTGCTC	CGCGGCACGA	AGCGTGACGA	AGTGGAACGC	550
GGCCAGGTTC	TCGCCGCTCC	CAAGAGCATC	ACGCCCCACA	AGAAGTTCAA	600
GGCTGAAGTG	TACGTTCTGT	CCAAGGAAGA	AGGCGGCCGC	CATACCCCGT	650
TCTTCACCGG	CTATCGTCCT	CAGTTCTACT	TCCGTACCAC	CGACATCACC	700
GGTATCATCG	CTCTTGAAGA	AGGCGTTGAA	ATGGTTATGC	CCGGCGATAA	750
CGCTACCTTT	AATGTCGAGC	TCATTACCCC	CATCGCCATG	GAAAAGGGC	799

2) INFORMATION FOR SEQ ID NO: 2272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevundimonas diminuta*
- (B) STRAIN: ATCC 11568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272

GATCCTGGTG	TGCTCGGCCG	CTGACGGCCC	GATGCCGCAG	ACCCGCGAGC	50
ACATCCTGCT	GTCGCGTCAG	GTCGGCGTTC	CGGCGCTGGT	GGTGTTCCTG	100
AACAAGGTCG	ACATGGTCGA	CGACGAGGAR	CTGCTGGAGC	TGGTCGAGAT	150
GGAAGTGCGC	GAGCTGCTGA	GCTCGTACCA	GTTCCCGGGC	GACGACATCC	200
CGGTGGTCAA	GGGCTCGGCC	CTGGCCGCGG	TGGAGGATCG	CGACCCGCAC	250
ATCGGCGCCG	AGCGCGTTCT	GGAGCTGATG	GCGGCGGTCG	ACAGCTACAT	300
CCCGCAGCCG	GAACGTCCGA	TCGACATGCC	GTTCTTGATG	CCGGTGGAAG	350
ACGTGTTCTC	GATCTCGGGC	CGCGGCACCG	TGGTGACGGG	TCGCGTCGAG	400
CGCGGCGTCG	TCAAGGTCGG	TGAAGAAGTC	GAAATCGTCG	GCATCCGTCC	450
GGTTCAGAAG	ACGACCTGCA	CGGGCGTCGA	AATGTTCCGC	AAGCTGCTGG	500
AYCAGGGTCA	RGCCGGCGAC	AACGTGGGCG	TGCTGCTGCG	CGGCACCAAG	550
CGTGAAGACG	TCGAGCGCGG	CCAGGTGCTG	TGCAAGCCGG	GTTGATCAC	600
CCCGCACACC	AAGTTCGTGG	CTGAAGCCTA	CATCCTGAAC	AAGGAAGAAG	650
GCGGCCGTCA	CACGCCGTTC	TTCACGAACT	ACCGTCCGCA	GTTCTACTTC	700
CGCACGACGG	ACGTGACCGG	CATCGTGCGC	CTGAAGGAAG	GCGTCGAGAT	750
GATCATGCCG	GGCGACAACG	CCGAGCTGGA	CGTCA		786

2) INFORMATION FOR SEQ ID NO: 2273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCTGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
ATTCCTCAAT	GGCCTTGGTA	TCAATTATCC	TGAGATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAGACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAG	TCTGGAAGT	GTACCAATGC	400
TGCAATCCCA	GGAGTTTATC	AAGCAGGTAA	AACTGGTACT	TCCAACATG	450
CAGATGATGA	GCTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAACATTT	TGTTGGCTAT	ACTCCACAAT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274

GCTACTTTGG	AAACATTACT	GTCCAATATG	CTCTTCAACA	ATCACGTAAT	50
GTCACAGCCG	TTGAAACTTT	GAATAAGGTC	GGTCTAGATA	AGGCTAAAGC	100
CTTCCTTAAT	GGGCTTGGTA	TTGATTATCC	AAGCATGCAT	TATGCAAACG	150
CCATTTCAAG	TAATACAAC	GAATCCAACA	AAAAATACGG	TGCAAGTAGT	200
GAAAAAATGG	CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTACCA	250
CAAGCCAATG	TACATCAATA	AAATCGTCTT	TAGCGACGGT	AGTGAGAAAG	300
AATTTTCTGA	TGCCGGCACA	CGAGCTATGA	AAGAACTAC	TGCCTATATG	350
ATGACTGAAA	TGATGAAAAC	AGTCCTAGTA	TACGGTACCG	GACGTGGAGC	400
CTACCTACCA	TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	450

CTGACGACGA	AATTGAAAAG	TATATCAAGA	ACACTGGCTA	CGTAGCCCCA	500
GATGAAATGT	TTGTAGGGTA	TACTCGTAAA	TATGCAATGG	CTGTTTGGAC	550
A					551

2) INFORMATION FOR SEQ ID NO: 2275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCAGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
G TTCCTCAAT	GGCCTTGGTA	TTAATTACCC	TGAAATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAAACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAA	TCTGGAAGTG	GTACCAATGC	400
TGCAATTCCA	GGAGTCTATC	AAGCAGGTAA	AACCGGCACT	TCCAAGTATG	450
CAGATGATGA	ACTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAGCTGTT	TGTTGGCTAC	ACTCCACAGT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276

TTATTTTGGG	AATATCACCA	TCCAATATGC	GCTCCAACAA	TCACGGAACG	50
TTACAGCCGT	AGAAACCTTG	AACAAAGTCG	GTTTGGATAG	AGCCAAGACC	100
TTCCTGAATG	GAATCGGTAT	TGACTATCCA	GATATGCACT	ATGCCAACGC	150
GATTTCAAGT	AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	200

AGAAAATGGC	TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	250
AAACCAATGT	ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	300
ATACGCTGAT	CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	350
TGACAGAAAT	GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	400
TATCTCCCTT	GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACCTATAC	450
AGATGATGAA	ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCCCCAG	500
ACGAAATGTT	TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	TGTWTGGACA	550

2) INFORMATION FOR SEQ ID NO: 2277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277

GCTCCTATCT	GGATTATGCG	ATGTCGGTCA	TTGTTGGCCG	TGCGCTGCCA	50
GATGTCCGAG	ATGGCCTGAA	GCCGGTACAC	CGTCGCGTAC	TTTACGCCAT	100
GAACGTACTA	GGCAATGACT	GGAACAAAGC	CTATAAAAAA	TCTGCCCCGTG	150
TCGTTGGTGA	CGTAATCGGT	AAATACCATC	CCCATGGTGA	CTCGGCGGTC	200
TATGACACGA	TCGTCCGCAT	GGCGCAGCCA	TTCTCGCTGC	GTTATATGCT	250
GGTAGACGGT	CAGGGTAACT	TCGGTTCTAT	CGACGGCGAC	TCTGCGGCGG	300
CAATGCGTTA	TACGGAAATC	CGTCTGGCGA	AAATTGCCCA	TGAACTGATG	350
GCCGAT					356

2) INFORMATION FOR SEQ ID NO: 2278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278

CTCTTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGC	GCGCTGCCGG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	CAGCCCCGTGT	150
CGTTGGTGAC	GTGATCGGTA	AATACCACCC	GCACGGCGAC	TCCGCGGTAT	200

ATGACACCAT	CGTTCGTATG	GCCCAGCCGT	TCTCGCTGCG	CTACATGCTG	250
GTGGATGGCC	AGGGGAACTT	CGGTTCAATC	GACGGCGACT	CCGCCGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCTCAC	GAAGTGA	347

2) INFORMATION FOR SEQ ID NO: 2279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 43886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279

AGAGCTCCTA	TCTGGATTAT	GCGATGTCGG	TCATTGTTGG	CCGTGCGCTG	50
CCAGATGTCC	GAGATGGCCT	GAAGCCGGTA	CACCGTCGCG	TACTTTACGC	100
CATGAACGTA	CTAGGCAATG	ACTGGAACAA	AGCCTATAAA	AAATCTGCCC	150
GTGTCGTTGG	TGACGTAATC	GGTAAATACC	ATCCCCATGG	TGACTCGGCG	200
GTCTATGACA	CGATCGTCCG	CATGGCGCAG	CCATTCTCGC	TGCGTTATAT	250
GCTGGTAGAC	GGTCAGGGTA	ACTTCGGTTC	TATCGACGGC	GACTCTGCGG	300
CGGCAATGCG	TTATACGGAA	ATCCGTCTGG	CGAAAATTGC	CCATGAACTG	350
ATGGCCGATC	TC				362

2) INFORMATION FOR SEQ ID NO: 2280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280

CTCCTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGT	GCGCTGCCAG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTACTAG	GCAATGACTG	GAACAAAGCC	TATAAAAAAT	CTGCCCCGTGT	150
CGTTGGTGAC	GTAATCGGTA	AATACCATCC	CCATGGTGAC	TCGGCGGTTT	200
ATGACACGAT	CGTCCGTATG	GCGCAGCCAT	TCTCGCTGCG	TTACATGCTG	250
GTAGACGGTC	AGGGTAACTT	CGGTTCCATC	GACGGCGACT	CTGCGGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCCCAT	GAAGTGATGG	350
CCGATCTC					358

2) INFORMATION FOR SEQ ID NO: 2281

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281

CCCCCAGCTG GGCGGCGGTA TCGATGGGGG

30

2) INFORMATION FOR SEQ ID NO: 2282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2282

AGRRGCIMAR ATGTATGA

18

2) INFORMATION FOR SEQ ID NO: 2283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283

ATITATGAYG GKITTCAGAG GC

22

2) INFORMATION FOR SEQ ID NO: 2284

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284

TCTGWGTRAC IGGYTCKGAG A

21

2) INFORMATION FOR SEQ ID NO: 2285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285

CMCCICCWGG TGGWGAWAC

19

2) INFORMATION FOR SEQ ID NO: 2286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286

AGTTGCTGTA TTAGGAAATG

20

2) INFORMATION FOR SEQ ID NO: 2287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287

TCGAAGTTGC TGTATTAGGA

20

2) INFORMATION FOR SEQ ID NO: 2288

1171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288

TAGAAGCTGG	CTCGTTTTTT	TATAAATAAG	TTATTCGTTT	ATTTTTGTTT	50
TGTGCTAAAA	TATGAGAGTA	AATCACTGAA	CGATTTAGAA	TACAGGAGGA	100
CAATCTTTTG	AAGATTACTT	TACTATATGG	CGGACGCAGC	GCAGAGCAGA	150
GCATGAAGTG	TCCATTCTTT	CCGCATTTTC	AGTTTTTAAAT	GCCATTTATT	200
ATAATTATTA	CCAAGTTCAA	CTCGTATTTA	TTACAAAAGA	AGGACAATGG	250
GTCAAAGGTC	CATTACTAAC	AGAAAAACCT	GCCAGCAAAG	ATGTCTTGCA	300
TCTTTCATGG	GACCCAAGTG	GACAGACAGA	GGAAGGCTTT	ACAGGAAAAG	350
TGATCAATCC	GGGCGAAATC	AAAGAAGAAG	GAGCCATCGT	TTTTCCAGTT	400
TTACATGGGC	CAAACGGGGA	AGATGGAACG	ATCCAAGGCT	TCTTAGAGAC	450
ATTGAATATG	CCTTATGTCG	GCGCAGGCGT	ATTGACCAGT	GCATGTGCCA	500
TGGATAAAAT	CATGACCAAG	TATATTTTAC	AAGCTGCTGG	TGTGCCGCAA	550
GTTCTTTATG	TACCAGTACT	TAAGAATCAA	TGGAAAGAAA	ATCCTAAAAA	600
AGTATTTGAT	CAATGTGAAG	GTTCTTTGCT	TTATCCGATG	TTTGTCAAAC	650
CGGCGAATAT	GGGTTCTAGT	GTCGGCATT	CAAAAGCAGA	AAACCGAGAA	700
GAGCTGCAAA	ATGCTTTAGC	AACAGCCTAT	CAGTATGATT	CTCGAGCAAT	750
CGTTGAACAA	GGAATTGAAG	CGCGCGAAAT	CGAAGTTGCT	GTATTAGGAA	800
ATGAAGACGT	TCGGACGACT	TTGCCTGGTG	AAGTCGTAAA	AGACGTAGCA	850
TTCTATGATT	ATGAAGCAAA	ATATATCAAT	AATAAAATCG	AAATGCAGAT	900
TCCAGCCGAA	GTGCCAGAAG	AAGTTTATCA	AAAAGCGCAA	GAGTACGCGA	950
AGTTAGCTTA	CACGATGTTA	GGTGAAGCG	GATTGAGCCG	GTGCGATTTT	1000
TTTTTTGACAA	ATAAAAATGA	ATTATTCCTG	AATGAATTAA	ACTCTATGCC	1050
AGGATTTACG	GAGTTCAGTA	TGTACCCACT	CTTATGGGAA	AATATGGGCT	1100
TGAAATACGG	TGATTTGATT	GAAGAACTGA	TCCAGTTAGG	AATGAATCGA	1150
TACCATCAGC	GTCAATCTTT	TTTTGAAAAA	AATGAATAAA	GAGAAATAAA	1200
GAAGAGGCTG	GAGTGATTGC	GTAACCGCGT	TCATTCTAGC		1240

2) INFORMATION FOR SEQ ID NO: 2289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289

CACCGAAGAA GATGAAAAAA

20

2) INFORMATION FOR SEQ ID NO: 2290

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290

TGGCACCGAA GAAGATGA

18

2) INFORMATION FOR SEQ ID NO: 2291

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291

ATTTTGGCAC CGAAGAAGA

19

2) INFORMATION FOR SEQ ID NO: 2292

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292

GAATCGGCAA GACAATATG

19

2) INFORMATION FOR SEQ ID NO: 2293

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1032 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: BM4147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293

ATGAATAGAA	TAAAAGTTGC	AATACTGTTT	GGGGGTTGCT	CAGAGGAGCA	50
TGACGTATCG	GTAAAATCTG	CAATAGAGAT	AGCCGCTAAC	ATTAATAAAG	100
AAAAATACGA	GCCGTTATAC	ATTGGAATTA	CGAAATCTGG	TGTATGGAAA	150
ATGTGCGAAA	AACCTTGCGC	GGAATGGGAA	AACGACAATT	GCTATTCAGC	200
TGTACTCTCG	CCGGATAAAA	AAATGCACGG	ATTACTTGTT	AAAAAGAACC	250
ATGAATATGA	AATCAACCAT	GTTGATGTAG	CATTTTCAGC	TTTGCATGGC	300
AAGTCAGGTG	AAGATGGATC	CATACAAGGT	CTGTTTGAAT	TGTCCGGTAT	350
CCCTTTTGTG	GGCTGCGATA	TTCAAAGCTC	AGCAATTTGT	ATGGACAAAT	400
CGTTGACATA	CATCGTTGCG	AAAAATGCTG	GGATAGCTAC	TCCCGCCTTT	450
TGGGTTATTA	ATAAAGATGA	TAGGCCGGTG	GCAGCTACGT	TTACCTATCC	500
TGTTTTTTGTT	AAGCCGGCGC	GTTCAGGCTC	ATCCTTCGGT	GTGAAAAAAG	550
TCAATAGCGC	GGACGAATTG	GACTACGCAA	TTGAATCGGC	AAGACAATAT	600
GACAGCAAAA	TCTTAATTGA	GCAGGCTGTT	TCGGGCTGTG	AGGTCGGTTG	650
TGCGGTATTG	GGAAACAGTG	CCGCGTTAGT	TGTTGGCGAG	GTGGACCAAA	700
TCAGGCTGCA	GTACGGAATC	TTTCGTATTC	ATCAGGAAGT	CGAGCCGGAA	750
AAAGGCTCTG	AAAACGCAGT	TATAACCGTT	CCC GCAGACC	TTTCAGCAGA	800
GGAGCGAGGA	CGGATACAGG	AAACGGCAAA	AAAAATATAT	AAAGCGCTCG	850
GCTGTAGAGG	TCTAGCCCGT	GTGGATATGT	TTTTACAAGA	TAACGGCCGC	900
ATTGTACTGA	ACGAAGTCAA	TACTCTGCCC	GGTTTCACGT	CATACAGTCG	950
TTATCCCCGT	ATGATGGCCG	CTGCAGGTAT	TGCACTTCCC	GAAGTGATTG	1000
ACCGCTTGAT	CGTATTAGCG	TTAAAGGGGT	GA		1032

2) INFORMATION FOR SEQ ID NO: 2294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294

AAACGAGGAT GATTGATTG

20

2) INFORMATION FOR SEQ ID NO: 2295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295

TTGAGCAAGC GATTTCGG

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2) INFORMATION FOR SEQ ID NO: 2296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
AAAAATTCGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTTCATG	AAAGAAAGAG	250
AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGCATG	GACAAATCAC	400
TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
CTTTGTGAAG	CCGGCACGGT	CAGGTTTCGTC	CTTTGGCGTA	ACCAAAGTAA	550
ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTTCG	GGCTGTGAGG	TCGGCTGCGC	650
GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAAACG	AGGTCAATAC	CCTGCCCGGT	TTTACATCGT	ACAGCCGCTA	950
TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 2297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297

TTCAGGAGGG GGATCGC

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 00/01150

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68 C07K14/00 C12N15/63 C12N05/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, SEQUENCE SEARCH, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 24059 A (MASSACHUSETTS INST TECHNOLOGY ;AIRD WILLIAM C (US); EDELBERG JAY M) 20 May 1999 (1999-05-20) page 26, line 12	24
X	WO 98 20157 A (BERGERON MICHEL G ;INFECTIO DIAGNOSTIC INC (CA); PICARD FRANCOIS J) 14 May 1998 (1998-05-14) the whole document	24

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

17 January 2002

Date of mailing of the international search report

12 04 2002

Name and mailing address of the ISA

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Authorized officer

REUTER, U

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CA 00/01150

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-44 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

The present application relates to nucleic acids that can be used in the detection of microorganisms, the provision and use of said nucleic acids and products that are derived from the nucleic acids.

In view of the extraordinary amount of combinations of sequences in the claims, which render the regrouping of sequences almost impossible, in view of the large number of sequences claimed, and in view of the wording of the claims presently on file, which render it difficult, if not impossible, to determine the matter for which protection is sought, the present application fails to comply with the clarity and conciseness requirements of Article 6 PCT (see also Rule 6.1(a) PCT) to such an extent that a meaningful search for the claims as they stand is impossible.

Additionally, present claims 1-44 relate to an extremely large number of possible compositions, nucleic acids, and combinations of nucleic acids. Present claims 4, 5, 8-10, 22-31, 33-43 relate to products defined by reference to a desirable characteristic or property, namely being obtainable by a method or being capable of hybridizing to a certain nucleic acid.

The claims cover all products having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such products. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT): An attempt is made to define the products by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible.

Notwithstanding the aforementioned, a search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely nucleic acid sequence Seq. ID. No. 543 (see non-unity ISA form 206), methods relating to said sequence, the use of the sequence and the products derived from or defined by the sequence.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-44 (all partially)

Invention 1:

Nucleic acid molecule with Sequence ID No 543, methods for the provision of the nucleic acid, methods using the nucleic acid, use of the nucleic acid, compositions and sets containing the nucleic acid, and products derived from or defined by the nucleic acid.

2. Claims: 1-44 (all partially)

Invention 2-2297:

Nucleic acid molecule with Sequence ID No n, wherein n is chosen among 1-543 and 545-2297, methods for the provision of the nucleic acid, methods using the nucleic acid, use of the nucleic acid, compositions and sets containing the nucleic acid, and products derived from or defined by the nucleic acid.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/CA 00/01150

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9924059	A	20-05-1999	AU 1454199 A	31-05-1999
			WO 9924059 A1	20-05-1999

WO 9820157	A	14-05-1998	US 5994066 A	30-11-1999
			AU 731850 B2	05-04-2001
			AU 4859897 A	29-05-1998
			BR 9713494 A	29-02-2000
			WO 9820157 A2	14-05-1998
			CN 1248295 A	22-03-2000
			EP 0943009 A2	22-09-1999
			JP 2001504330 T	03-04-2001
			NO 991976 A	02-07-1999
